GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: June 21, 2002, 12:02:57 ; Search time 338.08 Seconds
(without alignments)
2422.409 Million cell updates/sec

Title: US-09-763-498-7
Perfect score: 477
Sequence: 1 atggaaaaagcattgaaaat.....ggttaactatgctgttttaa 477

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802:*
1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
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23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	477	100.0	477	21	AAZ51247	Human Interleukin-
2	475.4	99.7	477	21	AAZ51248	Polymorphic human
3	461.2	96.7	819	22	AAD06911	Human interleukin-
4	349.8	73.3	391	22	AAF83870	Human interleukin-
5	238.6	50.0	809	19	AAV71960	Rodent interleukin
6	238.6	50.0	838	20	AAX86460	cDNA encoding a mu
7	213	44.7	213	21	AAZ51246	3' exon of human I
8	202	42.3	1073	22	AAD12296	Human interleukin-
9	202	42.3	1183	19	AAV42659	cDNA encoding Inte
10	202	42.3	1183	20	AAX90135	Human interleukin-
11	202	42.3	1183	22	AAS26842	Human cDNA encodin
12	202	42.3	1291	20	AAX86458	cDNA encoding a hu
13	201.6	42.3	673	22	AAS26915	Human cDNA encodin
14	201.6	42.3	673	22	AAD16762	Human novel protei
15	201.4	42.2	1377	20	AAX86459	cDNA encoding a hu
16	161.4	33.8	1321	21	AAA96351	cDNA encoding a no
17	161.4	33.8	1321	21	AAA51595	Human IL-1 recepto
18	134.2	28.1	520	22	AAF83869	Human interleukin-
19	134.2	28.1	585	22	AAC90487	Human IL-1 eta cDN
20	134.2	28.1	1244	22	AAD08531	Human Interleukin-
21	129.2	27.1	746	20	AAX86455	cDNA encoding a mu
22	127	26.6	219	19	AAV71959	Rodent interleukin
23	86.6	18.2	174	21	AAZ51249	Mouse Interleukin-
24	78.8	16.5	1710	20	AAV99953	Nucleotide sequenc
25	74.8	15.7	1877	21	AAA99192	Mouse interleukin-
26	74.2	15.6	654	21	AAD00213	Human zil1a4 degen
27	72.6	15.2	654	21	AAD00214	Human zil1a4-E200K
28	71.8	15.1	531	22	AAF85156	Nucleotide sequenc
29	71.8	15.1	603	22	AAF85157	Nucleotide sequenc
30	71.8	15.1	1577	19	AAV21578	Equine interleukin
31	71.8	15.1	1614	22	AAF85155	Nucleotide sequenc
32	70.8	14.8	456	14	AAQ40754	IL-1 inhibitor (IL
33	70.8	14.8	462	18	AAT38808	Recombinant human
34	70.8	14.8	462	19	AAV36455	Recombinant human
35	70.8	14.8	462	22	AAI70513	Human interleukin-
36	70.8	14.8	514	16	AAQ83763	Plasmid 15424. Sy
37	70.8	14.8	514	18	AAT72210	DNA encoding leade
38	70.8	14.8	514	20	AAX82158	Leaderless IL-1 re
39	70.8	14.8	531	17	AAT35255	Human interleukin-
40	70.8	14.8	531	17	AAT35256	Human interleukin-
41	70.8	14.8	531	17	AAT30157	Interleukin-1 rece
42	70.8	14.8	531	17	AAT30158	Interleukin-1 rece
43	70.8	14.8	531	17	AAT30159	Interleukin-1 rece
44	70.8	14.8	532	12	AAQ14693	IRAP gene. Homo s
45	70.8	14.8	540	10	AAN92441	Sequence of bps 61

ALIGNMENTS

RESULT 1
AAZ51247
ID AAZ51247 standard; DNA; 477 BP.
XX
AC AAZ51247;
XX
DT 06-JUN-2000 (first entry)
XX
DE Human Interleukin-1 epsilon DNA.
XX
KW Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;
KW gene mapping; immune system; treatment; inflammatory disease;
KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
KW psoriasis; human; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..477
FT /*tag= a
FT /product= "Interleukin-1 epsilon protein"
FT /note= "Homologous to mouse IL-1 epsilon protein"
XX
PN WO200011174-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US18771.
XX
PR 21-AUG-1998; 98US-0097413.
PR 31-AUG-1998; 98US-0098595.

PR 11-SEP-1998; 98US-0099974.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Sims JE, Smith DE;
XX
DR WPI; 2000-237653/20.
DR P-PSDB; AAY70217.
XX
PT Nucleotide sequences encoding human interleukin -1 epsilon, useful to
PT treat inflammatory and immune system-related diseases such as
PT rheumatoid arthritis and inflammatory bowel disease -
XX
PS Claim 1a; Fig 1; 76pp; English.
XX
CC The present sequence is the human Interleukin-1 (IL-1) epsilon DNA
CC encoding IL-1 epsilon protein. This gene is mapped to chromosome 2q and
CC is mainly expressed in spleen, lymph node, thymus, tonsil and leucocyte
CC tissues. IL-1 epsilon is a cytokine, with antiinflammatory,
CC immunosuppressant, antirheumatic, antiarthritic and antipsoriatic
CC activity. The DNA sequence can be used in chromosome identification,
CC gene mapping and study of immune system. IL-1 epsilon can be used in the
CC treatment of inflammatory or autoimmune diseases such as rheumatoid
CC arthritis, inflammatory bowel disease and psoriasis.
XX
SQ Sequence 477 BP; 124 A; 123 C; 117 G; 113 T; 0 other;

Query Match 100.0%; Score 477; DB 21; Length 477;
Best Local Similarity 100.0%; Pred. No. 5.5e-137;
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 cgggtgtgggttcttcaggaccagacgctcatagcagtcccgaggaaggaccgtatgtct 120
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Db      61 cgggtgtgggttcttcaggaccagacgctcatagcagtcccgaggaaggaccgtatgtct 120

Qy     121 ccagtcactattgccttaatctcatgccgacatgtggagaccttgagaaagacagaggg 180
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Db     121 ccagtcactattgccttaatctcatgccgacatgtggagaccttgagaaagacagaggg 180

Qy     181 aaccccatctacctgggcctgaatggactcaatctctgcctgatgtgtgctaaagtcggg 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 aaccccatctacctgggcctgaatggactcaatctctgcctgatgtgtgctaaagtcggg 240

Qy     241 gaccagcccacactgcagctgaaggaaaaggatataatggatttgtacaaccaacccgag 300
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Db     241 gaccagcccacactgcagctgaaggaaaaggatataatggatttgtacaaccaacccgag 300

Qy     301 cctgtgaagtcctttctcttctaccacagccagagtggcaggaactccaccttcgagtct 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 cctgtgaagtcctttctcttctaccacagccagagtggcaggaactccaccttcgagtct 360

Qy     361 gtggctttccctggctggttcatcgctgtcagctctgaaggaggctgtcctctcatcctt 420
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Db     361 gtggctttccctggctggttcatcgctgtcagctctgaaggaggctgtcctctcatcctt 420

Qy     421 acccaagaactggggaaagccaacactactgactttgggttaactatgctgttttaa 477
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 2
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ID AAZ51248 standard; DNA; 477 BP.
XX
AC AAZ51248;
XX
DT 06-JUN-2000 (first entry)
XX
DE Polymorphic human Interleukin-1 epsilon DNA.
XX
KW Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;
KW gene mapping; immune system; treatment; inflammatory disease;
KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
KW psoriasis; human; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..477
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FT /note= "Homologous to mouse IL-1 epsilon protein"
FT variation replace (35, A)
FT /*tag= b
XX
PN WO200011174-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US18771.
XX
PR 21-AUG-1998; 98US-0097413.
PR 31-AUG-1998; 98US-0098595.
PR 11-SEP-1998; 98US-0099974.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Sims JE, Smith DE;
XX
DR WPI; 2000-237653/20.
DR P-PSDB; AAY70218.
XX
PT Nucleotide sequences encoding human interleukin -1 epsilon, useful to
PT treat inflammatory and immune system-related diseases such as
PT rheumatoid arthritis and inflammatory bowel disease -
XX
PS Claim 1a; Fig 1; 76pp; English.
XX
CC The present sequence is the polymorphic human Interleukin-1 (IL-1)
CC epsilon DNA. This gene is mapped to chromosome 2q and is mainly
CC expressed in spleen, lymph node, thymus, tonsil and leucocyte
CC tissues. IL-1 epsilon is a cytokine, with antiinflammatory,
CC immunosuppressant, antirheumatic, antiarthritic and antipsoriatic
CC activity. The DNA sequence can be used in chromosome identification,
CC gene mapping and study of immune system. IL-1 epsilon can be used in the
CC treatment of inflammatory or autoimmune diseases such as rheumatoid
CC arthritis, inflammatory bowel disease and psoriasis.
XX
SQ Sequence 477 BP; 123 A; 123 C; 118 G; 113 T; 0 other;

Query Match 99.7%; Score 475.4; DB 21; Length 477;
Best Local Similarity 99.8%; Pred. No. 1.7e-136;
Matches 476; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy     121 ccagtcactattgccttaatctcatgccgacatgtggagaccttgagaaagacagaggg 180
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Qy     181 aaccccatctacctgggcctgaatggactcaatctctgcctgatgtgtgctaaagtcggg 240
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Db    241 gaccagcccacactgcagctgaaggaaaaggatataatggatttgtacaaccaacccgag 300

Qy    301 cctgtgaagtcctttctcttctaccacagccagagtggcaggaactccaccttcgagtct 360
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Qy    361 gtggctttccctggctggttcatcgctgtcagctctgaaggaggctgtcctctcatcctt 420
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Db    361 gtggctttccctggctggttcatcgctgtcagctctgaaggaggctgtcctctcatcctt 420

Qy    421 acccaagaactggggaaagccaacactactgactttgggttaactatgctgttttaa 477
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 acccaagaactggggaaagccaacactactgactttgggttaactatgctgttttaa 477
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RESULT 3
AAD06911
ID AAD06911 standard; cDNA; 819 BP.
XX
AC AAD06911;
XX
DT 03-AUG-2001 (first entry)
XX
DE Human interleukin-1 receptor antagonist-like (IL-1ra-L) cDNA.
XX
KW Human; interleukin-1 receptor antagonist-like protein; IL-1ra-L; therapy;
KW rheumatoid arthritis; psoriatic arthritis; inflammatory arthritis; lupus;
KW joint disease; autoimmune disease; multiple sclerosis; diabetes; obesity;
KW transplant rejection; graft versus host disease; strain; sprain; leprosy;
KW cartilage damage; hepatitis; human immunodeficiency virus; HIV; anorexia;
KW clostridium-associated diarrhoea; pulmonary tuberculosis; septic shock;
KW myopathy; Alzheimer's disease; Parkinson's disease; memory disorder;
KW acute respiratory disease syndrome; cystic fibrosis; asthma; psoriasis;
KW eczema; glomerulonephritis; osteoporosis; Paget's disease; lymphoma;
KW hypercalcaemia; haemorrhage; ischaemia; atherosclerosis; leukaemia;
KW infertility; endometriosis; retinal neuropathy; acute pancreatitis;
KW Kawasaki's disease; cancer; ss.
XX
OS Homo sapiens.
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FT /product= "Human interleukin-1 receptor antagonist-like
FT (IL-1ra-L) protein"
FT /note= "CDS does not include stop codon"
FT /partial
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PN WO200141792-A1.
XX
PD 14-JUN-2001.
XX
PF 04-DEC-2000; 2000WO-US32891.
XX
PR 10-DEC-1999; 99US-0170105.
PR 28-NOV-2000; 2000US-0724859.
XX
PA (AMGE-) AMGEN INC.
XX
PI Calzone FJ, Luethy R, Boedigheimer MJ, Zhu J, Chung Y, Jing S;
XX
DR WPI; 2001-381495/40.
DR P-PSDB; AAE03417.
XX
PT Novel Interleukin-1 Receptor Antagonist-Like nucleic acid molecule, the
PT polypeptide encoded by the nucleic acid is useful diagnosis, treatment,
PT and prevention of diseases such as arthritis, diabetes, transplant
PT rejection -
XX
PS Claim 1; Fig 1A; 127pp; English.
XX
CC The present sequence is human interleukin-1 receptor antagonist-like
CC (IL-1ra-L) cDNA. IL-1ra-L is useful for treating, preventing or
CC ameliorating IL-1ra-L polypeptide-related disease, condition or disorder
CC which include rheumatoid arthritis, psoriatic arthritis, inflammatory
CC arthritis, osteoarthritis, autoimmune disease, multiple sclerosis,
CC lupus, diabetes, transplant rejection, inflammatory joint disease, graft
CC versus host disease and inflammatory conditions resulting from strain,
CC sprain, cartilage damage, trauma, orthopaedic surgery, hepatitis, human
CC immunodeficiency virus (HIV) infection, clostridium-associated
CC diarrhoea, leprosy, pulmonary tuberculosis, septic shock, obesity,
CC anorexia, myopathies, Alzheimer's disease, Parkinson's disease, memory
CC disorders, acute respiratory disease syndrome, cystic fibrosis, asthma,
CC psoriasis, eczema, acute and chronic glomerulonephritis, osteoporosis,
CC Paget's disease, hypercalcaemia, haemorrhage, ischaemia, atherosclerosis,
CC lymphomas, lung and breast cancer, leukaemias, infertility,
CC endometriosis, retinal degeneration, retinal neuropathy, acute
CC pancreatitis and Kawasaki's disease.
XX
SQ Sequence 819 BP; 202 A; 196 C; 204 G; 217 T; 0 other;

Query Match 96.7%; Score 461.2; DB 22; Length 819;
Best Local Similarity 99.4%; Pred. No. 5.2e-132;
Matches 463; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy     69 ggttcttcaggaccagacgctcatagcagtcccgaggaaggaccgtatgtctccagtcac 128
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Qy    129 tattgccttaatctcatgccgacatgtggagacccttgagaaagacagagggaacccccat 188
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Qy    249 cacactgcagctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaa 308
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Qy    309 gtcctttctcttctaccacagccagagtggcaggaactccaccttcgagtctgtggcttt 368
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Qy    429 actggggaaagccaacactactgactttgggttaactatgctgttt 474
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RESULT 4
AAF83870
ID AAF83870 standard; cDNA; 391 BP.
XX
AC AAF83870;
XX
DT 06-AUG-2001 (first entry)
XX
DE Human interleukin-1 receptor antagonist (NOVINTRA C) encoding cDNA.
XX
KW NOVX; transmembrane protein; NOVTRAN; neuromedin peptide; NOVNEUR;
KW gonadotropin-like protein; NOVGON; interleukin-1; NOVINTRA; human;
KW cytostatic; neuroprotective; reproductive; antiinflammatory; cancer;
KW antibacterial; cerebroprotective; antidiabetic; antiarthritic;

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KW   antiasthmatic; antiallergic; ss.
XX
OS   Homo sapiens.
XX
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PN   WO200140291-A2.
XX
PD   07-JUN-2001.
XX
PF   06-DEC-2000; 2000WO-US33029.
XX
PR   06-DEC-1999;   99US-0169056.
PR   09-DEC-1999;   99US-0169866.
PR   09-DEC-1999;   99US-0169886.
PR   10-DEC-1999;   99US-0170252.
PR   12-JAN-2000; 2000US-0175740.
PR   05-DEC-2000; 2000US-0170252.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Burgess CE,  Prayaga SK,  Shimkets RA,  Rastelli L,  Zerhusen BD;
PI   Mezes PS;
XX
DR   WPI; 2001-374790/39.
DR   P-PSDB; AAB85001.
XX
PT   Novel isolated human transmembrane, neuromedin peptide
PT   gonadotropin-like protein and interleukin-1 receptor antagonist
PT   proteins, useful for treating cancer, immune response disorder,
PT   metabolic function disorders  -
XX
PS   Claim 50; Fig 15A; 138pp; English.
XX
CC   The invention provides novel polypeptides (NOVX) selected from human
CC   transmembrane protein (NOVTRAN), neuromedin peptide (NOVNEUR),
CC   gonadotropin-like protein (NOVGON) and two interleukin-1 receptor
CC   antagonist proteins (NOVINTRA A and B). The invention also provides
CC   methods in which a NOVX polypeptide, polynucleotide  and antibody are
CC   used in the detection, prevention and treatment of a broad range of
CC   pathological states. NOVTRAN can be used to treat is a cell signaling
CC   disorder such as cancer, immune  response disorder, hematopoietic
CC   disorder, neurodegenerative disorder. NOVNEUR can be used to treat
CC   endocrine disorder, muscle disorder, neurologic disorder, cancers of
CC   central nervous system, breast, colon, ovary, kidney, prostate and
CC   thyroid. NOVGON can be used to treat reproductive development disorder,
CC   metabolic function disorder and melanoma. NOVINTRA A and B can be used
CC   to treat bone metabolism or structure disorder, inflammatory response
CC   disorder, immune regulation disorder, septic shock, stroke, diabetes,
CC   arthritis and cancer. The present sequence represents a cDNA encoding
CC   the NOVINTRA C polypeptide.
XX
SQ   Sequence 391 BP; 94 A; 106 C; 99 G; 92 T; 0 other;
```

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  Query Match           73.3%;  Score 349.8;  DB 22;  Length 391;
  Best Local Similarity 96.5%;  Pred. No. 8.2e-98;
  Matches  383;  Conservative    0;  Mismatches    2;  Indels   12;  Gaps    2;

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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 gatatcaatcatcgggtgtgggttcttcaggaccagacgctcatagcagtcccgaggaag 60

Qy     109 gaccgtatgtctccagtcactattgccttaatctcatgccgacatgtggagacccttgag 168
           |      |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 g------tgttcccagtcactattgccttaatctcatgccgacatgtggagacccttgag 114

Qy     169 aaagacagagggaaccccatctacctgggcctgaatggactcaatctctgcctgatgtgt 228
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     115 aaagacagagggaaccccatctacctgggcctgaatggactcaatctctgcctgatgtgt 174

Qy     229 gctaaagtcggggaccagcccacactgcagctga------aggaaaaggatataatggat 282
           ||||||||||||||||||||||||||||||||      ||||||||||||||||||||
Db     175 gctaaagtcggggaccagcccacactgcagctgaagcttcaggaaaaggatataatggat 234

Qy     283 ttgtacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcagg 342
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     235 ttgtacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcagg 294

Qy     343 aactccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaagga 402
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     295 aactccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaagga 354

Qy     403 ggctgtcctctcatccttacccaagaactggggaaag 439
           |||||||||||||||||||||||||||||||||||||
Db     355 ggctgtcctctcatccttacccaagaactggggaaag 391
```

```
RESULT   5
AAV71960
ID   AAV71960 standard; cDNA; 809 BP.
XX
AC   AAV71960;
XX
DT   19-FEB-1999  (first entry)
XX
DE   Rodent interleukin (IL)-1 epsilon polypeptide encoding cDNA.
XX
KW   Interleukin; IL-1 delta; polyclonal antibody; IL-1 epsilon; cytokine;
KW   inflammatory response; immune system; diagnosis; agonist; antagonist;
KW   chemokine; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             90..572
FT                   /*tag= a
FT                   /product= "IL-1 epsilon polypeptide"
XX
PN   WO9847921-A1.
XX
PD   29-OCT-1998.
XX
PF   17-APR-1998;   98WO-US06879.
XX
PR   06-AUG-1997;   97US-0055111.
PR   21-APR-1997;   97US-0837627.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Bazan JF,  Hedrick JA,  Kastelein RA,  Sana TR;
XX
DR   WPI; 1998-609976/51.
DR   P-PSDB; AAW86286.
XX
PT   Mammalian interleukin 1-delta and 1-epsilon - useful for, e.g.
PT   regulating the immune system and inflammatory responses
XX
PS   Claim 14; Pages 92-93; 113pp; English.
XX
CC   This cDNA encodes a rodent interleukin (IL)-1 epsilon polypeptide. The
CC   invention relates to a recombinant polypeptide that specifically binds
CC   polyclonal antibodies (Abs) generated against a 12 consecutive amino acid
CC   segment of IL-1 delta or IL-1 epsilon. Agonists or antagonists of these
CC   IL polypeptides are used to regulate a cell involved in an inflammatory
CC   response. The IL-1 delta or IL-1 epsilon polypeptides and peptides are
CC   used to produce Abs and antigen-Ab complexes. The polypeptides, Abs and
CC   the corresponding nucleic acids regulate development and/or the immune
CC   system, and can be used to diagnose and treat conditions associated with
CC   abnormal expression of IL. Agonists or antagonists of IL-1 delta or IL-1
CC   epsilon polypeptides are used with agonists or antagonists of IL-1 alpha,
CC   IL-1RA, IL-1 beta, IL-1 gamma, IL-2 and/or IL-12. The IL-1 delta or IL-1
CC   epsilon polypeptides may be used as a soluble polypeptide or as a fusion
```

```
CC   protein with another cytokine or chemokine.
XX
SQ   Sequence 809 BP; 241 A; 180 C; 179 G; 209 T; 0 other;

  Query Match           50.0%;  Score 238.6;  DB 19;  Length 809;
  Best Local Similarity 68.8%;  Pred. No. 2.2e-63;
  Matches  328;  Conservative    0;  Mismatches  149;  Indels    0;  Gaps    0;

Qy      1 atggaaaaagcattgaaaattgacacacctcagcaggggagcattcaggatatcaatcat 60
          | ||| |||| | | | |   |   |||||  ||   |     |||||||| | | |  |
Db     96 aaggagaaagaactaagagcagcatcaccttcgcttagacatgttcaggatcttagtagt 155

Qy     61 cgggtgtgggttcttcaggaccagacgctcatagcagtcccgaggaaggaccgtatgtct 120
          || |||||| | || ||| || | |  |||| ||||||||  ||||| || |   |    |
Db    156 cgtgtgtggatcctgcagaacaatatcctcactgcagtcccaaggaaagagcaaacagtt 215

Qy    121 ccagtcactattgccttaatctcatgccgacatgtggagacccttgagaaagacagaggg 180
          ||||||||||||| ||||  || |||||| | || |||| || |||||||   |||| |||
Db    216 ccagtcactattaccttgctcccatgccaatatctggacactcttgagacgaacaggggg 275

Qy    181 aaccccatctacctgggcctgaatggactcaatctctgcctgatgtgtgctaaagtcggg 240
           | ||||  ||| ||||  || |  | |  |    ||||||| | ||  | || |  |||
Db    276 gatcccacgtacatgggagtgcaaaggccgatgagctgcctgttctgcacaaaggatggg 335

Qy    241 gaccagcccacactgcagctgaaggaaaaggatataatggatttgtacaaccaacccgag 300
          || |||||    || |||||   ||||  | | ||||||||  ||||||||  ||   ||
Db    336 gagcagcctgtgctacagcttggggaagggaacataatggaaatgtacaacaaaaaggaa 395

Qy    301 cctgtgaagtcctttctcttctaccacagccagagtggcaggaactccaccttcgagtct 360
          |||||  ||  ||| |||||||||  ||||   |||||||  |  | ||| || || ||||||
Db    396 cctgtaaaagcctctctcttctatcacaagaagagtggtacaacctctacatttgagtct 455

Qy    361 gtggctttccctggctggttcatcgctgtcagctctgaaggaggctgtcctctcatcctt 420
          |  || |||||||| |||||||||||||||| ||||| ||||  |||| || |||||  ||
Db    456 gcagccttccctggttggttcatcgctgtctgctctaaagggagctgcccactcattctg 515

Qy    421 acccaagaactggggaaagccaacactactgactttgggttaactatgctgttttaa 477
          |||||||||||||| ||  |  ||  |||||||| | | | | | || |   ||||
Db    516 acccaagaactgggggaaatcttcatcactgacttcgagatgattgtggtacattaa 572


RESULT   6
AAX86460
ID   AAX86460 standard; cDNA; 838 BP.
XX
AC   AAX86460;
XX
DT   30-SEP-1999  (first entry)
XX
DE   cDNA encoding a murine SPOIL-II protein.
XX
KW   SPOIL-II; interleukin-1 receptor antagonist; IL-1ra; modulating agent;
KW   bone metabolism disorder; proinflammatory disorder; immune disorder;
KW   inflammatory disease; septic shock; stroke; diabetes; arthritis;
KW   intercolitis; pneumonitis; epithelial cell; skin disease;
KW   proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;
KW   epithelial cancer; squamous cell carcinoma; bone resorption disorder;
KW   osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;
KW   osteogenesis imperfecta; fibrous displasia; hypophosphatasia;
KW   bone sarcoma; myeloma bone disorder; osteolytic bone lesion;
KW   hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;
KW   bone fracture; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             96..578
FT                   /*tag=  a
FT                   /product= SPOIL-II
XX
PN   WO9937662-A1.
XX
PD   29-JUL-1999.
XX
PF   26-JAN-1999;   99WO-US01575.
XX
PR   27-JAN-1998;   98US-0013810.
XX
PA   (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI   Busfield SJ;
XX
DR   WPI; 1999-458675/38.
DR   P-PSDB; AAY24049.
XX
PT   New isolated SPOIL proteins, used to develop products for treating,
PT   e.g. inflammatory and immune disorders
XX
PS   Claim 1; Fig 6; 126pp; English.
XX
CC   The present sequence encodes a SPOIL-II protein. The SPOIL proteins have
CC   homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.
CC   The SPOIL proteins are used as modulating agents in regulating a variety
CC   of cellular processes. The products can be used for treating disorders
CC   characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone
CC   metabolism disorder, a proinflammatory disorder or an immune disorder.
CC   They can be used for treating e.g. inflammatory diseases and disorders
CC   e.g. inflammation, septic shock, stroke, diabetes, arthritis,
CC   intercolitis and pneumonitis, epithelial cell and/or skin diseases and
CC   disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma
CC   and Kaposi's sarcoma and other epithelial cancers including squamous cell
CC   carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and
CC   bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's
CC   disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,
CC   fibrous displasia, hypophosphatasia, bone sarcoma, myeloma bone disorder
CC   (e.g. osteolytic bone lesions) and hypercalcemia. SPOIL molecules and
CC   SPOIL modulators are useful for regulation of bone mass (e.g. increase in
CC   bone mass and/or inhibit bone loss), management of bone fragility (e.g.
CC   decrease bone fragility); and prevention and/or treatment of bone pain,
CC   bone deformities and/or bone fractures. The products can also be used for
CC   detection, diagnosis and screening assays.
XX
SQ   Sequence 838 BP; 256 A; 188 C; 184 G; 210 T; 0 other;

  Query Match           50.0%;  Score 238.6;  DB 20;  Length 838;
  Best Local Similarity 68.8%;  Pred. No. 2.2e-63;
  Matches  328;  Conservative    0;  Mismatches  149;  Indels    0;  Gaps    0;

Qy      1 atggaaaaagcattgaaaattgacacacctcagcaggggagcattcaggatatcaatcat 60
          | ||| |||| | | | |   |   |||||  ||   |     |||||||| | | |  |
Db    102 aaggagaaagaactaagagcagcatcaccttcgcttagacatgttcaggatcttagtagt 161

Qy     61 cgggtgtgggttcttcaggaccagacgctcatagcagtcccgaggaaggaccgtatgtct 120
          || |||||| | || ||| || | |  |||| ||||||||  ||||| || |   |    |
Db    162 cgtgtgtggatcctgcagaacaatatcctcactgcagtcccaaggaaagagcaaacagtt 221

Qy    121 ccagtcactattgccttaatctcatgccgacatgtggagacccttgagaaagacagaggg 180
          ||||||||||||| ||||  || |||||| | || |||| || |||||||   |||| |||
Db    222 ccagtcactattaccttgctcccatgccaatatctggacactcttgagacgaacaggggg 281

Qy    181 aaccccatctacctgggcctgaatggactcaatctctgcctgatgtgtgctaaagtcggg 240
           | ||||  ||| ||||  || |  | |  |    ||||||| | ||  | || |  |||
Db    282 gatcccacgtacatgggagtgcaaaggccgatgagctgcctgttctgcacaaaggatggg 341

Qy    241 gaccagcccacactgcagctgaaggaaaaggatataatggatttgtacaaccaacccgag 300
          || |||||    || |||||   ||||  | | ||||||||  ||||||||  ||   ||
Db    342 gagcagcctgtgctacagcttggggaagggaacataatggaaatgtacaacaaaaaggaa 401

Qy    301 cctgtgaagtcctttctcttctaccacagccagagtggcaggaactccaccttcgagtct 360
          |||||  ||  ||| |||||||||  ||||   |||||||  |  | ||| || || ||||||
Db    402 cctgtaaaagcctctctcttctatcacaagaagagtggtacaacctctacatttgagtct 461

Qy    361 gtggctttccctggctggttcatcgctgtcagctctgaaggaggctgtcctctcatcctt 420
          |  || |||||||| |||||||||||||||| ||||| ||||  |||| || |||||  ||
Db    462 acccaagaactgggggaaatcttcatcactgacttcgagatgattgtggtacattaa 519
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Db    462 gcagccttccctggttggttcatcgctgtctgctctaaagggagctgcccactcattctg 521

Qy    421 acccaagaactggggaaagccaacactactgactttgggttaactatgctgttttaa 477
          ||||||||||||||| ||  |  ||  |||||||| | | | | | || |   ||||
Db    522 acccaagaactgggggaaatcttcatcactgacttcgagatgattgtggtacattaa 578
```

RESULT 7
AAZ51246
ID AAZ51246 standard; DNA; 213 BP.
XX
AC AAZ51246;
XX
DT 06-JUN-2000 (first entry)
XX
DE 3' exon of human Interleukin-1 epsilon DNA.
XX
KW Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;
KW gene mapping; immune system; treatment; inflammatory disease;
KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
KW psoriasis; human; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..213
FT /*tag= a
FT /partial
FT /product= "Partial human IL-1 epsilon protein"
FT /note= "Homologous to mouse IL-1 epsilon protein"
XX
PN WO200011174-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US18771.
XX
PR 21-AUG-1998; 98US-0097413.
PR 31-AUG-1998; 98US-0098595.
PR 11-SEP-1998; 98US-0099974.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Sims JE, Smith DE;
XX
DR WPI; 2000-237653/20.
DR P-PSDB; AAY70216.
XX
PT Nucleotide sequences encoding human interleukin -1 epsilon, useful to
PT treat inflammatory and immune system-related diseases such as
PT rheumatoid arthritis and inflammatory bowel disease -
XX
PS Claim 1a; Fig 1; 76pp; English.
XX
CC The present sequence is the 3' exon of human Interleukin-1 (IL-1)
CC epsilon DNA. IL-1 epsilon gene is mapped to chromosome 2q and is mainly
CC expressed in spleen, lymph node, thymus, tonsil and leucocyte tissues.
CC IL-1 epsilon is a cytokine, with antiinflammatory, immunosuppressant,
CC antirheumatic, antiarthritic and antipsoriatic activity. The DNA
CC sequence can be used in chromosome identification, gene mapping and
CC study of immune system. IL-1 epsilon can be used in the treatment of
CC inflammatory or autoimmune diseases such as rheumatoid arthritis,
CC inflammatory bowel disease and psoriasis.
XX
SQ Sequence 213 BP; 51 A; 56 C; 48 G; 58 T; 0 other;

Query Match 44.7%; Score 213; DB 21; Length 213;
Best Local Similarity 100.0%; Pred. No. 9.3e-56;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    265 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 324
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 60

Qy    325 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 384
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120

Qy    385 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 444
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180

Qy    445 actactgactttgggttaactatgctgttttaa 477
          |||||||||||||||||||||||||||||||||
Db    181 actactgactttgggttaactatgctgttttaa 213
```

RESULT 8
AAD12296
ID AAD12296 standard; DNA; 1073 BP.
XX
AC AAD12296;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human interleukin-1epsilon (IL-1epsilon) protein DNA.
XX
KW Human; interleukin-1epsilon; IL-1epsilon; virucide; hepatotropic; fever;
KW immunological disorder; tumour; inflammatory disorder; hypoglycaemia;
KW autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;
KW psoriasis; viral infection; allergy; cytokine; HIV; drug screening; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 67..576
FT /*tag= a
FT /product= "Human interleukin-1epsilon (IL-1epsilon)
FT protein"
XX
PN WO200157219-A2.
XX
PD 09-AUG-2001.
XX
PF 01-FEB-2001; 2001WO-US03285.
XX
PR 02-FEB-2000; 2000US-0179638.
XX
PA (SCHE) SCHERING CORP.
XX
PI Debets JEMA, Timans JC, Bazan JF, Kastelein RA;
XX
DR WPI; 2001-488886/53.
DR P-PSDB; AAE06656.
XX
PT Novel isolated or recombinant antigenic interleukin-1 delta or epsilon
PT polypeptide useful for treating conditions exhibiting abnormal
PT expression of interleukin such as immunological disorders, tumor and
PT allergy -
XX
PS Claim 18; Page 86-87; 103pp; English.
XX
CC The invention relates to recombinant antigenic interleukin-1 like
CC molecules and their corresponding nucleic acid sequences, designated
CC as interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon).
CC IL-1delta and IL-1epsilon are useful for treating conditions exhibiting
CC abnormal expression of the interleukin such as immunological disorders,
CC tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis,
CC allergy, autoimmune diseases and infectious diseases (e.g., pulmonary
CC tuberculosis, leprosy, fulminant hepatitis, and viral infections such as
CC HIV). The invention also relates to methods of using the composition
CC containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic
CC utilities. IL-1delta is used as an immunogen for the production of
CC antisera or antibodies specific, e.g., capable of distinguishing between

```
CC   IL-1 family members and an IL-1delta, for the interleukin or its
CC   fragment. The purified interleukin is used as a reagent to detect any
CC   antibodies generated in response to the presence of elevated levels of
CC   expression, or immunological disorders which lead to antibody production
CC   to the endogenous cytokine. The invention also contemplates the use of
CC   competitive drug screening assays. The present DNA sequence encodes human
CC   interleukin-1epsilon (IL-1epsilon) protein.
XX
SQ   Sequence 1073 BP; 281 A; 241 C; 255 G; 296 T; 0 other;


  Query Match             42.3%;  Score 202;  DB 22;  Length 1073;
  Best Local Similarity   67.1%;  Pred. No. 4.7e-52;
  Matches  302;  Conservative    0;  Mismatches  145;  Indels    3;  Gaps    1;

Qy      18 aattgacacacctcagcaggggagcattcaggatatcaatcatcgggtgtgggttcttca 77
           |||    | ||||      ||||  ||| | ||| | ||||| |  ||||||   |||||
Db     120 aatgtgtaaacctattactgggactattaatgatttgaatcagcaagtgtggacccttca 179

Qy      78 ggaccagacgctcatagcagtcccgaggaaggaccgtatgtctccagtcactattgcctt 137
           ||  ||||  ||  | ||||| ||  | |  ||| || || | ||||||||| ||||  |
Db     180 gggtcagaaccttgtggcagttccacgaagtgacagtgtgaccccagtcactgttgctgt 239

Qy     138 aatctcatgccgacatgtggagacccttgagaaagacagagggaaccccatctacctggg 197
            ||| |||||    ||   ||| | |||||| ||| ||||||| | ||||| ||  ||||
Db     240 tatcacatgcaagtatccagaggctcttgagcaaggcagaggggatcccatttatttggg 299

Qy     198 cctgaatggactcaatctctgcctgatgtgtgctaaagtcggggaccagcccacactgca 257
           |  |    |   | | ||  ||   ||||  || || || || |||||||| ||||
Db     300 aatccagaatccagaaatgtgtttgtattgtgagaaggttggagaacagcccacattgca 359

Qy     258 gctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttct 317
           ||| || ||  || | || |||||| ||||   |||||||||||| |||||  |||| ||
Db     360 gctaaaagagcagaagatcatggatctgtatggccaacccgagcccgtgaaacccttcct 419

Qy     318 cttctaccacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctg 377
           |||||||    | ||| ||| |||| ||||||| | |||||||||||| ||||| | |||
Db     420 tttctaccgtgccaagactggtaggacctccacccttgagtctgtggccttcccggactg 479

Qy     378 gttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaa 437
           ||||||   || |  |||  |  ||| |   ||  |||| || ||   |||||| |||||
Db     480 gttcat---tgcctcctccaagagagaccagcccatcattctgacttcagaacttgggaa 536

Qy     438 agccaacactactgactttgggttaactat 467
             |  |||  |||| |||||  |||| |||
Db     537 gtcatacaacactgcctttgaattaaatat 566


RESULT   9
AAV42659
ID   AAV42659 standard; cDNA; 1183 BP.
XX
AC   AAV42659;
XX
DT   14-OCT-1998  (first entry)
XX
DE   cDNA encoding Interleukin-1 receptor antagonist beta (IL-1ra-beta).
XX
KW   Interleukin-1 receptor antagonist beta; IL-1ra-beta; IL-1 alpha;
KW   IL-1 beta; inflammatory response; treatment; inflammation; septicaemia;
KW   cancer; anaemia; arthritis; inflammatory bowel disease;
KW   graft vs. host rejection; autoimmunity; stroke; cardiac ischaemia;
KW   acute respiratory disease syndrome; psoriasis; restenosis;
KW   traumatic brain injury; acquired immune deficiency syndrome;
KW   cachexia; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             75..584
FT                   /*tag=  a
FT                   /product= IL-1ra-beta
XX
```

```
PN   EP855404-A1.
XX
PD   29-JUL-1998.
XX
PF   27-JAN-1998;   98EP-0300572.
XX
PR   28-JAN-1997;   97US-0790032.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Young PR;
XX
DR   WPI; 1998-389778/34.
DR   P-PSDB; AAW63136.
XX
PT   New nucleic acid encoding human interleukin-1 receptor antagonist
PT   beta polypeptides - and related expression systems, transformed
PT   cells, proteins, antibodies, agonists and antagonists, useful for
PT   treatment, prevention and diagnosis of inflammation, septicaemia,
PT   cancer etc
XX
PS   Claim 3; Fig 1; 20pp; English.
XX
CC   The present sequence encodes human Interleukin-1 receptor antagonist
CC   beta (IL-ra-beta). IL-1 alpha and IL-1 beta play key roles in
CC   inflammatory responses, and are produced as zymogens which are cleaved
CC   upon secretion to yield mature carboxyl terminal 17 kD fragments.
CC   IL-1ra-beta polypeptides and polynucleotides are useful in treatment of
CC   chronic and acute inflammation, septicaemia, cancer, anaemia, arthritis,
CC   inflammatory bowel disease, graft vs. host rejection, autoimmunity,
CC   stroke, cardiac ischaemia, acute respiratory disease syndrome (ARDS),
CC   psoriasis, restenosis, traumatic brain injury, acquired immune
CC   deficiency syndrome (AIDS) and cachexia. These conditions (or
CC   susceptibility to them) may be diagnosed by detecting mutations in the
CC   IL-1ra-beta coding sequence analysing a sample for presence or amount
CC   of IL-1ra-beta.
XX
SQ   Sequence 1183 BP; 329 A; 249 C; 269 G; 336 T; 0 other;


  Query Match             42.3%;  Score 202;  DB 19;  Length 1183;
  Best Local Similarity   67.1%;  Pred. No. 4.9e-52;
  Matches  302;  Conservative    0;  Mismatches  145;  Indels    3;  Gaps    1;

Qy      18 aattgacacacctcagcaggggagcattcaggatatcaatcatcgggtgtgggttcttca 77
           |||    | ||||      ||||  ||| | ||| | ||||| |  ||||||   |||||
Db     128 aatgtgtaaacctattactgggactattaatgatttgaatcagcaagtgtggacccttca 187

Qy      78 ggaccagacgctcatagcagtcccgaggaaggaccgtatgtctccagtcactattgcctt 137
           ||  ||||  ||  | ||||| ||  | |  ||| || || | ||||||||| ||||  |
Db     188 gggtcagaaccttgtggcagttccacgaagtgacagtgtgaccccagtcactgttgctgt 247

Qy     138 aatctcatgccgacatgtggagacccttgagaaagacagagggaaccccatctacctggg 197
            ||| |||||    ||   ||| | |||||| ||| ||||||| | ||||| ||  ||||
Db     248 tatcacatgcaagtatccagaggctcttgagcaaggcagaggggatcccatttatttggg 307

Qy     198 cctgaatggactcaatctctgcctgatgtgtgctaaagtcggggaccagcccacactgca 257
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Db     308 aatccagaatccagaaatgtgtttgtattgtgagaaggttggagaacagcccacattgca 367

Qy     258 gctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttct 317
           ||| || ||  || | || |||||| ||||   |||||||||||| |||||  |||| ||
Db     368 gctaaaagagcagaagatcatggatctgtatggccaacccgagcccgtgaaacccttcct 427

Qy     318 cttctaccacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctg 377
           |||||||    | ||| ||| |||| ||||||| | ||||||||||| ||||| | |||
Db     428 tttctaccgtgccaagactggtaggacctccacccttgagtctgtggccttcccggactg 487

Qy     378 gttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaa 437
           ||||||   || |  |||  |  ||| |   ||  |||| || ||   |||||| |||||
Db     488 gttcat---tgcctcctccaagagagaccagcccatcattctgacttcagaacttgggaa 544

Qy     438 agccaacactactgactttgggttaactat 467
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           |  |||  |||| |||||  |||| |||
Db    545 gtcatacaacactgcctttgaattaaatat 574
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RESULT 10
AAX90135
ID AAX90135 standard; cDNA; 1183 BP.
XX
AC AAX90135;
XX
DT 20-SEP-1999 (first entry)
XX
DE Human interleukin-1 receptor antagonist beta encoding cDNA.
XX
KW Human; interleukin-1 receptor antagonist beta; IL-1RA beta; septicemia;
KW chronic inflammation; acute inflammation; arthritis; autoimmunity;
KW inflammatory bowel disease; graft vs. host disease; stroke; psoriasis;
KW cardiac ischaemia; acute respiratory disease syndrome; ARDS; restenosis;
KW traumatic brain injury; AIDS; cachexia; allergy; parasite infection;
KW allergic rhinitis; allergic asthma; atopic dermatitis; gene therapy;
KW allergic inflammatory disease; delayed hypersensitivity; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO9936541-A1.
XX
PD 22-JUL-1999.
XX
PF 14-JAN-1999; 99WO-US00847.
XX
PR 29-APR-1998; 98US-0069619.
PR 14-JAN-1998; 98US-0007464.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Marshall L, Young PR;
XX
DR WPI; 1999-430615/36.
DR P-PSDB; AAY24395.
XX
PT New interleukin-1 receptor antagonist beta, useful for treating
PT inflammation and autoimmune diseases
XX
PS Claim 5; Fig 1; 34pp; English.
XX
CC The present sequence encodes human interleukin-1 receptor antagonist
CC beta (IL-1RA beta). IL-1RA beta polypeptides and polynucleotides are
CC useful for diagnosing diseases (or susceptibility to diseases) related
CC to the expression or activity of IL-1RA beta, by determining mutations
CC in the IL-1RA beta nucleic acid sequences and/or analysing for the
CC presence or amount of IL-1RA beta polypeptide. IL-1RA beta polypeptides
CC are also useful for screening for compounds which affect activity of the
CC protein. These can be used in treatment to inhibit (antagonist) or
CC enhance (agonist) IL-1RA beta activity, in addition to direct
CC administration of IL-1RA beta polypeptides to treat conditions, or
CC direct administration of antisense sequences to prevent expression.
CC IL-1RA beta polypeptides (administered directly, in a vector i.e. gene
CC therapy, and as a vaccine) and antibodies induce an immune response to
CC immunise and prevent disease. Diseases diagnosed, prevented or treated
CC include chronic and acute inflammation, septicemia, arthritis,
CC inflammatory bowel disease, graft vs. host disease, autoimmunity,
CC stroke, cardiac ischaemia, acute respiratory disease syndrome (ARDS),
CC psoriasis, restenosis, traumatic brain injury, AIDS, cachexia, allergy,
CC parasite infection, allergic rhinitis, allergic asthma, atopic
CC dermatitis, allergic inflammatory diseases and delayed hypersensitivity.
XX
SQ Sequence 1183 BP; 329 A; 249 C; 269 G; 336 T; 0 other;

Query Match 42.3%; Score 202; DB 20; Length 1183;
Best Local Similarity 67.1%; Pred. No. 4.9e-52;
Matches 302; Conservative 0; Mismatches 145; Indels 3; Gaps 1;

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Qy     18 aattgacacacctcagcaggggagcattcaggatatcaatcatcgggtgtgggttcttca 77
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Db    128 aatgtgtaaacctattactgggactattaatgatttgaatcagcaagtgtggacccttca 187

Qy     78 ggaccagacgctcatagcagtcccgaggaaggaccgtatgtctccagtcactattgcctt 137
          ||  ||||  ||  | |||||  ||  | |  ||| || || | ||||||||| ||||  |
Db    188 gggtcagaaccttgtggcagttccacgaagtgacagtgtgaccccagtcactgttgctgt 247

Qy    138 aatctcatgccgacatgtggagacccttgagaaagacagagggaaccccatctacctggg 197
          ||| |||||    ||   ||| | |||||| ||| ||||||| | |||||  ||  ||||
Db    248 tatcacatgcaagtatccagaggctcttgagcaaggcagaggggatcccatttatttggg 307

Qy    198 cctgaatggactcaatctctgcctgatgtgtgctaaagtcggggaccagcccacactgca 257
            |   |   |  | | ||  ||   ||||  || || || || |||||||||  ||||
Db    308 aatccagaatccagaaatgtgtttgtattgtgagaaggttggagaacagcccacattgca 367

Qy    258 gctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtccttttct 317
          ||| || ||  || | || ||||||  ||||   ||||||||||||  |||||  |||| ||
Db    368 gctaaaagagcagaagatcatggatctgtatggccaacccgagcccgtgaaacccttcct 427

Qy    318 cttctaccacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctg 377
          |||||||    | ||| ||| |||| |||||||  | ||||||||||| |||||  | |||
Db    428 tttctaccgtgccaagactggtaggacctccacccttgagtctgtggccttcccggactg 487

Qy    378 gttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaa 437
          ||||||   || |  |||  | |||  |   ||  |||| || ||   |||||| |||||
Db    488 gttcat---tgcctcctccaagagagaccagcccatcattctgacttcagaacttgggaa 544

Qy    438 agccaacactactgactttgggttaactat 467
            |  |||  |||| |||||  |||| |||
Db    545 gtcatacaacactgcctttgaattaaatat 574
```

RESULT 11
AAS26842
ID AAS26842 standard; cDNA; 1183 BP.
XX
AC AAS26842;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human cDNA encoding a novel secreted protein, SEQ ID 34.
XX
KW Human; immunosuppressive; antiarthritic; ss; antirheumatic;
KW cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;
KW neuroprotective; antibacterial; virucide; fungicide; opthalmalogical;
KW vulnerary; secreted protein; rheumatoid arthritis;
KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;
KW corneal infection; wound healing; epithelial cell proliferation;
KW skin ageing; food additive; preservative; antiproliferative.
XX
OS Homo sapiens.
XX
PN WO200155441-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01320.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.

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PR 01-SEP-2000; 2000US-0229345.
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PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
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PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
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PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
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PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
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PR 17-NOV-2000; 2000US-0249209.
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PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
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PR 17-NOV-2000; 2000US-0249297.
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PR 01-DEC-2000; 2000US-0250160.
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PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-476222/51.
DR P-PSDB; AAU16937.
XX
PT Novel polypeptides and polynucleotides useful as diagnostic reagents to
PT diagnose diseases or disorders associated with aberrant expression or
PT activity of polypeptides, for treating blood clotting disorder,
PT haemophilia -
XX
PS Claim 1; SEQ ID No 34; 601pp; English.
XX
CC The invention relates to isolated nucleic acid molecules and their
CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They
CC are also used in diagnosing a pathological condition or susceptibility
CC to a pathological condition. Antibodies to the proteins can also
CC be used in alleviating symptoms associated with the disorders and in

CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked
CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated
CC include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi
CC and ocular disorders e.g. corneal infection, and many other
CC disorders listed in the specification. The polypeptides can also
CC be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present

Query Match 42.3%; Score 202; DB 22; Length 1183;
Best Local Similarity 67.1%; Pred. No. 4.9e-52;
Matches 302; Conservative 0; Mismatches 145; Indels 3; Gaps 1;

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Qy      18 aattgacacacctcagcaggggagcattcaggatatcaatcatcgggtgtgggttcttca 77
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Db     128 aatgtgtaaacctattactgggactattaatgatttgaatcagcaagtgtggacccttca 187

Qy      78 ggaccagacgctcatagcagtcccgaggaaggaccgtatgtctccagtcactattgcctt 137
           ||  ||||  ||  | ||||| ||  | |  ||| || || | ||||||||| ||||  |
Db     188 gggtcagaaccttgtggcagttccacgaagtgacagtgtgaccccagtcactgttgctgt 247

Qy     138 aatctcatgccgacatgtggagacccttgagaaagacagagggaaccccatctacctggg 197
            ||| |||||    ||   ||| | |||||| ||| ||||||| | ||||| ||  ||||
Db     248 tatcacatgcaagtatccagaggctcttgagcaaggcagaggggatcccatttatttggg 307

Qy     198 cctgaatggactcaatctctgcctgatgtgtgctaaagtcggggaccagcccacactgca 257
             |  |    |  | | ||  ||   |||| || || || || |||||||| ||||
Db     308 aatccagaatccagaaatgtgtttgtattgtgagaaggttggagaacagcccacattgca 367

Qy     258 gctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtccttttct 317
           ||| || ||  || | || |||||| ||||   |||||||||||| |||||  |||| ||
Db     368 gctaaaagagcagaagatcatggatctgtatggccaacccgagcccgtgaaacccttcct 427

Qy     318 cttctaccacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctg 377
           |||||||    | ||| ||| |||| ||||||| | ||||||||||| ||||| | |||
Db     428 tttctaccgtgccaagactggtaggacctccaccttgagtctgtggccttcccggactg 487

Qy     378 gttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaa 437
           ||||||   || |  |||  |  ||| |   ||  |||| || ||   |||||| |||||
Db     488 gttcat---tgcctcctccaagagagaccagcccatcattctgacttcagaacttgggaa 544

Qy     438 agccaacactactgactttgggttaactat 467
             |  |||  |||| |||||  |||| |||
Db     545 gtcatacaacactgcctttgaattaaatat 574
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RESULT 12
AAX86458
ID AAX86458 standard; DNA; 1291 BP.
XX
AC AAX86458;
XX
DT 30-SEP-1999 (first entry)
XX
DE cDNA encoding a human SPOIL-I protein (also known as hTANGO 080-I).
XX
KW SPOIL-I; interleukin-1 receptor antagonist; IL-1ra; modulating agent;
KW bone metabolism disorder; proinflammatory disorder; immune disorder;
KW inflammatory disease; septic shock; stroke; diabetes; arthritis;
KW intercolitis; pneumonitis; epithelial cell; skin disease;
KW proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;
KW epithelial cancer; squamous cell carcinoma; bone resorption disorder;
KW osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;
KW osteogenesis imperfecta; fibrous displasia; hypophosphatasia;
KW bone sarcoma; myeloma bone disorder; osteolytic bone lesion;
KW hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;
KW bone fracture; hTANGO 80-I; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 124..633
FT /*tag= a
FT /product= SPOIL-1
XX
PN WO9937662-A1.
XX
PD 29-JUL-1999.
XX
PF 26-JAN-1999; 99WO-US01575.
XX
PR 27-JAN-1998; 98US-0013810.
XX
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI Busfield SJ;
XX
DR WPI; 1999-458675/38.
DR P-PSDB; AAY24043.
XX
PT New isolated SPOIL proteins, used to develop products for treating,
PT e.g. inflammatory and immune disorders
XX
PS Example 1; Fig 4A-B; 126pp; English.
XX
CC The present sequence encodes a SPOIL-I protein. The SPOIL proteins have
CC homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.
CC The SPOIL proteins are used as modulating agents in regulating a variety
CC of cellular processes. The products can be used for treating disorders
CC characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone
CC metabolism disorder, a proinflammatory disorder or an immune disorder.
CC They can be used for treating e.g. inflammatory diseases and disorders
CC e.g. inflammation, septic shock, stroke, diabetes, arthritis,
CC intercolitis and pneumonitis, epithelial cell and/or skin diseases and
CC disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma
CC and Kaposi's sarcoma and other epithelial cancers including squamous cell
CC carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and
CC bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's
CC disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,
CC fibrous displasia, hypophosphatasia, bone sarcoma, myeloma bone disorder
CC (e.g. osteolytic bone lesions) and hypercalcemia. SPOIL molecules and
CC SPOIL modulators are useful for regulation of bone mass (e.g. increase in
CC bone mass and/or inhibit bone loss), management of bone fragility (e.g.
CC decrease bone fragility); and prevention and/or treatment of bone pain,
CC bone deformities and/or bone fractures. The products can also be used for
CC detection, diagnosis and screening assays.
XX
SQ Sequence 1291 BP; 375 A; 271 C; 291 G; 354 T; 0 other;

Query Match 42.3%; Score 202; DB 20; Length 1291;
Best Local Similarity 67.1%; Pred. No. 5.1e-52;
Matches 302; Conservative 0; Mismatches 145; Indels 3; Gaps 1;

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Qy      18 aattgacacacctcagcaggggagcattcaggatatcaatcatcgggtgtgggttcttca 77
           |||    | ||||      ||||  ||| | ||| | ||||| |  ||||||   |||||
Db     177 aatgtgtaaacctattactgggactattaatgatttgaatcagcaagtgtggacccttca 236

Qy      78 ggaccagacgctcatagcagtcccgaggaaggaccgtatgtctccagtcactattgcctt 137
           ||  ||||  ||  | ||||| ||  | |  ||| || || | ||||||||| ||||  |
Db     237 gggtcagaaccttgtggcagttccacgaagtgacagtgtgaccccagtcactgttgctgt 296

Qy     138 aatctcatgccgacatgtggagacccttgagaaagacagagggaaccccatctacctggg 197
            ||| |||||    ||   ||| | |||||| ||| ||||||| | ||||| ||  ||||
Db     297 tatcacatgcaagtatccagaggctcttgagcaaggcagaggggatcccatttatttggg 356

Qy     198 cctgaatggactcaatctctgcctgatgtgtgctaaagtcggggaccagcccacactgca 257
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Db     357 aatccagaatccagaaatgtgtttgtattgtgagaaggttggagaacagcccacattgca 416

Qy     258 gctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttct 317
           ||| || ||  || | || ||||| ||||   |||||||||||| |||||  |||| ||
Db     417 gctaaaagagcagaagatcatggatctgtatggccaacccgagcccgtgaaacccttcct 476

Qy     318 cttctaccacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctg 377
            |||||||    | ||| ||| |||| ||||||| | |||||||||| ||||| | |||
Db     477 tttctaccgtgccaagactggtaggacctccaccttgagtctgtggccttcccggactg 536

Qy     378 gttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaa 437
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Db     537 gttcat---tgcctcctccaagagagaccagcccatcattctgacttcagaacttgggaa 593

Qy     438 agccaacactactgactttgggttaactat 467
             |  |||  |||| |||||  |||| |||
Db     594 gtcatacaacactgcctttgaattaaatat 623


RESULT  13
AAS26915
ID   AAS26915 standard; cDNA; 673 BP.
XX
AC   AAS26915;
XX
DT   07-NOV-2001  (first entry)
XX
DE   Human cDNA encoding a novel secreted protein, SEQ ID 107.
XX
KW   Human; immunosuppressive; antiarthritic; ss; antirheumatic;
KW   cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;
KW   neuroprotective; antibacterial; virucide; fungicide; opthalmalogical;
KW   vulnerary; secreted protein; rheumatoid arthritis;
KW   hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
KW   cerebrovascular disorder; cerebral ischaemia; angiogenesis;
KW   nervous system disorder; Alzheimer's disease; infection; ocular disorder;
KW   corneal infection; wound healing; epithelial cell proliferation;
KW   skin ageing; food additive; preservative; antiproliferative.
XX
OS   Homo sapiens.
XX
PN   WO200155441-A2.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US01320.
XX
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PR 05-DEC-2000; 2000US-0251030.
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PR 08-DEC-2000; 2000US-0251856.
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PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-476222/51.
DR P-PSDB; AAU17010.
XX
PT Novel polypeptides and polynucleotides useful as diagnostic reagents to
PT diagnose diseases or disorders associated with aberrant expression or
PT activity of polypeptides, for treating blood clotting disorder,
PT haemophilia -
XX
PS Claim 1; SEQ ID No 107; 601pp; English.
XX
CC The invention relates to isolated nucleic acid molecules and their
CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They
CC are also used in diagnosing a pathological condition or susceptibility
CC to a pathological condition. Antibodies to the proteins can also
CC be used in alleviating symptoms associated with the disorders and in
CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked
CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated
CC include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi
CC and ocular disorders e.g. corneal infection, and many other
CC disorders listed in the specification. The polypeptides can also
CC be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present

Query Match 42.3%; Score 201.6; DB 22; Length 673;
Best Local Similarity 66.9%; Pred. No. 5.1e-52;
Matches 301; Conservative 1; Mismatches 145; Indels 3; Gaps 1;

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AC AAD16762;
XX
DT 22-NOV-2001 (first entry)
XX
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XX
KW Human; cytostatic; gene therapy; inflammatory disorder; neural disorder;
KW Parkinson's disease; Alzheimer's disease; immune system disorder; AIDS;
KW autoimmune disease; rheumatoid arthritis; muscular disorder; ischaemia;
KW reproductive disorder; Crohn's disease; pulmonary disorder; cancer;
KW myocardial infarction; glomerulonephritis; nephrotic syndrome; tumour;
KW haematopoietic disorder; rhinitis; asthma; diabetes; atherosclerosis;
KW anti-sense therapy; endocrine disorder; leukaemia; ss.
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FT /note= "CDS does not include start and stop codon; Xaa
FT is an unknown amino acid"
FT /partial
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PN WO200155202-A1.
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PD 02-AUG-2001.
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PF 17-JAN-2001; 2001WO-US01325.
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PR 31-JAN-2000; 2000US-0179065.
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PR 16-MAR-2000; 2000US-0189874.
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PR 19-MAY-2000; 2000US-0205515.
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PR 01-DEC-2000; 2000US-0250391.
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XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-451925/48.
DR P-PSDB; AAE09702.
XX

PT Isolated polypeptide for treating, preventing and/ or prognosing
PT medical disorders and also for testing and detection e.g. diagnosis and
PT screening for agonists -
XX
PS Claim 1; SEQ ID No 23; 469pp; English.
XX
CC AAD16750-AAD16775 represent cDNAs corresponding to novel human protein
CC genes, and AAE09690-AAE09715 represent the proteins they encode. AAD16777
CC -AAD16780 represent novel human genomic DNA fragments. The novel proteins
CC and their DNAs are useful for diagnosing, treating, preventing and/or
CC prognosing inflammatory disorders (bursitis or tendonitis); neural
CC disorders (e.g. Parkinson's disease, Alzheimer's disease); immune system
CC disorders; AIDS; autoimmune diseases (e.g., rheumatoid arthritis);
CC muscular disorders; reproductive disorders; gastrointestinal disorders
CC (malabsorption syndrome, Crohn's disease); pulmonary disorders;
CC cardiovascular disorders (myocardial infarction, ischaemia, arrhythmias);
CC renal disorders (glomerulonephritis, nephrotic syndrome); cancerous
CC disease and conditions (breast cancer); hyperproliferative disorders
CC (leukaemia, hyperplasia); tumours; foetal and developmental
CC abnormalities; haematopoietic disorders; respiratory disorders (rhinitis,
CC asthma); angiogenic disorders; diabetes; atherosclerosis; endocrine
CC disorders; pregnancy-related disorders and infections. The novel protein
CC DNA is useful in gene therapy and anti-sense therapy. The proteins can

Query Match 42.3%; Score 201.6; DB 22; Length 673;
Best Local Similarity 66.9%; Pred. No. 5.1e-52;
Matches 301; Conservative 1; Mismatches 145; Indels 3; Gaps 1;

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Qy     78 ggaccagacgctcatagcagtcccgaggaaggaccgtatgtctccagtcactattgcctt 137
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Qy    138 aatctcatgccgacatgtggagacccttgagaaagacagagggaaccccatctacctggg 197
          ||| |||||    ||   ||| | |||||| ||| ||||||| | ||||| ||  ||||
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Qy    258 gctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtccttttct 317
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Qy    318 cttctaccacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctg 377
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RESULT 15
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XX
DT 30-SEP-1999 (first entry)
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KW bone metabolism disorder; proinflammatory disorder; immune disorder;
KW inflammatory disease; septic shock; stroke; diabetes; arthritis;
KW intercolitis; pneumonitis; epithelial cell; skin disease;
KW proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;
KW epithelial cancer; squamous cell carcinoma; bone resorption disorder;
KW osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;
KW osteogenesis imperfecta; fibrous displasia; hypophosphatasia;
KW bone sarcoma; myeloma bone disorder; osteolytic bone lesion;
KW hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;
KW bone fracture; hTANGO 80-I; ss.
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XX
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XX
PF 26-JAN-1999; 99WO-US01575.
XX
PR 27-JAN-1998; 98US-0013810.
XX
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI Busfield SJ;
XX
DR WPI; 1999-458675/38.
DR P-PSDB; AAY24044.
XX
PT New isolated SPOIL proteins, used to develop products for treating,
PT e.g. inflammatory and immune disorders
XX
PS Claim 1; Fig 5; 126pp; English.
XX
CC The present sequence encodes a SPOIL-II protein. The SPOIL proteins have
CC homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.
CC The SPOIL proteins are used as modulating agents in regulating a variety
CC of cellular processes. The products can be used for treating disorders
CC characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone
CC metabolism disorder, a proinflammatory disorder or an immune disorder.
CC They can be used for treating e.g. inflammatory diseases and disorders
CC e.g. inflammation, septic shock, stroke, diabetes, arthritis,
CC intercolitis and pneumonitis, epithelial cell and/or skin diseases and
CC disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma
CC and Kaposi's sarcoma and other epithelial cancers including squamous cell
CC carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and
CC bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's
CC disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,
CC fibrous displasia, hypophosphatasia, bone sarcoma, myeloma bone disorder
CC (e.g. osteolytic bone lesions) and hypercalcemia. SPOIL molecules and
CC SPOIL modulators are useful for regulation of bone mass (e.g. increase in
CC bone mass and/or inhibit bone loss), management of bone fragility (e.g.
CC decrease bone fragility); and prevention and/or treatment of bone pain,
CC bone deformities and/or bone fractures. The products can also be used for
CC detection, diagnosis and screening assays.
XX
SQ Sequence 1377 BP; 377 A; 304 C; 316 G; 380 T; 0 other;

Query Match 42.2%; Score 201.4; DB 20; Length 1377;
Best Local Similarity 67.5%; Pred. No. 8.1e-52;
Matches 299; Conservative 0; Mismatches 141; Indels 3; Gaps 1;

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Db    275 aaacctattactgggactattaatgatttgaatcagcaagtgtggacccttcagggtcag 334

Qy     85 acgctcatagcagtcccgaggaaggaccgtatgtctccagtcactattgccttaatctca 144
          |  ||  | ||||| ||  | |  ||| || || | ||||||||| ||||  | ||| ||
Db    335 aaccttgtggcagttccacgaagtgacagtgtgaccccagtcactgttgctgttatcaca 394
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Qy    145 tgccgacatgtggagacccttgagaaagacagagggaaccccatctacctgggcctgaat 204
          |||    ||   ||| | |||||| ||| ||||||| | ||||| ||  ||||  |  |
Db    395 tgcaagtatccagaggctcttgagcaaggcagaggggatcccatttatttgggaatccag 454

Qy    205 ggactcaatctctgcctgatgtgtgctaaagtcggggaccagcccacactgcagctgaag 264
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Db    455 aatccagaaatgtgtttgtattgtgagaaggttggagaacagcccacattgcagctaaaa 514

Qy    265 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 324
          ||  || | || |||||| ||||   ||||||||||||| |||||  |||| || ||||||
Db    515 gagcagaagatcatggatctgtatggccaacccgagcccgtgaaaccttcctttttctac 574

Qy    325 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 384
          |    | ||| ||| |||| ||||||| | |||||||||||| ||||| | |||||||||
Db    575 cgtgccaagactggtaggacctccacccttgagtctgtggccttcccggactggttcat- 633

Qy    385 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 444
            || |  |||  |  ||| |   ||  |||| || ||   |||||| |||||  |  ||
Db    634 --tgcctcctccaagagagaccagcccatcattctgacttcagaacttgggaagtcatac 691

Qy    445 actactgactttgggttaactat 467
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Db    692 aacactgcctttgaattaaatat 714
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Search completed: June 21, 2002, 12:02:58
Job time: 14921 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: June 21, 2002, 11:56:00 ; Search time 2781.56 Seconds
(without alignments)
3588.619 Million cell updates/sec

Title: US-09-763-498-7
Perfect score: 477
Sequence: 1 atggaaaaagcattgaaaat.....ggttaactatgctgttttaa 477

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
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20: em_om:*
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22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
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28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	477	100.0	477	9	AF201831	AF201831 Homo sapi
	2	349.8	73.3	391	6	AX193589	AX193589 Sequence
	3	238.6	50.0	483	10	AF200493	AF200493 Mus muscu
	4	238.6	50.0	795	10	AF206697	AF206697 Mus muscu
	5	222	46.5	244	6	AX193660	AX193660 Sequence
	6	215.8	45.2	197308	9	AC016724	AC016724 Homo sapi
	7	202	42.3	1073	6	AX207820	AX207820 Sequence
	8	202	42.3	1177	9	AF206696	AF206696 Homo sapi
	9	202	42.3	1183	6	E54910	E54910 Interleukin
	10	202	42.3	1183	9	AF200492	AF200492 Homo sapi
	11	134.2	28.1	520	6	AX193587	AX193587 Sequence
	12	134.2	28.1	585	6	AX052581	AX052581 Sequence
	13	134.2	28.1	585	9	AF201833	AF201833 Homo sapi
	14	134.2	28.1	1244	6	AX167128	AX167128 Sequence
	15	129.2	27.1	746	6	AR137703	AR137703 Sequence
	16	127	26.6	243	6	AR137705	AR137705 Sequence
	17	127	26.6	294	6	AR137704	AR137704 Sequence
	18	112	23.5	329	6	AX193643	AX193643 Sequence
	19	106.4	22.3	186587	2	AC106686	AC106686 Rattus no
c	20	79.4	16.6	184626	2	AC096974	AC096974 Rattus no
	21	78.8	16.5	1036	4	AY026462	AY026462 Canis fam
	22	77.2	16.2	563	4	AF216526	AF216526 Canis fam
	23	74.8	15.7	520	10	MUSILRA	M63100 M.musculus
	24	74.8	15.7	542	10	S64082	S64082 interleukin
	25	74.8	15.7	604	10	AF001795	AF001795 Mus muscu
	26	74.8	15.7	1576	10	MUSIL1RAA	M57525 Mouse inter
	27	74.8	15.7	1877	6	E55194	E55194 Interleukin
	28	74.8	15.7	1877	10	MUSILIRN	M74294 Mouse IL-1r
	29	74.8	15.7	1940	10	MUSIL1RA	M64404 Mus domesti
	30	71.8	15.1	531	6	AX127225	AX127225 Sequence
	31	71.8	15.1	603	6	AX127227	AX127227 Sequence
	32	71.8	15.1	1590	4	D83714	D83714 Equus cabal
	33	71.8	15.1	1590	6	E15594	E15594 cDNA encodi
	34	71.8	15.1	1614	4	ECU92482	U92482 Equus cabal
	35	71.8	15.1	1614	6	AX127224	AX127224 Sequence
c	36	71.2	14.9	197308	9	AC016724	AC016724 Homo sapi
	37	71	14.9	574	4	S68977	S68977 sIL-1ra=int
	38	70.8	14.8	462	6	AR105636	AR105636 Sequence
	39	70.8	14.8	474	6	A50276	A50276 Sequence 10
	40	70.8	14.8	474	6	AR001464	AR001464 Sequence
	41	70.8	14.8	474	6	AR055509	AR055509 Sequence
	42	70.8	14.8	474	6	AR085392	AR085392 Sequence
	43	70.8	14.8	514	6	I42450	I42450 Sequence 41
	44	70.8	14.8	531	6	A49726	A49726 Sequence 1
	45	70.8	14.8	531	6	A50144	A50144 Sequence 1

ALIGNMENTS

RESULT 1
AF201831
LOCUS AF201831 477 bp mRNA linear PRI 16-JAN-2000
DEFINITION Homo sapiens FIL1 epsilon mRNA, complete cds.
ACCESSION AF201831
VERSION AF201831.1 GI:6694389
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 477)
AUTHORS Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garka,K.E. and Sims,J.E.
TITLE Four new members expand the interleukin-1 superfamily
JOURNAL J. Biol. Chem. 275 (2), 1169-1175 (2000)
MEDLINE 20092888
REFERENCE 2 (bases 1 to 477)
AUTHORS Sims,J.E.
TITLE Direct Submission
JOURNAL Submitted (04-NOV-1999) Molecular Genetics, Immunex Corporation, 51 University Street, Seattle, WA 98101, USA
FEATURES Location/Qualifiers

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                     /db_xref="taxon:9606"
                     /chromosome="2"
                     /map="2q; between D2S121 and D2S110"
     CDS             1. .477
                     /note="similar to IL-1"
                     /codon_start=1
                     /product="FIL1 epsilon"
                     /protein_id="AAF25211.1"
                     /db_xref="GI:6694390"
                     /translation="MEKALKIDTPQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTI
                     ALISCRHVETLEKDRGNPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPV
                     KSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTMLF"
BASE COUNT      124 a    123 c    117 g    113 t
ORIGIN
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Query Match 100.0%; Score 477; DB 9; Length 477;
Best Local Similarity 100.0%; Pred. No. 2.1e-133;
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 cgggtgtgggttcttcaggaccagacgctcatagcagtcccgaggaaggaccgtatgtct 120
Db      61 CGGGTGTGGGTTCTTCAGGACCAGACGCTCATAGCAGTCCCGAGGAAGGACCGTATGTCT 120

Qy     121 ccagtcactattgccttaatctcatgccgacatgtggagacccttgagaaagacagaggg 180
Db     121 CCAGTCACTATTGCCTTAATCTCATGCCGACATGTGGAGACCCTTGAGAAAGACAGAGGG 180

Qy     181 aaccccatctacctgggcctgaatggactcaatctctgcctgatgtgtgctaaagtcggg 240
Db     181 AACCCCATCTACCTGGGCCTGAATGGACTCAATCTCTGCCTGATGTGTGCTAAAGTCGGG 240

Qy     241 gaccagcccacactgcagctgaaggaaaaggatataatggatttgtacaaccaacccgag 300
Db     241 GACCAGCCCACACTGCAGCTGAAGGAAAAGGATATAATGGATTTGTACAACCAACCCGAG 300

Qy     301 cctgtgaagtcctttctcttctaccacagccagagtggcaggaactccaccttcgagtct 360
Db     301 CCTGTGAAGTCCTTTCTCTTCTACCACAGCCAGAGTGGCAGGAACTCCACCTTCGAGTCT 360

Qy     361 gtggctttccctggctggttcatcgctgtcagctctgaaggaggctgtcctctcatcctt 420
Db     361 GTGGCTTTCCCTGGCTGGTTCATCGCTGTCAGCTCTGAAGGAGGCTGTCCTCTCATCCTT 420

Qy     421 acccaagaactggggaaagccaacactactgactttgggttaactatgctgttttaa 477
Db     421 ACCCAAGAACTGGGGAAAGCCAACACTACTGACTTTGGGTTAACTATGCTGTTTTAA 477
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RESULT   2
AX193589
LOCUS       AX193589                391 bp    DNA     linear   PAT 15-AUG-2001
DEFINITION  Sequence 11 from Patent WO0140291.
ACCESSION   AX193589
VERSION     AX193589.1  GI:15211518
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 391)
  AUTHORS   Burgess,C.E., Prayaga,S.K., Shimkets,R.A., Rastelli,L.,
            Zerhusen,B.D. and Mezes,P.S.
  TITLE     Proteins and nucleic acids encoding the same
  JOURNAL   Patent: WO 0140291-A 11 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
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     source          1. .391
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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ORIGIN
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Best Local Similarity 96.5%; Pred. No. 6.8e-95;
Matches 383; Conservative 0; Mismatches 2; Indels 12; Gaps 2;

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Qy     109 gaccgtatgtctccagtcactattgccttaatctcatgccgacatgtggagacccttgag 168
Db      61 G------TGTTCCCAGTCACTATTGCCTTAATCTCATGCCGACATGTGGAGACCCTTGAG 114

Qy     169 aaagacagagggaacccccatctacctgggcctgaatggactcaatctctgcctgatgtgt 228
Db     115 AAAGACAGAGGGAACCCCATCTACCTGGGCCTGAATGGACTCAATCTCTGCCTGATGTGT 174

Qy     229 gctaaagtcggggaccagcccacactgcagctga------aggaaaaggatataatggat 282
Db     175 GCTAAAGTCGGGGACCAGCCCACACTGCAGCTGAAGCTTCAGGAAAAGGATATAATGGAT 234

Qy     283 ttgtacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcagg 342
Db     235 TTGTACAACCAACCCGAGCCTGTGAAGTCCTTTCTCTTCTACCACAGCCAGAGTGGCAGG 294

Qy     343 aactccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaagga 402
Db     295 AACTCCACCTTCGAGTCTGTGGCTTTCCCTGGCTGGTTCATCGCTGTCAGCTCTGAAGGA 354

Qy     403 ggctgtcctctcatccttacccaagaactggggaaag 439
Db     355 GGCTGTCCTCTCATCCTTACCCAAGAACTGGGGAAAG 391
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RESULT   3
AF200493
LOCUS       AF200493                483 bp    mRNA    linear   ROD 11-MAY-2000
DEFINITION  Mus musculus interleukin-1 homolog 1 mRNA, complete cds.
ACCESSION   AF200493
VERSION     AF200493.1  GI:7769113
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 483)
  AUTHORS   Kumar,S., McDonnell,P.C., Lehr,R., Tierney,L., Tzimas,M.N.,
            Griswold,D.E., Capper,E.A., Tal-Singer,R., Wells,G.I., Doyle,M.L.
            and Young,P.R.
  TITLE     Identification and initial characterization of four novel members
            of the interleukin-1 family
  JOURNAL   J. Biol. Chem. 275 (14), 10308-10314 (2000)
  MEDLINE   20209405
   PUBMED   10744718
REFERENCE   2  (bases 1 to 483)
  AUTHORS   Kumar,S., McDonnell,P.C. and Young,P.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-NOV-1999) Bone and Cartilage Biology, UW 2109,
            SmithKline Beecham Pharmaceuticals, 709 Swedeland Rd., King of
            Prussia, PA 19406, USA
FEATURES             Location/Qualifiers
     source          1. .483
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     CDS             1. .483
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                     /note="cytokine; mIL-1H1"
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BASE COUNT      139 a    113 c    117 g    114 t
ORIGIN


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Qy      61 cgggtgtgggttcttcaggaccagacgctcatagcagtcccgaggaaggaccgtatgtct 120
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Db      67 CGTGTGTGGATCCTGCAGAACAATATCCTCACTGCAGTCCCAAGGAAAGAGCAAACAGTT 126

Qy     121 ccagtcactattgccttaatctcatgccgacatgtggagacccttgagaaagacagaggg 180
           |||||||||||| ||||  || |||||| | || |||| || |||||||   |||| |||
Db     127 CCAGTCACTATTACCTTGCTCCCATGCCAATATCTGGACACTCTTGAGACGAACAGGGGG 186

Qy     181 aaccccatctacctgggcctgaatggactcaatctctgcctgatgtgtgctaaagtcggg 240
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Qy     241 gaccagcccacactgcagctgaaggaaaaggatataatggatttgtacaaccaacccgag 300
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Qy     301 cctgtgaagtcctttctcttctaccacagccagagtggcaggaactccaccttcgagtct 360
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Qy     361 gtggctttccctggctggttcatcgctgtcagctctgaaggaggctgtcctctcatcctt 420
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Qy     421 acccaagaactggggaaagccaacactactgactttgggttaactatgctgttttaa 477
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Db     427 ACCCAAGAACTGGGGGAAATCTTCATCACTGACTTCGAGATGATTGTGGTTCATTAA 483


RESULT   4
AF206697
LOCUS       AF206697                795 bp    mRNA    linear   ROD 01-NOV-2001
DEFINITION  Mus musculus interleukin-1 epsilon (Il1e) mRNA, complete cds.
ACCESSION   AF206697
VERSION     AF206697.1  GI:11493849
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 795)
  AUTHORS   Debets,R., Timans,J.C., Homey,B., Zurawski,S., Sana,T.R., Lo,S.,
            Wagner,J., Edwards,G., Clifford,T., Menon,S., Bazan,J.F. and
            Kastelein,R.A.
  TITLE     Two novel IL-1 family members, IL-1 delta and IL-1 epsilon,
            function as an antagonist and agonist of NF-kappa B activation
            through the orphan IL-1 receptor-related protein 2
  JOURNAL   J. Immunol. 167 (3), 1440-1446 (2001)
  MEDLINE   21359532
   PUBMED   11466363
REFERENCE   2  (bases 1 to 795)
  AUTHORS   Debets,R., Timans,J.C., Zurawski,S., Bazan,J.F. and Kastelein,R.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-NOV-1999) Molecular Biology, DNAX Research Institute
            of Molecular and Cellular Biology, Inc., 901 California Avenue,
            Palo Alto, CA 94304-1104, USA
FEATURES             Location/Qualifiers
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     CDS             76. .558
                     /gene="Il1e"
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                     and IL-1ra; highly expressed in skin tissue; acts through
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                     signaling cascade; antagonized by IL-1d"
                     /codon_start=1
                     /product="interleukin-1 epsilon"
                     /protein_id="AAG35671.1"
                     /db_xref="GI:11493850"
                     /translation="MNKEKELRAASPSLRHVQDLSSRVWILQNNILTAVPRKEQTVPV
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BASE COUNT      237 a    177 c    174 g    207 t
ORIGIN


  Query Match             50.0%;  Score 238.6;  DB 10;  Length 795;
  Best Local Similarity   68.8%;  Pred. No. 3.4e-61;
  Matches  328;  Conservative    0;  Mismatches  149;  Indels    0;  Gaps    0;

Qy       1 atggaaaaagcattgaaaattgacacacctcagcaggggagcattcaggatatcaatcat 60
           | ||| |||| | | | |   |   |||||  ||   |     |||||||| | | |  |
Db      82 AAGGAGAAAGAACTAAGAGCAGCATCACCTTCGCTTAGACATGTTCAGGATCTTAGTAGT 141

Qy      61 cgggtgtgggttcttcaggaccagacgctcatagcagtcccgaggaaggaccgtatgtct 120
           || |||||| | || ||| || | |  |||| ||||||||  ||||| || |   |    |
Db     142 CGTGTGTGGATCCTGCAGAACAATATCCTCACTGCAGTCCCAAGGAAAGAGCAAACAGTT 201

Qy     121 ccagtcactattgccttaatctcatgccgacatgtggagacccttgagaaagacagaggg 180
           |||||||||||| ||||  || |||||| | || |||| || |||||||   |||| |||
Db     202 CCAGTCACTATTACCTTGCTCCCATGCCAATATCTGGACACTCTTGAGACGAACAGGGGG 261

Qy     181 aaccccatctacctgggcctgaatggactcaatctctgcctgatgtgtgctaaagtcggg 240
            | ||||  ||| ||||  || |  | |  |    |||||||  | ||  | || |  |||
Db     262 GATCCCACGTACATGGGAGTGCAAAGGCCGATGAGCTGCCTGTTCTGCACAAAGGATGGG 321

Qy     241 gaccagcccacactgcagctgaaggaaaaggatataatggatttgtacaaccaacccgag 300
           || |||||    || |||||   ||||  | | ||||||||  |||||||| ||   ||
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Qy     301 cctgtgaagtcctttctcttctaccacagccagagtggcaggaactccaccttcgagtct 360
           |||||  ||  ||| |||||||||  ||||   |||||||  |  | ||| || || ||||||
Db     382 CCTGTAAAAGCCTCTCTCTTCTATCACAAGAAGAGTGGTACAACCTCTACATTTGAGTCT 441

Qy     361 gtggctttccctggctggttcatcgctgtcagctctgaaggaggctgtcctctcatcctt 420
           |  || |||||||| |||||||||||||||| |||||  ||||  ||||  || ||||| ||
Db     442 GCAGCCTTCCCTGGTTGGTTCATCGCTGTCTGCTCTAAAGGGAGCTGCCCACTCATTCTG 501

Qy     421 acccaagaactggggaaagccaacactactgactttgggttaactatgctgttttaa 477
           |||||||||||||| ||  |  ||  |||||||| | | | | | || |   ||||
Db     502 ACCCAAGAACTGGGGGAAATCTTCATCACTGACTTCGAGATGATTGTGGTACATTAA 558


RESULT   5
AX193660
LOCUS       AX193660                244 bp    DNA     linear   PAT 15-AUG-2001
DEFINITION  Sequence 82 from Patent WO0140291.
ACCESSION   AX193660
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VERSION     AX193660.1  GI:15211539
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 244)
  AUTHORS   Burgess,C.E., Prayaga,S.K., Shimkets,R.A., Rastelli,L.,
            Zerhusen,B.D. and Mezes,P.S.
  TITLE     Proteins and nucleic acids encoding the same
  JOURNAL   Patent: WO 0140291-A 82 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .244
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT       53 a     71 c     58 g     62 t
ORIGIN
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  Query Match           46.5%;  Score 222;  DB 6;  Length 244;
  Best Local Similarity 97.5%;  Pred. No. 3.2e-56;
  Matches  238;  Conservative    0;  Mismatches    0;  Indels    6;  Gaps    1;

Qy     188 tctacctgggcctgaatggactcaatctctgcctgatgtgtgctaaagtcggggaccagc 247
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TCTACCTGGGCCTGAATGGACTCAATCTCTGCCTGATGTGTGCTAAAGTCGGGGACCAGC 60

Qy     248 ccacactgcagctga------aggaaaaggatataatggatttgtacaaccaacccgagc 301
           |||||||||||||||      ||||||||||||||||||||||||||||||||||||||
Db      61 CCACACTGCAGCTGAAGCTTCAGGAAAAGGATATAATGGATTTGTACAACCAACCCGAGC 120

Qy     302 ctgtgaagtccttttctcttctaccacagccagagtggcaggaactccaccttcgagtctg 361
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CTGTGAAGTCCTTTCTCTTCTACCACAGCCAGAGTGGCAGGAACTCCACCTTCGAGTCTG 180

Qy     362 tggctttccctggctggttcatcgctgtcagctctgaaggaggctgtcctctcatcctta 421
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TGGCTTTCCCTGGCTGGTTCATCGCTGTCAGCTCTGAAGGAGGCTGTCCTCTCATCCTTA 240

Qy     422 ccca 425
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Db     241 CCCA 244
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RESULT   6
AC016724
LOCUS       AC016724              197308 bp    DNA     linear   PRI 09-JAN-2002
DEFINITION  Homo sapiens BAC clone RP11-339F22 from 2, complete sequence.
ACCESSION   AC016724
VERSION     AC016724.11  GI:14718389
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 197308)
  AUTHORS   Sulston,J.E. and Waterston,R.
  TITLE     Toward a complete human genome sequence
  JOURNAL   Genome Res. 8 (11), 1097-1108 (1998)
  MEDLINE   99063792
REFERENCE   2  (bases 1 to 197308)
  AUTHORS   Armstrong,J. and Haakenson,W.
  TITLE     The sequence of Homo sapiens BAC clone RP11-339F22
  JOURNAL   Unpublished (2001)
REFERENCE   3  (bases 1 to 197308)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-DEC-1999) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   4  (bases 1 to 197308)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JUL-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   5  (bases 1 to 197308)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JAN-2002) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT     On Jul 14, 2001 this sequence version replaced gi:13431151.
            -------------- Genome Center
                Center: Washington University Genome Sequencing Center
                Center code: WUGSC
                Web site: http://genome.wustl.edu/gsc
                Contact: sapiens@watson.wustl.edu
            -------------- Summary Statistics
                Center project name: H_NH0339F22
            --------------.

            NOTICE:  This sequence may not represent the entire insert of this
            clone.  It may be shorter because we only sequence overlapping
            clone sections once, or longer because we provide a small overlap
            between neighboring data submissions.

            This sequence was finished as follows unless otherwise noted:
            all regions were double stranded, sequenced with an alternate
            chemistry, or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by sequence
            from more than one subclone; and the assembly was confirmed by
            restriction digest.

            MAPPING INFORMATION:
            Mapping information for this clone was provided by Dr. John D.
            McPherson, Department of Genetics, Washington University, St. Louis
            MO.  For additional information about the map position of this
            sequence, see http://genome.wustl.edu/gsc

            SOURCE INFORMATION:
            The RPCI-11 human BAC library was made from the blood of one male
            donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
            Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
            approach for construction of bacterial artificial chromosome
            libraries.  Genomics 51:1-8.  The clone may be obtained either from
            Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
            and coworkers at the Roswell Park Cancer Institute
            (http://bacpac.med.buffalo.edu)
            VECTOR:  pBACe3.6
            NEIGHBORING SEQUENCE INFORMATION:
            The clone sequenced to the left is RP11-725J3; the clone sequenced
            to the right is RP11-97J14.  Actual start of this clone is at base
            position 1 of RP11-339F22; actual end is at base position 197308 of
            RP11-339F22.

            Data from AC084280 and AC024704 was used to finish this clone,
            AC016724.  Polymorphisms have been identified between AC024704 and
            AC016724.

            Sequence derived from pcr from base position 148683 to 149264.
FEATURES             Location/Qualifiers
     source          1. .197308
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="2"
                     /map="2"
                     /clone="RP11-339F22"
                     /clone_lib="RPCI-11"
     repeat_region   6. .275
                     /rpt_family="L1"
     repeat_region   274. .740
                     /rpt_family="L1"
     repeat_region   744. .907
                     /rpt_family="ERV1"
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repeat_region   917. .1361
                /rpt_family="L1"
repeat_region   1362. .1814
                /rpt_family="L1"
repeat_region   1838. .1952
                /rpt_family="ERV1"
repeat_region   2105. .2161
                /rpt_family="ERV1"
repeat_region   2245. .2587
                /rpt_family="L1"
repeat_region   2588. .2877
                /rpt_family="Alu"
repeat_region   2878. .3244
                /rpt_family="L1"
repeat_region   3235. .4195
                /rpt_family="L1"
repeat_region   3460. .3481
                /rpt_family="AT_rich"
repeat_region   4311. .4450
                /rpt_family="MIR"
repeat_region   4822. .4957
                /rpt_family="MER1_type"
repeat_region   5152. .5337
                /rpt_family="MER1_type"
repeat_region   6118. .7901
                /rpt_family="L2"
repeat_region   8008. .8145
                /rpt_family="L2"
repeat_region   8146. .8343
                /rpt_family="MER1_type"
repeat_region   8344. .8429
                /rpt_family="L2"
repeat_region   8661. .8827
                /rpt_family="ERV1"
repeat_region   8999. .9029
                /rpt_family="(T)n"
misc_feature    9003. .9030
                /note="similar to Homo sapiens EST BI091273
                (NID:g14509603)"
misc_feature    9011. .9031
                /note="similar to Homo sapiens EST AA587127 (NID:g2397941)
                nn70c01.s1"
misc_feature    9013. .9031
                /note="similar to Homo sapiens EST AI034379 (NID:g3255332)
                ox20g11.x1"
repeat_region   9167. .9564
                /rpt_family="L2"
repeat_region   10187. .10267
                /rpt_family="MIR"
repeat_region   11074. .11122
                /rpt_family="(CTG)n"
repeat_region   11587. .11611
                /rpt_family="(TG)n"
repeat_region   11651. .11884
                /rpt_family="MaLR"
repeat_region   12198. .12353
                /rpt_family="MIR"
repeat_region   12578. .12714
                /rpt_family="MER1_type"
repeat_region   13540. .13855
                /rpt_family="Alu"
repeat_region   13985. .14843
                /rpt_family="L1"
repeat_region   14923. .15243
                /rpt_family="MER2_type"
repeat_region   15980. .16836
                /rpt_family="L1"
repeat_region   17526. .17822
                /rpt_family="Alu"
repeat_region   18067. .18089
                /rpt_family="AT_rich"
repeat_region   19365. .19493
                /rpt_family="MER1_type"
repeat_region   19604. .20083
                /rpt_family="ERVL"
repeat_region   20084. .20447
                /rpt_family="MaLR"
repeat_region   20448. .21020
                /rpt_family="ERVL"
repeat_region   21033. .21306
                /rpt_family="L1"
repeat_region   21315. .21656
                /rpt_family="ERVL"
repeat_region   21906. .22079
                /rpt_family="ERVL"
repeat_region   22533. .22637
                /rpt_family="MER2_type"
repeat_region   22668. .22977
                /rpt_family="ERVL"
repeat_region   23349. .23852
                /rpt_family="L1"
repeat_region   25801. .25931
                /rpt_family="ERVL"
misc_feature    27616. .28020
                /note="match to EST AW937349 (NID:g8112771)"
repeat_region   28055. .28149
                /rpt_family="L2"
repeat_region   28743. .28984
                /rpt_family="CR1"
repeat_region   29010. .29092
                /rpt_family="L2"

  Query Match            45.2%;  Score 215.8;  DB 9;  Length 197308;
  Best Local Similarity  99.1%;  Pred. No. 4.6e-54;
  Matches  217;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    259 ctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtccttttctc 318
          ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  57056 CTTCAGGAAAAGGATATAATGGATTTGTACAACCAACCCGAGCCTGTGAAGTCCTTTCTC 57115

Qy    319 ttctaccacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctgg 378
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  57116 TTCTACCACAGCCAGAGTGGCAGGAACTCCACCTTCGAGTCTGTGGCTTTCCCTGGCTGG 57175

Qy    379 ttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaa 438
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  57176 TTCATCGCTGTCAGCTCTGAAGGAGGCTGTCCTCTCATCCTTACCCAAGAACTGGGGAAA 57235

Qy    439 gccaacactactgactttgggttaactatgctgttttaa 477
          |||||||||||||||||||||||||||||||||||||||
Db  57236 GCCAACACTACTGACTTTGGGTTAACTATGCTGTTTTAA 57274


RESULT   7
AX207820
LOCUS       AX207820                1073 bp    DNA     linear   PAT 31-AUG-2001
DEFINITION  Sequence 3 from Patent WO0157219.
ACCESSION   AX207820
VERSION     AX207820.1  GI:15422467
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   Debets,J.E., Timans,J.C., Bazan,J.F. and Kastelein,R.A.
  TITLE     Mammalian interleukin-1-delta and -epsilon. Their use in
            therapeutic and diagnostic methods
  JOURNAL   Patent: WO 0157219-A 3 09-AUG-2001;
            SCHERING CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .1073
                     /organism="unidentified"
                     /db_xref="taxon:32644"
                     /note="Description of Unknown Organism: primate; surmised
                     Homo sapiens"
     CDS             67. .576
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                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC60373.1"
                     /db_xref="GI:15422468"
                     /translation="MRGTPGDADGGGRAVYQSMCKPITGTINDLNQQVWTLQGQNLVA
                     VPRSDSVTPVTVAVITCKYPEALEQGRGDPIYLGIQNPEMCLYCEKVGEQPTLQLKEQ
                     KIMDLYGQPEPVKPFLFYRAKTGRTSTLESVAFPDWFIASSKRDQPIILTSELGKSYN
                     TAFELNIND"
BASE COUNT      281 a    241 c    255 g    296 t
ORIGIN


  Query Match             42.3%;  Score 202;  DB 6;  Length 1073;
  Best Local Similarity   67.1%;  Pred. No. 4.2e-50;
  Matches  302;  Conservative    0;  Mismatches  145;  Indels    3;  Gaps    1;

Qy      18 aattgacacacctcagcaggggagcattcaggatatcaatcatcgggtgtgggttcttca 77
           |||    | ||||      ||||  ||| | ||| | ||||| |  ||||||   |||||
Db     120 AATGTGTAAACCTATTACTGGGACTATTAATGATTTGAATCAGCAAGTGTGGACCCTTCA 179

Qy      78 ggaccagacgctcatagcagtcccgaggaaggaccgtatgtctccagtcactattgcctt 137
           ||  ||||  ||  | |||||  ||  | |  ||| || || | |||||||||  ||||  |
Db     180 GGGTCAGAACCTTGTGGCAGTTCCACGAAGTGACAGTGTGACCCCAGTCACTGTTGCTGT 239

Qy     138 aatctcatgccgacatgtggagacccttgagaaagacagagggaaccccatctacctggg 197
           |||  |||||    ||   ||| | |||||| ||| ||||||| | |||||  ||  ||||
Db     240 TATCACATGCAAGTATCCAGAGGCTCTTGAGCAAGGCAGAGGGGATCCCATTTATTTGGG 299

Qy     198 cctgaatggactcaatctctgcctgatgtgtgctaaagtcggggaccagcccacactgca 257
             |  |    |   | | ||  ||   ||||  || || || || |||||||||  ||||
Db     300 AATCCAGAATCCAGAAATGTGTTTGTATTGTGAGAAGGTTGGAGAACAGCCCACATTGCA 359

Qy     258 gctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttct 317
           |||  ||  ||  || | || |||||  ||||   ||||||||||||  |||||  ||||  ||
Db     360 GCTAAAAGAGCAGAAGATCATGGATCTGTATGGCCAACCCGAGCCCGTGAAACCCTTCCT 419

Qy     318 cttctaccacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctg 377
           |||||||    | ||| ||| |||| |||||||  |  ||||||||||  |||||  | |||
Db     420 TTTCTACCGTGCCAAGACTGGTAGGACCTCCACCCTTGAGTCTGTGGCCTTCCCGGACTG 479

Qy     378 gttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaa 437
           ||||||   ||  |  |||  |  |||  |   ||  |||| || ||   |||||| |||||
Db     480 GTTCAT---TGCCTCCTCCAAGAGAGACCAGCCCATCATTCTGACTTCAGAACTTGGGAA 536

Qy     438 agccaacactactgactttgggttaactat 467
             |  |||  |||| |||||  |||| |||
Db     537 GTCATACAACACTGCCTTTGAATTAAATAT 566


RESULT   8
AF206696
LOCUS       AF206696                1177 bp    mRNA    linear   PRI 01-NOV-2001
DEFINITION  Homo sapiens interleukin-1 epsilon (IL1E) mRNA, complete cds.
ACCESSION   AF206696
VERSION     AF206696.1  GI:11493847
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1177)
  AUTHORS   Debets,R., Timans,J.C., Homey,B., Zurawski,S., Sana,T.R., Lo,S.,
            Wagner,J., Edwards,G., Clifford,T., Menon,S., Bazan,J.F. and
            Kastelein,R.A.
  TITLE     Two novel IL-1 family members, IL-1 delta and IL-1 epsilon,
            function as an antagonist and agonist of NF-kappa B activation
            through the orphan IL-1 receptor-related protein 2
  JOURNAL   J. Immunol. 167 (3), 1440-1446 (2001)
  MEDLINE   21359532
   PUBMED   11466363
REFERENCE   2  (bases 1 to 1177)
  AUTHORS   Debets,R., Timans,J.C., Zurawski,S., Bazan,J.F. and Kastelein,R.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-NOV-1999) Molecular Biology, DNAX Research Institute
            of Molecular and Cellular Biology, Inc., 901 California Avenue,
            Palo Alto, CA 94304-1104, USA
FEATURES             Location/Qualifiers
     source          1. .1177
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /tissue_type="airway epithelial cells induced with TNF
                     alpha and IFN"
     gene            1. .1177
                     /gene="IL1E"
     CDS             67. .576
                     /gene="IL1E"
                     /note="interleukin-1-like protein; similar to IL-1a, IL-1b
                     and IL-1ra; highly expressed in skin tissue; acts through
                     an IL-1-like receptor IL-1Rrp2 resulting in IL-1-like
                     signaling cascade; antagonized by IL-1d"
                     /codon_start=1
                     /product="interleukin-1 epsilon"
                     /protein_id="AAG35670.1"
                     /db_xref="GI:11493848"
                     /translation="MRGTPGDADGGGRAVYQSMCKPITGTINDLNQQVWTLQGQNLVA
                     VPRSDSVTPVTVAVITCKYPEALEQGRGDPIYLGIQNPEMCLYCEKVGEQPTLQLKEQ
                     KIMDLYGQPEPVKPFLFYRAKTGRTSTLESVAFPDWFIASSKRDQPIILTSELGKSYN
                     TAFELNIND"
BASE COUNT      320 a    249 c    267 g    341 t
ORIGIN


  Query Match             42.3%;  Score 202;  DB 9;  Length 1177;
  Best Local Similarity   67.1%;  Pred. No. 4.3e-50;
  Matches  302;  Conservative    0;  Mismatches  145;  Indels    3;  Gaps    1;

Qy      18 aattgacacacctcagcaggggagcattcaggatatcaatcatcgggtgtgggttcttca 77
           |||    | ||||      ||||  ||| | ||| | ||||| |  ||||||   |||||
Db     120 AATGTGTAAACCTATTACTGGGACTATTAATGATTTGAATCAGCAAGTGTGGACCCTTCA 179

Qy      78 ggaccagacgctcatagcagtcccgaggaaggaccgtatgtctccagtcactattgcctt 137
           ||  ||||  ||  | |||||  ||  | |  ||| || || | |||||||||  ||||  |
Db     180 GGGTCAGAACCTTGTGGCAGTTCCACGAAGTGACAGTGTGACCCCAGTCACTGTTGCTGT 239

Qy     138 aatctcatgccgacatgtggagacccttgagaaagacagagggaaccccatctacctggg 197
           |||  |||||    ||   ||| | |||||| ||| ||||||| | |||||  ||  ||||
Db     240 TATCACATGCAAGTATCCAGAGGCTCTTGAGCAAGGCAGAGGGGATCCCATTTATTTGGG 299

Qy     198 cctgaatggactcaatctctgcctgatgtgtgctaaagtcggggaccagcccacactgca 257
             |  |    |   | | ||  ||   ||||  || || || || |||||||||  ||||
Db     300 AATCCAGAATCCAGAAATGTGTTTGTATTGTGAGAAGGTTGGAGAACAGCCCACATTGCA 359

Qy     258 gctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttct 317
           |||  ||  ||  || | || |||||  ||||   ||||||||||||  |||||  ||||  ||
Db     360 GCTAAAAGAGCAGAAGATCATGGATCTGTATGGCCAACCCGAGCCCGTGAAACCCTTCCT 419

Qy     318 cttctaccacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctg 377
           |||||||    | ||| ||| |||| |||||||  |  ||||||||||  |||||  | |||
Db     420 TTTCTACCGTGCCAAGACTGGTAGGACCTCCACCCTTGAGTCTGTGGCCTTCCCGGACTG 479

Qy     378 gttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaa 437
           ||||||   ||  |  |||  |  |||  |   ||  |||| || ||   |||||| |||||
Db     480 GTTCAT---TGCCTCCTCCAAGAGAGACCAGCCCATCATTCTGACTTCAGAACTTGGGAA 536

Qy     438 agccaacactactgactttgggttaactat 467
             |  |||  |||| |||||  |||| |||
Db     537 GTCATACAACACTGCCTTTGAATTAAATAT 566


RESULT   9
E54910
LOCUS       E54910                  1183 bp    DNA     linear   PAT 07-FEB-2001
DEFINITION  Interleukin-1 receptor antagonist beta (IL-1RA-beta) polypeptide.
ACCESSION   E54910
VERSION     E54910.1  GI:13019313
KEYWORDS    JP 2000032990-A/1.
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SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1183)
  AUTHORS   Peter,R.Y.
  TITLE     Interleukin-1 receptor antagonist beta (IL-1RA-beta) polypeptide
  JOURNAL   Patent: JP 2000032990-A 1 02-FEB-2000;
            SMITHKLINE BEECHAM CORP
COMMENT     OS   Unidentified
            PN   JP 2000032990-A/1
            PD   02-FEB-2000
            PF   14-MAY-1999 JP 1999134172
            PR   28-JAN-1997 US    08/790032
            PI   PETER R YOUNG
            PC   C12N15/09,A61K38/00,A61K39/395,A61K45/00,C07K14/545,C07K16/24,
            PC   C12P21/02,
            PC   C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53//A61K31/00, PC
              A61K31/00,
            PC   A61K31/00,A61K31/00,C12N15/00,A61K37/02
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .1183
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .1183
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                      /db_xref="taxon:32644"
BASE COUNT      329 a    249 c    269 g    336 t
ORIGIN
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  Query Match             42.3%;  Score 202;  DB 6;  Length 1183;
  Best Local Similarity   67.1%;  Pred. No. 4.3e-50;
  Matches  302;  Conservative    0;  Mismatches  145;  Indels    3;  Gaps    1;

Qy      18 aattgacacacctcagcaggggagcattcaggatatcaatcatcgggtgtgggttcttca 77
           |||    | ||||      ||||  ||| | ||| | |||||  |  ||||||   |||||
Db     128 AATGTGTAAACCTATTACTGGGACTATTAATGATTTGAATCAGCAAGTGTGGACCCTTCA 187

Qy      78 ggaccagacgctcatagcagtcccgaggaaggaccgtatgtctccagtcactattgcctt 137
           ||  ||||  ||  | |||||  ||  | |  ||| || || | |||||||||  ||||  |
Db     188 GGGTCAGAACCTTGTGGCAGTTCCACGAAGTGACAGTGTGACCCCAGTCACTGTTGCTGT 247

Qy     138 aatctcatgccgacatgtggagacccttgagaaagacagagggaaccccatctacctggg 197
           |||  |||||    ||   ||| | |||||| ||| ||||||| | |||||  ||  ||||
Db     248 TATCACATGCAAGTATCCAGAGGCTCTTGAGCAAGGCAGAGGGGATCCCATTTATTTGGG 307

Qy     198 cctgaatggactcaatctctgcctgatgtgtgctaaagtcggggaccagcccacactgca 257
           |  |    |   | | ||  ||   ||||  || || || || |||||||||  ||||
Db     308 AATCCAGAATCCAGAAATGTGTTTGTATTGTGAGAAGGTTGGAGAACAGCCCACATTGCA 367

Qy     258 gctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttct 317
           ||| || ||  || | || ||||||  ||||   ||||||||||| |||||  |||| ||
Db     368 GCTAAAAGAGCAGAAGATCATGGATCTGTATGGCCAACCCGAGCCCGTGAAACCCTTCCT 427

Qy     318 cttctaccacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctg 377
           |||||||    | ||| ||| |||| |||||||  | ||||||||||  |||||  | |||
Db     428 TTTCTACCGTGCCAAGACTGGTAGGACCTCCACCCTTGAGTCTGTGGCCTTCCCGGACTG 487

Qy     378 gttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaa 437
           ||||||   || |  |||  |  ||| |   ||  |||| || ||   ||||||  |||||
Db     488 GTTCAT---TGCCTCCTCCAAGAGAGACCAGCCCATCATTCTGACTTCAGAACTTGGGAA 544

Qy     438 agccaacactactgactttgggttaactat 467
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Db     545 GTCATACAACACTGCCTTTGAATTAAATAT 574
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RESULT  10
AF200492
LOCUS       AF200492               1183 bp    mRNA    linear   PRI 11-MAY-2000
DEFINITION  Homo sapiens interleukin-1 homolog 1 mRNA, complete cds.
ACCESSION   AF200492
VERSION     AF200492.1  GI:7769111
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1183)
  AUTHORS   Kumar,S., McDonnell,P.C., Lehr,R., Tierney,L., Tzimas,M.N.,
            Griswold,D.E., Capper,E.A., Tal-Singer,R., Wells,G.I., Doyle,M.L.
            and Young,P.R.
  TITLE     Identification and initial characterization of four novel members
            of the interleukin-1 family
  JOURNAL   J. Biol. Chem. 275 (14), 10308-10314 (2000)
  MEDLINE   20209405
   PUBMED   10744718
REFERENCE   2  (bases 1 to 1183)
  AUTHORS   Kumar,S., McDonnell,P.C. and Young,P.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-NOV-1999) Bone and Cartilage Biology, UW 2109,
            SmithKline Beecham Pharmaceuticals, 709 Swedeland Rd., King of
            Prussia, PA 19406, USA
FEATURES             Location/Qualifiers
     source          1. .1183
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="2"
                     /map="2q12-q21; close to IL-1 locus"
                     /cell_type="primary keratinocytes; epithelial"
     CDS             75. .584
                     /note="cytokine; IL-1H1"
                     /codon_start=1
                     /product="interleukin-1 homolog 1"
                     /protein_id="AAF69248.1"
                     /db_xref="GI:7769112"
                     /translation="MRGTPGDADGGGRAVYQSMCKPITGTINDLNQQVWTLQGQNLVA
                     VPRSDSVTPVTVAVITCKYPEALEQGRGDPIYLGIQNPEMCLYCEKVGEQPTLQLKEQ
                     KIMDLYGQPEPVKPFLFYRAKTGRTSTLESVAFPDWFIASSKRDQPIILTSELGKSYN
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BASE COUNT      329 a    249 c    269 g    336 t
ORIGIN
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  Query Match             42.3%;  Score 202;  DB 9;  Length 1183;
  Best Local Similarity   67.1%;  Pred. No. 4.3e-50;
  Matches  302;  Conservative    0;  Mismatches  145;  Indels    3;  Gaps    1;

Qy      18 aattgacacacctcagcaggggagcattcaggatatcaatcatcgggtgtgggttcttca 77
           |||    | ||||      ||||  ||| | ||| | |||||  |  ||||||   |||||
Db     128 AATGTGTAAACCTATTACTGGGACTATTAATGATTTGAATCAGCAAGTGTGGACCCTTCA 187

Qy      78 ggaccagacgctcatagcagtcccgaggaaggaccgtatgtctccagtcactattgcctt 137
           ||  ||||  ||  | |||||  ||  | |  ||| || || | |||||||||  ||||  |
Db     188 GGGTCAGAACCTTGTGGCAGTTCCACGAAGTGACAGTGTGACCCCAGTCACTGTTGCTGT 247

Qy     138 aatctcatgccgacatgtggagacccttgagaaagacagagggaaccccatctacctggg 197
           |||  |||||    ||   ||| | |||||| ||| ||||||| | |||||  ||  ||||
Db     248 TATCACATGCAAGTATCCAGAGGCTCTTGAGCAAGGCAGAGGGGATCCCATTTATTTGGG 307

Qy     198 cctgaatggactcaatctctgcctgatgtgtgctaaagtcggggaccagcccacactgca 257
           |  |    |   | | ||  ||   ||||  || || || || |||||||||  ||||
Db     308 AATCCAGAATCCAGAAATGTGTTTGTATTGTGAGAAGGTTGGAGAACAGCCCACATTGCA 367

Qy     258 gctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttct 317
           ||| || ||  || | || ||||||  ||||   ||||||||||| |||||  |||| ||
Db     368 GCTAAAAGAGCAGAAGATCATGGATCTGTATGGCCAACCCGAGCCCGTGAAACCCTTCCT 427

Qy     318 cttctaccacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctg 377
           |||||||    | ||| ||| |||| |||||||  | ||||||||||  |||||  | |||
Db     428 TTTCTACCGTGCCAAGACTGGTAGGACCTCCACCCTTGAGTCTGTGGCCTTCCCGGACTG 487

Qy     378 gttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaa 437
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Db    488 GTTCAT---TGCCTCCTCCAAGAGAGACCAGCCCATCATTCTGACTTCAGAACTTGGGAA 544

Qy    438 agccaacactactgactttgggttaactat 467
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Db    545 GTCATACAACACTGCCTTTGAATTAAATAT 574


RESULT  11
AX193587
LOCUS       AX193587                 520 bp    DNA     linear   PAT 15-AUG-2001
DEFINITION  Sequence 9 from Patent WO0140291.
ACCESSION   AX193587
VERSION     AX193587.1  GI:15211517
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 520)
  AUTHORS   Burgess,C.E., Prayaga,S.K., Shimkets,R.A., Rastelli,L.,
            Zerhusen,B.D. and Mezes,P.S.
  TITLE     Proteins and nucleic acids encoding the same
  JOURNAL   Patent: WO 0140291-A 9 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .520
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      147 a    127 c    112 g    134 t
ORIGIN


  Query Match             28.1%;  Score 134.2;  DB 6;  Length 520;
  Best Local Similarity   56.8%;  Pred. No. 1.3e-29;
  Matches  247;  Conservative    0;  Mismatches  188;  Indels    0;  Gaps    0;

Qy     43 attcaggatatcaatcatcgggtgtgggttcttcaggaccagacgctcatagcagtcccg 102
          ||||  |||      ||   ||||||||| ||    |   |  |  | |||||||  ||
Db     79 ATTCGTGATTCTCGACAGATGGTGTGGGTCCTGAGTGGAAATTCTTTAATAGCAGCTCCT 138

Qy    103 aggaaggaccgtatgtctccagtcactattgccttaatctcatgccgacatgtggagacc 162
          |    | | ||    || |||||| ||    |||||  | ||  || | |    ||   |
Db    139 CTTAGCCGCAGCATTAAGCCTGTCACTCTTCATTTAATAGCCTGTAGAGACACAGAATTC 198

Qy    163 cttgagaaagacagagggaaccccatctacctgggcctgaatggactcaatctctgcctg 222
          |||  || || |  || ||     | ||||||||  | || |||    |||||||  ||
Db    199 AGTGACAAGGAAAAGGGTAATATGGTTTACCTGGGAATCAAGGGAAAAGATCTCTGTCTC 258

Qy    223 atgtgtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggatataatggat 282
          | |||||  || |   || | |||| ||  ||||||| ||||||||  |||| |||||
Db    259 TTCTGTGCAGAAATTCAGGGCAAGCCTACTTTGCAGCTTAAGGAAAAAAATATCATGGAC 318

Qy    283 ttgtacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcagg 342
          ||||    |     |  |   |||| |||||||||| | |||||   |    |||
Db    319 CTGTATGTGGAGAAGAAAGCACAGAAGCCCTTTCTCTTTTTCCACAATAAAGAAGGCTCC 378

Qy    343 aactccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaagga 402
          |  ||   |||  |||| ||  ||| ||||||||||||||| ||   |  | |  |  |
Db    379 ACTTCTGTCTTTCAGTCAGTCTCTTACCCTGGCTGGTTCATAGCCACCTCCACCACATCA 438

Qy    403 ggctgtcctctcatccttacccaagaactggggaaagccaacactactgactttgggtta 462
          ||    ||  || | || ||| | ||    || | | | || |  ||| ||||    |||
Db    439 GGACAGCCCATCTTTCTCACCAAGGAGAGAGGCATAACTAATAACACTAACTTCTACTTA 498

Qy    463 actatgctgttttaa 477
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Db    499 GATTCTGTGGAATAA 513


RESULT  12
AX052581
LOCUS       AX052581                 585 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 1 from Patent WO0071720.
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ACCESSION   AX052581
VERSION     AX052581.1  GI:12226796
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 585)
  AUTHORS   Sims,J.E. and Renshaw,B.R.
  TITLE     Il-1 eta dna and polypeptides
  JOURNAL   Patent: WO 0071720-A 1 30-NOV-2000;
            IMMUNEX CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .585
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             112. .585
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC21807.1"
                     /db_xref="GI:12226797"
                     /translation="MNPQREAAPKSYAIRDSRQMVWVLSGNSLIAAPLSRSIKPVTLH
                     LIACRDTEFSDKEKGNMVYLGIKGKDLCLFCAEIQGKPTLQLKEKNIMDLYVEKKAQK
                     PFLFFHNKEGSTSVFQSVSYPGWFIATSTTSGQPIFLTKERGITNNTNFYLDSVE"
BASE COUNT      161 a    154 c    110 g    160 t
ORIGIN


  Query Match             28.1%;  Score 134.2;  DB 6;  Length 585;
  Best Local Similarity   56.8%;  Pred. No. 1.3e-29;
  Matches  247;  Conservative    0;  Mismatches  188;  Indels    0;  Gaps    0;

Qy     43 attcaggatatcaatcatcgggtgtgggttcttcaggaccagacgctcatagcagtcccg 102
          ||||  |||      ||   ||||||||| ||    |   |  |  | |||||||  ||
Db    151 ATTCGTGATTCTCGACAGATGGTGTGGGTCCTGAGTGGAAATTCTTTAATAGCAGCTCCT 210

Qy    103 aggaaggaccgtatgtctccagtcactattgccttaatctcatgccgacatgtggagacc 162
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Db    211 CTTAGCCGCAGCATTAAGCCTGTCACTCTTCATTTAATAGCCTGTAGAGACACAGAATTC 270

Qy    163 cttgagaaagacagagggaaccccatctacctgggcctgaatggactcaatctctgcctg 222
          |||  || || |  || ||     | ||||||||  | || |||    |||||||  ||
Db    271 AGTGACAAGGAAAAGGGTAATATGGTTTACCTGGGAATCAAGGGAAAAGATCTCTGTCTC 330

Qy    223 atgtgtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggatataatggat 282
          | |||||  || |   || | |||| ||  ||||||| ||||||||  |||| |||||
Db    331 TTCTGTGCAGAAATTCAGGGCAAGCCTACTTTGCAGCTTAAGGAAAAAAATATCATGGAC 390

Qy    283 ttgtacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcagg 342
          ||||    |     |  |   |||| |||||||||| | |||||   |    |||
Db    391 CTGTATGTGGAGAAGAAAGCACAGAAGCCCTTTCTCTTTTTCCACAATAAAGAAGGCTCC 450

Qy    343 aactccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaagga 402
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Db    451 ACTTCTGTCTTTCAGTCAGTCTCTTACCCTGGCTGGTTCATAGCCACCTCCACCACATCA 510

Qy    403 ggctgtcctctcatccttacccaagaactggggaaagccaacactactgactttgggtta 462
          ||    ||  || | || ||| | ||    || | | | || |  ||| ||||    |||
Db    511 GGACAGCCCATCTTTCTCACCAAGGAGAGAGGCATAACTAATAACACTAACTTCTACTTA 570

Qy    463 actatgctgttttaa 477
          |    ||   |||
Db    571 GATTCTGTGGAATAA 585


RESULT  13
AF201833
LOCUS       AF201833                 585 bp    mRNA    linear   PRI 16-JAN-2000
DEFINITION  Homo sapiens FIL1 eta mRNA, complete cds.
ACCESSION   AF201833
VERSION     AF201833.1  GI:6694393
KEYWORDS    .
SOURCE      human.
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 585)
  AUTHORS   Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garka,K.E. and
            Sims,J.E.
  TITLE     Four new members expand the interleukin-1 superfamily
  JOURNAL   J. Biol. Chem. 275 (2), 1169-1175 (2000)
  MEDLINE   20092888
REFERENCE   2  (bases 1 to 585)
  AUTHORS   Sims,J.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-NOV-1999) Molecular Genetics, Immunex Corporation, 51
            University Street, Seattle, WA 98101, USA
FEATURES             Location/Qualifiers
     source          1. .585
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="2"
                     /map="2q; between D2S121 and D2S110"
     CDS             112. .585
                     /note="similar to IL-1"
                     /codon_start=1
                     /product="FIL1 eta"
                     /protein_id="AAF25213.1"
                     /db_xref="GI:6694394"
                     /translation="MNPQREAAPKSYAIRDSRQMVWVLSGNSLIAAPLSRSIKPVTLH
                     LIACRDTEFSDKEKGNMVYLGIKGKDLCLFCAEIQGKPTLQLKEKNIMDLYVEKKAQK
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BASE COUNT      161 a    154 c    110 g    160 t
ORIGIN
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  Query Match             28.1%;  Score 134.2;  DB 9;  Length 585;
  Best Local Similarity   56.8%;  Pred. No. 1.3e-29;
  Matches  247;  Conservative    0;  Mismatches  188;  Indels    0;  Gaps    0;

Qy      43 attcaggatatcaatcatcgggtgtgggttcttcaggaccagacgctcatagcagtcccg 102
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Db     151 ATTCGTGATTCTCGACAGATGGTGTGGGTCCTGAGTGGAAATTCTTTAATAGCAGCTCCT 210

Qy     103 aggaaggaccgtatgtctccagtcactattgccttaatctcatgccgacatgtggagacc 162
             |    | | ||    || |||||| ||   |||||  | ||  || |    ||   |
Db     211 CTTAGCCGCAGCATTAAGCCTGTCACTCTTCATTTAATAGCCTGTAGAGACACAGAATTC 270

Qy     163 cttgagaaagacagagggaaccccatctacctgggcctgaatggactcaatctctgcctg 222
             ||| || || |  || ||     | ||||||||  | || |||    |||||||  ||
Db     271 AGTGACAAGGAAAAGGGTAATATGGTTTACCTGGGAATCAAGGGAAAAGATCTCTGTCTC 330

Qy     223 atgtgtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggatataatggat 282
             | |||||  || |   || | |||| ||  ||||||| ||||||||  |||| |||||
Db     331 TTCTGTGCAGAAATTCAGGGCAAGCCTACTTTGCAGCTTAAGGAAAAAAATATCATGGAC 390

Qy     283 ttgtacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcagg 342
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Db     391 CTGTATGTGGAGAAGAAAGCACAGAAGCCCTTTCTCTTTTTCCACAATAAAGAAGGCTCC 450

Qy     343 aactccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaagga 402
           |  ||   |||  |||| ||  ||| ||||||||||||||| ||   |  | |   |  |
Db     451 ACTTCTGTCTTTCAGTCAGTCTCTTACCCTGGCTGGTTCATAGCCACCTCCACCACATCA 510

Qy     403 ggctgtcctctcatccttacccaagaactggggaaagccaacactactgactttgggtta 462
           ||    ||  || | || ||| | ||    || | | | || |  ||| ||||   |||
Db     511 GGACAGCCCATCTTTCTCACCAAGGAGAGAGGCATAACTAATAACACTAACTTCTACTTA 570

Qy     463 actatgctgttttaa 477
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Db     571 GATTCTGTGGAATAA 585
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RESULT  14
AX167128
LOCUS       AX167128               1244 bp    DNA     linear   PAT 03-JUL-2001
DEFINITION  Sequence 1 from Patent WO0142305.
ACCESSION   AX167128
VERSION     AX167128.1  GI:14596616
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1244)
  AUTHORS   Welcher,A.A., Luethy,R. and Jing,S.
  TITLE     Interleukin-1 receptor antagonist-like molecules and uses thereof
  JOURNAL   Patent: WO 0142305-A 1 14-JUN-2001;
            Amgen Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1244
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             301. .774
                     /note="unnamed protein product"
                     /codon_start=1
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                     /db_xref="GI:14596617"
                     /translation="MNPQREAAPKSYAIRDSRQMVWVLSGNSLIAAPLSRSIKPVTLH
                     LIACRDTEFSDKEKGNMVYLGIKGKDLCLFCAEIQGKPTLQLKEKNIMDLYVEKKAQK
                     PFLFFHNKEGSTSVFQSVSYPGWFIATSTTSGQPIFLTKERGITNNTNFYLDSVE"
BASE COUNT      354 a    323 c    227 g    340 t
ORIGIN
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  Query Match             28.1%;  Score 134.2;  DB 6;  Length 1244;
  Best Local Similarity   56.8%;  Pred. No. 1.4e-29;
  Matches  247;  Conservative    0;  Mismatches  188;  Indels    0;  Gaps    0;

Qy      43 attcaggatatcaatcatcgggtgtgggttcttcaggaccagacgctcatagcagtcccg 102
           ||||  |||       ||   |||||||||  ||    |   |  | | |||||||  ||
Db     340 ATTCGTGATTCTCGACAGATGGTGTGGGTCCTGAGTGGAAATTCTTTAATAGCAGCTCCT 399

Qy     103 aggaaggaccgtatgtctccagtcactattgccttaatctcatgccgacatgtggagacc 162
             |    | | ||    || |||||| ||   |||||  | ||  || |    ||   |
Db     400 CTTAGCCGCAGCATTAAGCCTGTCACTCTTCATTTAATAGCCTGTAGAGACACAGAATTC 459

Qy     163 cttgagaaagacagagggaaccccatctacctgggcctgaatggactcaatctctgcctg 222
             ||| || || |  || ||     | ||||||||  | || |||    |||||||  ||
Db     460 AGTGACAAGGAAAAGGGTAATATGGTTTACCTGGGAATCAAGGGAAAAGATCTCTGTCTC 519

Qy     223 atgtgtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggatataatggat 282
             | |||||  || |   || | |||| ||  ||||||| ||||||||  |||| |||||
Db     520 TTCTGTGCAGAAATTCAGGGCAAGCCTACTTTGCAGCTTAAGGAAAAAAATATCATGGAC 579

Qy     283 ttgtacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcagg 342
             ||||     |      |  |   |||| |||||||||| | |||||   |    |||
Db     580 CTGTATGTGGAGAAGAAAGCACAGAAGCCCTTTCTCTTTTTCCACAATAAAGAAGGCTCC 639

Qy     343 aactccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaagga 402
           |  ||   |||  |||| ||  ||| ||||||||||||||| ||   |  | |   |  |
Db     640 ACTTCTGTCTTTCAGTCAGTCTCTTACCCTGGCTGGTTCATAGCCACCTCCACCACATCA 699

Qy     403 ggctgtcctctcatccttacccaagaactggggaaagccaacactactgactttgggtta 462
           ||    ||  || | || ||| | ||    || | | | || |  ||| ||||   |||
Db     700 GGACAGCCCATCTTTCTCACCAAGGAGAGAGGCATAACTAATAACACTAACTTCTACTTA 759

Qy     463 actatgctgttttaa 477
             |    ||   |||
Db     760 GATTCTGTGGAATAA 774
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RESULT  15
AR137703
LOCUS       AR137703               746 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 1 from patent US 6197551.
ACCESSION   AR137703
VERSION     AR137703.1  GI:14479212
KEYWORDS    .
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 746)
  AUTHORS   Busfield,S.J.
  TITLE     Spoil-1 protein and nucleic acid molecules and uses therefor
  JOURNAL   Patent: US 6197551-A 1 06-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .746
                     /organism="unknown"
BASE COUNT      275 a    150 c    142 g    179 t
ORIGIN
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Query Match 27.1%; Score 129.2; DB 6; Length 746;
Best Local Similarity 73.9%; Pred. No. 4.5e-28;
Matches 164; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

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          ||| |  |||||  | | ||||||||  ||||||||  ||   || |||||  ||  ||| |
Db    210 CAGTTCCAGGAAGGGAACATAATGGAAATGTACAACAAAAAGGAACCTGTAAAAGCCTCT 269

Qy    316 ctcttctaccacagccagagtggcaggaactccaccttcgagtctgtggctttccctggc 375
          ||||||||  ||||   |||||||  |  | |||  ||  ||  |||||||  ||  ||||||||
Db    270 CTCTTCTATCACAAGAAGAGTGGTACAACCTCTACATTTGAGTCTGCAGCCTTCCCTGGT 329

Qy    376 tggttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaagaactgggg 435
          ||||||||||||||  |||||  ||||  ||||  ||  |||||  ||  ||||||||||||||
Db    330 TGGTTCATCGCTGTCTGCTCTAAAGGGAGCTGCCCACTCATTCTGACCCAAGAACTGGGG 389

Qy    436 aaagccaacactactgactttgggttaactatgctgttttaa 477
            ||  |  ||  ||||||||  |  |  |  |  ||  |   ||||
Db    390 GAAATCTTCATCACTGACTTCGAGATGATTGTGGTACATTAA 431
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Search completed: June 21, 2002, 11:56:23
Job time: 15396 sec

08 12/1/04 (01)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2002, 07:39:47 ; Search time 2781.56 Seconds
(without alignments)
1602.465 Million cell updates/sec

Title: US-09-763-498-5
Perfect score: 213
Sequence: 1 gaaaaggatataatggattt.....ggttaactatgctgttttaa 213

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	213	100.0	477	9	AF201831	AF201831 Homo sapi
	2	213	100.0	197308	9	AC016724	AC016724 Homo sapi
	3	175	82.2	391	6	AX193589	AX193589 Sequence
	4	161	75.6	244	6	AX193660	AX193660 Sequence
	5	125	58.7	483	10	AF200493	AF200493 Mus muscu
	6	125	58.7	746	6	AR137703	AR137703 Sequence
	7	125	58.7	795	10	AF206697	AF206697 Mus muscu
	8	122.8	57.7	243	6	AR137705	AR137705 Sequence
	9	122.8	57.7	294	6	AR137704	AR137704 Sequence
	10	106.4	50.0	186587	2	AC106686	AC106686 Rattus no
	11	97.4	45.7	1073	6	AX207820	AX207820 Sequence
	12	97.4	45.7	1177	9	AF206696	AF206696 Homo sapi
	13	97.4	45.7	1183	6	E54910	E54910 Interleukin
	14	97.4	45.7	1183	9	AF200492	AF200492 Homo sapi
c	15	75.2	35.3	184626	2	AC096974	AC096974 Rattus no
	16	65.8	30.9	520	6	AX193587	AX193587 Sequence
	17	65.8	30.9	585	6	AX052581	AX052581 Sequence
	18	65.8	30.9	585	9	AF201833	AF201833 Homo sapi
	19	65.8	30.9	1244	6	AX167128	AX167128 Sequence
c	20	65.8	30.9	197308	9	AC016724	AC016724 Homo sapi
	21	64.6	30.3	329	6	AX193643	AX193643 Sequence
	22	51	23.9	1036	4	AY026462	AY026462 Canis fam
	23	49.8	23.4	574	4	S68977	S68977 sIL-1ra=int
	24	49.4	23.2	563	4	AF216526	AF216526 Canis fam
	25	48.8	22.9	465	6	AX080399	AX080399 Sequence
	26	48.8	22.9	468	6	AX069335	AX069335 Sequence
	27	48.8	22.9	471	10	AF230378	AF230378 Mus muscu
	28	48.8	22.9	1283	10	AF200495	AF200495 Mus muscu
	29	48.8	22.9	1284	6	AX080392	AX080392 Sequence
	30	48.8	22.9	1284	10	MMU250429	AJ250429 Mus muscu
	31	48.6	22.8	218	6	AX193630	AX193630 Sequence
	32	48.6	22.8	221	4	AF072476	AF072476 Equus cab
	33	48.6	22.8	531	6	AX127225	AX127225 Sequence
	34	48.6	22.8	603	6	AX127227	AX127227 Sequence
	35	48.6	22.8	1590	4	D83714	D83714 Equus cabal
	36	48.6	22.8	1590	6	E15594	E15594 cDNA encodi
	37	48.6	22.8	1614	4	ECU92482	U92482 Equus cabal
	38	48.6	22.8	1614	6	AX127224	AX127224 Sequence
	39	47.2	22.2	8032	6	AX069334	AX069334 Sequence
	40	46.8	22.0	357	6	AX069304	AX069304 Sequence
	41	46.8	22.0	465	6	AX080398	AX080398 Sequence
	42	46.8	22.0	468	9	AF230377	AF230377 Homo sapi
	43	46.8	22.0	985	6	AX069305	AX069305 Sequence
	44	46.8	22.0	1025	6	AX207818	AX207818 Sequence
	45	46.8	22.0	1282	6	AX069307	AX069307 Sequence

ALIGNMENTS

RESULT 1
AF201831
LOCUS AF201831 477 bp mRNA linear PRI 16-JAN-2000
DEFINITION Homo sapiens FIL1 epsilon mRNA, complete cds.
ACCESSION AF201831
VERSION AF201831.1 GI:6694389
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 477)
AUTHORS Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garka,K.E. and Sims,J.E.
TITLE Four new members expand the interleukin-1 superfamily
JOURNAL J. Biol. Chem. 275 (2), 1169-1175 (2000)
MEDLINE 20092888
REFERENCE 2 (bases 1 to 477)
AUTHORS Sims,J.E.
TITLE Direct Submission
JOURNAL Submitted (04-NOV-1999) Molecular Genetics, Immunex Corporation, 51 University Street, Seattle, WA 98101, USA
FEATURES Location/Qualifiers

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     source          1. .477
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="2"
                     /map="2q; between D2S121 and D2S110"
     CDS             1. .477
                     /note="similar to IL-1"
                     /codon_start=1
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                     /protein_id="AAF25211.1"
                     /db_xref="GI:6694390"
                     /translation="MEKALKIDTPQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTI
                     ALISCRHVETLEKDRGNPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPV
                     KSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTMLF"
BASE COUNT      124 a    123 c    117 g    113 t
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  Query Match             100.0%;  Score 213;  DB 9;  Length 477;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-56;
  Matches  213;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db     265 GAAAAGGATATAATGGATTTGTACAACCAACCCGAGCCTGTGAAGTCCTTTCTCTTCTAC 324

Qy      61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     325 CACAGCCAGAGTGGCAGGAACTCCACCTTCGAGTCTGTGGCTTTCCCTGGCTGGTTCATC 384

Qy     121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     385 GCTGTCAGCTCTGAAGGAGGCTGTCCTCTCATCCTTACCCAAGAACTGGGGAAAGCCAAC 444

Qy     181 actactgactttgggttaactatgctgttttaa 213
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Db     445 ACTACTGACTTTGGGTTAACTATGCTGTTTTAA 477
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RESULT   2
AC016724
LOCUS       AC016724               197308 bp    DNA     linear   PRI 09-JAN-2002
DEFINITION  Homo sapiens BAC clone RP11-339F22 from 2, complete sequence.
ACCESSION   AC016724
VERSION     AC016724.11  GI:14718389
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 197308)
  AUTHORS   Sulston,J.E. and Waterston,R.
  TITLE     Toward a complete human genome sequence
  JOURNAL   Genome Res. 8 (11), 1097-1108 (1998)
  MEDLINE   99063792
REFERENCE   2  (bases 1 to 197308)
  AUTHORS   Armstrong,J. and Haakenson,W.
  TITLE     The sequence of Homo sapiens BAC clone RP11-339F22
  JOURNAL   Unpublished (2001)
REFERENCE   3  (bases 1 to 197308)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-DEC-1999) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   4  (bases 1 to 197308)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JUL-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   5  (bases 1 to 197308)
  AUTHORS   Waterston,R.
```

```
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JAN-2002) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT     On Jul 14, 2001 this sequence version replaced gi:13431151.
            -------------- Genome Center
                Center: Washington University Genome Sequencing Center
                Center code: WUGSC
                Web site: http://genome.wustl.edu/gsc
                Contact: sapiens@watson.wustl.edu
            -------------- Summary Statistics
                Center project name: H_NH0339F22
            --------------.

            NOTICE:  This sequence may not represent the entire insert of this
            clone.  It may be shorter because we only sequence overlapping
            clone sections once, or longer because we provide a small overlap
            between neighboring data submissions.

            This sequence was finished as follows unless otherwise noted:
            all regions were double stranded, sequenced with an alternate
            chemistry, or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by sequence
            from more than one subclone; and the assembly was confirmed by
            restriction digest.

            MAPPING INFORMATION:
            Mapping information for this clone was provided by Dr. John D.
            McPherson, Department of Genetics, Washington University, St. Louis
            MO.  For additional information about the map position of this
            sequence, see http://genome.wustl.edu/gsc

            SOURCE INFORMATION:
            The RPCI-11 human BAC library was made from the blood of one male
            donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
            Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
            approach for construction of bacterial artificial chromosome
            libraries. Genomics 51:1-8. The clone may be obtained either from
            Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
            and coworkers at the Roswell Park Cancer Institute
            (http://bacpac.med.buffalo.edu)
            VECTOR:  pBACe3.6
            NEIGHBORING SEQUENCE INFORMATION:
            The clone sequenced to the left is RP11-725J3; the clone sequenced
            to the right is RP11-97J14.  Actual start of this clone is at base
            position 1 of RP11-339F22; actual end is at base position 197308 of
            RP11-339F22.

            Data from AC084280 and AC024704 was used to finish this clone,
            AC016724.  Polymorphisms have been identified between AC024704 and
            AC016724.

            Sequence derived from pcr from base position 148683 to 149264.
FEATURES             Location/Qualifiers
     source          1. .197308
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="2"
                     /map="2"
                     /clone="RP11-339F22"
                     /clone_lib="RPCI-11"
     repeat_region   6. .275
                     /rpt_family="L1"
     repeat_region   274. .740
                     /rpt_family="L1"
     repeat_region   744. .907
                     /rpt_family="ERV1"
     repeat_region   917. .1361
                     /rpt_family="L1"
     repeat_region   1362. .1814
                     /rpt_family="L1"
     repeat_region   1838. .1952
                     /rpt_family="ERV1"
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repeat_region   2105. .2161
                /rpt_family="ERV1"
repeat_region   2245. .2587
                /rpt_family="L1"
repeat_region   2588. .2877
                /rpt_family="Alu"
repeat_region   2878. .3244
                /rpt_family="L1"
repeat_region   3235. .4195
                /rpt_family="L1"
repeat_region   3460. .3481
                /rpt_family="AT_rich"
repeat_region   4311. .4450
                /rpt_family="MIR"
repeat_region   4822. .4957
                /rpt_family="MER1_type"
repeat_region   5152. .5337
                /rpt_family="MER1_type"
repeat_region   6118. .7901
                /rpt_family="L2"
repeat_region   8008. .8145
                /rpt_family="L2"
repeat_region   8146. .8343
                /rpt_family="MER1_type"
repeat_region   8344. .8429
                /rpt_family="L2"
repeat_region   8661. .8827
                /rpt_family="ERV1"
repeat_region   8999. .9029
                /rpt_family="(T)n"
misc_feature    9003. .9030
                /note="similar to Homo sapiens EST BI091273
                (NID:g14509603)"
misc_feature    9011. .9031
                /note="similar to Homo sapiens EST AA587127 (NID:g2397941)
                nn70c01.s1"
misc_feature    9013. .9031
                /note="similar to Homo sapiens EST AI034379 (NID:g3255332)
                ox20g11.x1"
repeat_region   9167. .9564
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repeat_region   10187. .10267
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repeat_region   11074. .11122
                /rpt_family="(CTG)n"
repeat_region   11587. .11611
                /rpt_family="(TG)n"
repeat_region   11651. .11884
                /rpt_family="MaLR"
repeat_region   12198. .12353
                /rpt_family="MIR"
repeat_region   12578. .12714
                /rpt_family="MER1_type"
repeat_region   13540. .13855
                /rpt_family="Alu"
repeat_region   13985. .14843
                /rpt_family="L1"
repeat_region   14923. .15243
                /rpt_family="MER2_type"
repeat_region   15980. .16836
                /rpt_family="L1"
repeat_region   17526. .17822
                /rpt_family="Alu"
repeat_region   18067. .18089
                /rpt_family="AT_rich"
repeat_region   19365. .19493
                /rpt_family="MER1_type"
repeat_region   19604. .20083
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repeat_region   20084. .20447
                /rpt_family="MaLR"
repeat_region   20448. .21020
                /rpt_family="ERVL"
repeat_region   21033. .21306
                /rpt_family="L1"
repeat_region   21315. .21656
                /rpt_family="ERVL"
repeat_region   21906. .22079
                /rpt_family="ERVL"
repeat_region   22533. .22637
                /rpt_family="MER2_type"
repeat_region   22668. .22977
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misc_feature    27616. .28020
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repeat_region   28055. .28149
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Best Local Similarity 100.0%; Pred. No. 1e-55;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   57062 GAAAAGGATATAATGGATTTGTACAACCAACCCGAGCCTGTGAAGTCCTTTCTCTTCTAC 57121

Qy      61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   57122 CACAGCCAGAGTGGCAGGAACTCCACCTTCGAGTCTGTGGCTTTCCCTGGCTGGTTCATC 57181

Qy     121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
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Db   57182 GCTGTCAGCTCTGAAGGAGGCTGTCCTCTCATCCTTACCCAAGAACTGGGGAAAGCCAAC 57241

Qy     181 actactgactttgggttaactatgctgttttaa 213
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Db   57242 ACTACTGACTTTGGGTTAACTATGCTGTTTTAA 57274
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RESULT   3
AX193589
LOCUS       AX193589                391 bp    DNA     linear   PAT 15-AUG-2001
DEFINITION  Sequence 11 from Patent WO0140291.
ACCESSION   AX193589
VERSION     AX193589.1  GI:15211518
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 391)
  AUTHORS   Burgess,C.E., Prayaga,S.K., Shimkets,R.A., Rastelli,L.,
            Zerhusen,B.D. and Mezes,P.S.
  TITLE     Proteins and nucleic acids encoding the same
  JOURNAL   Patent: WO 0140291-A 11 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .391
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT       94 a    106 c     99 g     92 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 5.6e-44;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    217 GAAAAGGATATAATGGATTTGTACAACCAACCCGAGCCTGTGAAGTCCTTTCTCTTCTAC 276

Qy     61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    277 CACAGCCAGAGTGGCAGGAACTCCACCTTCGAGTCTGTGGCTTTCCCTGGCTGGTTCATC 336

Qy    121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaag 175
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    337 GCTGTCAGCTCTGAAGGAGGCTGTCCTCTCATCCTTACCCAAGAACTGGGGAAAG 391
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RESULT 4
AX193660
LOCUS AX193660 244 bp DNA linear PAT 15-AUG-2001
DEFINITION Sequence 82 from Patent WO0140291.
ACCESSION AX193660
VERSION AX193660.1 GI:15211539
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 244)
AUTHORS Burgess,C.E., Prayaga,S.K., Shimkets,R.A., Rastelli,L.,
Zerhusen,B.D. and Mezes,P.S.
TITLE Proteins and nucleic acids encoding the same
JOURNAL Patent: WO 0140291-A 82 07-JUN-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1. .244
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 53 a 71 c 58 g 62 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.3e-39;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db     84 GAAAAGGATATAATGGATTTGTACAACCAACCCGAGCCTGTGAAGTCCTTTCTCTTCTAC 143

Qy     61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
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Db    144 CACAGCCAGAGTGGCAGGAACTCCACCTTCGAGTCTGTGGCTTTCCCTGGCTGGTTCATC 203

Qy    121 gctgtcagctctgaaggaggctgtcctctcatccttaccca 161
          |||||||||||||||||||||||||||||||||||||||
Db    204 GCTGTCAGCTCTGAAGGAGGCTGTCCTCTCATCCTTACCCA 244
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RESULT 5
AF200493
LOCUS AF200493 483 bp mRNA linear ROD 11-MAY-2000
DEFINITION Mus musculus interleukin-1 homolog 1 mRNA, complete cds.
ACCESSION AF200493
VERSION AF200493.1 GI:7769113
KEYWORDS .
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 483)
AUTHORS Kumar,S., McDonnell,P.C., Lehr,R., Tierney,L., Tzimas,M.N.,
Griswold,D.E., Capper,E.A., Tal-Singer,R., Wells,G.I., Doyle,M.L.
and Young,P.R.
TITLE Identification and initial characterization of four novel members
of the interleukin-1 family
JOURNAL J. Biol. Chem. 275 (14), 10308-10314 (2000)
MEDLINE 20209405
PUBMED 10744718
REFERENCE 2 (bases 1 to 483)
AUTHORS Kumar,S., McDonnell,P.C. and Young,P.R.
TITLE Direct Submission
JOURNAL Submitted (01-NOV-1999) Bone and Cartilage Biology, UW 2109,
SmithKline Beecham Pharmaceuticals, 709 Swedeland Rd., King of
Prussia, PA 19406, USA
FEATURES Location/Qualifiers
source 1. .483
/organism="Mus musculus"
/db_xref="taxon:10090"
/cell_line="PAM 212"
/cell_type="keratinocyte"
CDS 1. .483
/note="cytokine; mIL-1H1"
/codon_start=1
/product="interleukin-1 homolog 1"
/protein_id="AAF69249.1"
/db_xref="GI:7769114"
/translation="MNKEKELRAASPSLRHVQDLSSRVWILQNNILTAVPRKEQTVPV
TITLLPCQYLDTLETNRGDPTYMGVQRPMSCLFCTKDGEQPVLQLGEGNIMEMYNKKE
PVKASLFYHKKSGTTSTFESAAFPGWFIAVCSKGSCPLILTQELGEIFITDFEMIVVH
"
BASE COUNT 139 a 113 c 117 g 114 t
ORIGIN

Query Match 58.7%; Score 125; DB 10; Length 483;
Best Local Similarity 74.2%; Pred. No. 2.5e-28;
Matches 158; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

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Qy      1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtccttttctcttctac 60
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Db    271 GAAGGGAACATAATGGAAATGTACAACAAAAAGGAACCTGTAAAAGCCTCTCTCTTCTAT 330

Qy     61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
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Db    331 CACAAGAAGAGTGGTACAACCTCTACATTTGAGTCTGCAGCCTTCCCTGGTTGGTTCATC 390

Qy    121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
          ||||||  |||||  ||||  ||||  ||  |||||  ||  ||||||||||||||||  ||  |  |
Db    391 GCTGTCTGCTCTAAAGGGAGCTGCCCACTCATTCTGACCCAAGAACTGGGGGAAATCTTC 450

Qy    181 actactgactttgggttaactatgctgttttaa 213
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Db    451 ATCACTGACTTCGAGATGATTGTGGTTCATTAA 483
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RESULT 6
AR137703
LOCUS AR137703 746 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 1 from patent US 6197551.
ACCESSION AR137703
VERSION AR137703.1 GI:14479212
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 746)
AUTHORS Busfield,S.J.
TITLE Spoil-1 protein and nucleic acid molecules and uses therefor
JOURNAL Patent: US 6197551-A 1 06-MAR-2001;
FEATURES Location/Qualifiers
source 1. .746
/organism="unknown"
BASE COUNT 275 a 150 c 142 g 179 t
ORIGIN

Query Match 58.7%; Score 125; DB 6; Length 746;
Best Local Similarity 74.2%; Pred. No. 2.6e-28;
Matches 158; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

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Qy      1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtccttttctcttctac 60
          |||  | | ||||||||  ||||||||  ||   || |||||  ||  ||| |||||||||
Db    219 GAAGGGAACATAATGGAAATGTACAACAAAAAGGAACCTGTAAAAGCCTCTCTCTTCTAT 278

Qy     61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
          ||||   |||||||  |  | ||| ||  ||  |||||||  ||  |||||||| |||||||||
Db    279 CACAAGAAGAGTGGTACAACCTCTACATTTGAGTCTGCAGCCTTCCCTGGTTGGTTCATC 338

Qy    121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
          ||||||  |||||  ||||  ||||  ||  |||||  ||  ||||||||||||||  ||  |  |
Db    339 GCTGTCTGCTCTAAAGGGAGCTGCCCACTCATTCTGACCCAAGAACTGGGGGAAATCTTC 398

Qy    181 actactgactttgggttaactatgctgttttaa 213
          |  ||||||||  |  |  |  |  ||  |   ||||
Db    399 ATCACTGACTTCGAGATGATTGTGGTACATTAA 431
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```
RESULT   7
AF206697
LOCUS       AF206697                795 bp    mRNA    linear   ROD 01-NOV-2001
DEFINITION  Mus musculus interleukin-1 epsilon (Ille) mRNA, complete cds.
ACCESSION   AF206697
VERSION     AF206697.1  GI:11493849
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 795)
  AUTHORS   Debets,R., Timans,J.C., Homey,B., Zurawski,S., Sana,T.R., Lo,S.,
            Wagner,J., Edwards,G., Clifford,T., Menon,S., Bazan,J.F. and
            Kastelein,R.A.
  TITLE     Two novel IL-1 family members, IL-1 delta and IL-1 epsilon,
            function as an antagonist and agonist of NF-kappa B activation
            through the orphan IL-1 receptor-related protein 2
  JOURNAL   J. Immunol. 167 (3), 1440-1446 (2001)
  MEDLINE   21359532
   PUBMED   11466363
REFERENCE   2  (bases 1 to 795)
  AUTHORS   Debets,R., Timans,J.C., Zurawski,S., Bazan,J.F. and Kastelein,R.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-NOV-1999) Molecular Biology, DNAX Research Institute
            of Molecular and Cellular Biology, Inc., 901 California Avenue,
            Palo Alto, CA 94304-1104, USA
FEATURES             Location/Qualifiers
     source          1. .795
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /chromosome="2"
                     /map="proximal region; near Il1d"
                     /dev_stage="17 day embryo"
     gene            1. .795
                     /gene="Il1e"
     CDS             76. .558
                     /gene="Il1e"
                     /note="interleukin-1-like protein; similar to IL-1a, IL-1b
                     and IL-1ra; highly expressed in skin tissue; acts through
                     an IL-1-like receptor IL-1Rrp2 resulting in IL-1-like
                     signaling cascade; antagonized by IL-1d"
                     /codon_start=1
                     /product="interleukin-1 epsilon"
                     /protein_id="AAG35671.1"
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                     PVKASLFYHKKSGTTSTFESAAFPGWFIAVCSKGSCPLILTQELGEIFITDFEMIVVH
                     "
BASE COUNT      237 a    177 c    174 g    207 t
ORIGIN
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  Query Match           58.7%;  Score 125;  DB 10;  Length 795;
  Best Local Similarity 74.2%;  Pred. No. 2.6e-28;
  Matches  158;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy      1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtccttttctcttctac 60
          |||  | | ||||||||  ||||||||  ||   || |||||  ||  ||| |||||||||
Db    346 GAAGGGAACATAATGGAAATGTACAACAAAAAGGAACCTGTAAAAGCCTCTCTCTTCTAT 405

Qy     61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
          ||||   |||||||  |  | ||| ||  ||  |||||||  ||  |||||||| |||||||||
Db    406 CACAAGAAGAGTGGTACAACCTCTACATTTGAGTCTGCAGCCTTCCCTGGTTGGTTCATC 465

Qy    121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
          ||||||  |||||  ||||  ||||  ||  |||||  ||  ||||||||||||||  ||  |  |
Db    466 GCTGTCTGCTCTAAAGGGAGCTGCCCACTCATTCTGACCCAAGAACTGGGGGAAATCTTC 525

Qy    181 actactgactttgggttaactatgctgttttaa 213
          |  ||||||||  |  |  |  |  ||  |   ||||
Db    526 ATCACTGACTTCGAGATGATTGTGGTACATTAA 558
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```
RESULT   8
AR137705
LOCUS       AR137705                243 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 4 from patent US 6197551.
ACCESSION   AR137705
VERSION     AR137705.1  GI:14479214
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 243)
  AUTHORS   Busfield,S.J.
  TITLE     Spoil-1 protein and nucleic acid molecules and uses therefor
  JOURNAL   Patent: US 6197551-A 4 06-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .243
                     /organism="unknown"
BASE COUNT       73 a     58 c     54 g     58 t
ORIGIN
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  Best Local Similarity 74.8%;  Pred. No. 1.2e-27;
  Matches  154;  Conservative    0;  Mismatches   52;  Indels    0;  Gaps    0;

Qy      1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtccttttctcttctac 60
          |||  | | ||||||||  ||||||||  ||   || |||||  ||  ||| |||||||||
Db     34 GAAGGGAACATAATGGAAATGTACAACAAAAAGGAACCTGTAAAAGCCTCTCTCTTCTAT 93

Qy     61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
          ||||   |||||||  |  | ||| ||  ||  |||||||  ||  |||||||| |||||||||
Db     94 CACAAGAAGAGTGGTACAACCTCTACATTTGAGTCTGCAGCCTTCCCTGGTTGGTTCATC 153

Qy    121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
          ||||||  |||||  ||||  ||||  ||  |||||  ||  ||||||||||||||  ||  |  |
Db    154 GCTGTCTGCTCTAAAGGGAGCTGCCCACTCATTCTGACCCAAGAACTGGGGGAAATCTTC 213

Qy    181 actactgactttgggttaactatgct 206
          |  ||||||||  |  |  |  |  ||  |
Db    214 ATCACTGACTTCGAGATGATTGTGGT 239
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```
RESULT   9
AR137704
LOCUS       AR137704                294 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 3 from patent US 6197551.
ACCESSION   AR137704
VERSION     AR137704.1  GI:14479213
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 294)
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```
  AUTHORS   Busfield,S.J.
  TITLE     Spoil-1 protein and nucleic acid molecules and uses therefor
  JOURNAL   Patent: US 6197551-A 3 06-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .294
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BASE COUNT       86 a     68 c     66 g     74 t
ORIGIN


  Query Match             57.7%;  Score 122.8;  DB 6;  Length 294;
  Best Local Similarity   74.8%;  Pred. No. 1.2e-27;
  Matches  154;  Conservative    0;  Mismatches   52;  Indels    0;  Gaps    0;

Qy       1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtccttttctcttctac 60
           |||  | | ||||||||  |||||||| ||   || ||||| ||  ||| |||||||||
Db      85 GAAGGGAACATAATGGAAATGTACAACAAAAAGGAACCTGTAAAAGCCTCTCTCTTCTAT 144

Qy      61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
           ||||   ||||||| |  | ||| || || |||||||  || ||||||| |||||||||
Db     145 CACAAGAAGAGTGGTACAACCTCTACATTTGAGTCTGCAGCCTTCCCTGGTTGGTTCATC 204

Qy     121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
           |||||| ||||| |||| |||| || ||||| || ||||||||||||||| ||  |  |
Db     205 GCTGTCTGCTCTAAAGGGAGCTGCCCACTCATTCTGACCCAAGAACTGGGGGAAATCTTC 264

Qy     181 actactgactttgggttaactatgct 206
           |  |||||||| | | | | | || |
Db     265 ATCACTGACTTCGAGATGATTGTGGT 290


RESULT  10
AC106686
LOCUS       AC106686              186587 bp    DNA     linear   HTG 12-JAN-2002
DEFINITION  Rattus norvegicus clone CH230-62D13, *** SEQUENCING IN PROGRESS
            ***, 85 unordered pieces.
ACCESSION   AC106686
VERSION     AC106686.1  GI:18139210
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 186587)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
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            Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
            Weinstock,G. and Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 186587)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JAN-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: GLUV
                Center clone name: CH230-62D13
            -------------- Summary Statistics
                Assembly program: Phrap; version 0.990329First call to
            findPhrapList
                Consensus quality: 133186 bases at least Q40
                Consensus quality: 144645 bases at least Q30
                Consensus quality: 154301 bases at least Q20
                Estimated insert size: 143906; sum-of-contigs estimation
                Quality coverage: 0x in Q20 bases; agarose-fp estimation
                Quality coverage: 1.9x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 85 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     3313: contig of 3313 bp in length
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            *     3414     9926: contig of 6513 bp in length
            *     9927    10026: gap of unknown length
            *    10027    14917: contig of 4891 bp in length
            *    14918    15017: gap of unknown length
            *    15018    19779: contig of 4762 bp in length
            *    19780    19879: gap of unknown length
            *    19880    23114: contig of 3235 bp in length
            *    23115    23214: gap of unknown length
            *    23215    26939: contig of 3725 bp in length
            *    26940    27039: gap of unknown length
            *    27040    31422: contig of 4383 bp in length
            *    31423    31522: gap of unknown length
            *    31523    33705: contig of 2183 bp in length
            *    33706    33805: gap of unknown length
            *    33806    36600: contig of 2795 bp in length
            *    36601    36700: gap of unknown length
            *    36701    39809: contig of 3109 bp in length
            *    39810    39909: gap of unknown length
            *    39910    43147: contig of 3238 bp in length
            *    43148    43247: gap of unknown length
            *    43248    47076: contig of 3829 bp in length
            *    47077    47176: gap of unknown length
            *    47177    49962: contig of 2786 bp in length
            *    49963    50062: gap of unknown length
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*    50063    53178: contig of 3116 bp in length
*    53179    53278: gap of unknown length
*    53279    56629: contig of 3351 bp in length
*    56630    56729: gap of unknown length
*    56730    59913: contig of 3184 bp in length
*    59914    60013: gap of unknown length
*    60014    62348: contig of 2335 bp in length
*    62349    62448: gap of unknown length
*    62449    65282: contig of 2834 bp in length
*    65283    65382: gap of unknown length
*    65383    67417: contig of 2035 bp in length
*    67418    67517: gap of unknown length
*    67518    69887: contig of 2370 bp in length
*    69888    69987: gap of unknown length
*    69988    72720: contig of 2733 bp in length
*    72721    72820: gap of unknown length
*    72821    74923: contig of 2103 bp in length
*    74924    75023: gap of unknown length
*    75024    77710: contig of 2687 bp in length
*    77711    77810: gap of unknown length
*    77811    80958: contig of 3148 bp in length
*    80959    81058: gap of unknown length
*    81059    82954: contig of 1896 bp in length
*    82955    83054: gap of unknown length
*    83055    84642: contig of 1588 bp in length
*    84643    84742: gap of unknown length
*    84743    87581: contig of 2839 bp in length
*    87582    87681: gap of unknown length
*    87682    89846: contig of 2165 bp in length
*    89847    89946: gap of unknown length
*    89947    92904: contig of 2958 bp in length
*    92905    93004: gap of unknown length
*    93005    94651: contig of 1647 bp in length
*    94652    94751: gap of unknown length
*    94752    96832: contig of 2081 bp in length
*    96833    96932: gap of unknown length
*    96933    98402: contig of 1470 bp in length
*    98403    98502: gap of unknown length
*    98503   100989: contig of 2487 bp in length
*   100990   101089: gap of unknown length
*   101090   102635: contig of 1546 bp in length
*   102636   102735: gap of unknown length
*   102736   104654: contig of 1919 bp in length
*   104655   104754: gap of unknown length
*   104755   106969: contig of 2215 bp in length
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*   107070   109658: contig of 2589 bp in length
*   109659   109758: gap of unknown length
*   109759   111691: contig of 1933 bp in length
*   111692   111791: gap of unknown length
*   111792   113882: contig of 2091 bp in length
*   113883   113982: gap of unknown length
*   113983   115694: contig of 1712 bp in length
*   115695   115794: gap of unknown length
*   115795   117673: contig of 1879 bp in length
*   117674   117773: gap of unknown length
*   117774   119905: contig of 2132 bp in length
*   119906   120005: gap of unknown length
*   120006   122398: contig of 2393 bp in length
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*   125613   127054: contig of 1442 bp in length
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*   128465   130365: contig of 1901 bp in length
*   130366   130465: gap of unknown length
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*   132332   133577: contig of 1246 bp in length
*   133578   133677: gap of unknown length
*   133678   134908: contig of 1231 bp in length
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*   135009   136313: contig of 1305 bp in length
*   136314   136413: gap of unknown length
*   136414   137977: contig of 1564 bp in length
*   137978   138077: gap of unknown length
*   138078   139553: contig of 1476 bp in length
*   139554   139653: gap of unknown length
*   139654   140909: contig of 1256 bp in length
*   140910   141009: gap of unknown length
*   141010   142701: contig of 1692 bp in length
*   142702   142801: gap of unknown length
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  Query Match             50.0%;  Score 106.4;  DB 2;  Length 186587;
  Best Local Similarity   71.4%;  Pred. No. 2.3e-22;
  Matches  140;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy      18 tttgtacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcag 77
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Db 171113 TATGTATCCCCAGAAGGAACGTGTAAAAGCCTCTCTCTTCTATCACAAGAAGAGTGGTAC 171172

Qy      78 gaactccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaagg 137
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Qy     138 aggctgtcctctcatccttacccaagaactggggaaagccaacactactgactttgggtt 197
             |||| || ||| |  | ||||||||||| |||||| ||  ||  ||||| |||| | |
Db 171233 GAGCTGCCCACTCGTTTTGACCCAAGAACTTGGGAAAACCTTCATCACTGATTTTGAGAT 171292

Qy     198 aactatgctgttttaa 213
             ||| |  |   ||||
Db 171293 GACTGTAGTACATTAA 171308


RESULT  11
AX207820
LOCUS       AX207820               1073 bp    DNA     linear   PAT 31-AUG-2001
DEFINITION  Sequence 3 from Patent WO0157219.
ACCESSION   AX207820
VERSION     AX207820.1  GI:15422467
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   Debets,J.E., Timans,J.C., Bazan,J.F. and Kastelein,R.A.
  TITLE     Mammalian interleukin-1-delta and -epsilon. Their use in
            therapeutic and diagnostic methods
  JOURNAL   Patent: WO 0157219-A 3 09-AUG-2001;
            SCHERING CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .1073
                     /organism="unidentified"
                     /db_xref="taxon:32644"
                     /note="Description of Unknown Organism: primate; surmised
                     Homo sapiens"
     CDS             67. .576
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC60373.1"
                     /db_xref="GI:15422468"
                     /translation="MRGTPGDADGGGRAVYQSMCKPITGTINDLNQQVWTLQGQNLVA
                     VPRSDSVTPVTVAVITCKYPEALEQGRGDPIYLGIQNPEMCLYCEKVGEQPTLQLKEQ
                     KIMDLYGQPEPVKPFLFYRAKTGRTSTLESVAFPDWFIASSKRDQPIILTSELGKSYN
                     TAFELNIND"
BASE COUNT      281 a    241 c    255 g    296 t
ORIGIN


  Query Match             45.7%;  Score 97.4;  DB 6;  Length 1073;
  Best Local Similarity   70.9%;  Pred. No. 1.1e-19;
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  Matches  144;  Conservative    0;  Mismatches   56;  Indels    3;  Gaps    1;

Qy       1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtccttttctcttctac 60
           ||  || | || |||||| ||||   |||||||||||| |||||  |||| || ||||||
Db     367 GAGCAGAAGATCATGGATCTGTATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTAC 426

Qy      61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
           |    | ||| ||| |||| ||||||| | |||||||||||| ||||| | |||||||||
Db     427 CGTGCCAAGACTGGTAGGACCTCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT- 485

Qy     121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
             || |  |||  |  ||| |   ||  |||| || ||   |||||| ||||| |  ||
Db     486 --TGCCTCCTCCAAGAGAGACCAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATAC 543

Qy     181 actactgactttgggttaactat 203
           |  |||| |||||  |||| |||
Db     544 AACACTGCCTTTGAATTAAATAT 566


RESULT  12
AF206696
LOCUS       AF206696               1177 bp    mRNA    linear   PRI 01-NOV-2001
DEFINITION  Homo sapiens interleukin-1 epsilon (IL1E) mRNA, complete cds.
ACCESSION   AF206696
VERSION     AF206696.1  GI:11493847
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1177)
  AUTHORS   Debets,R., Timans,J.C., Homey,B., Zurawski,S., Sana,T.R., Lo,S.,
            Wagner,J., Edwards,G., Clifford,T., Menon,S., Bazan,J.F. and
            Kastelein,R.A.
  TITLE     Two novel IL-1 family members, IL-1 delta and IL-1 epsilon,
            function as an antagonist and agonist of NF-kappa B activation
            through the orphan IL-1 receptor-related protein 2
  JOURNAL   J. Immunol. 167 (3), 1440-1446 (2001)
  MEDLINE   21359532
   PUBMED   11466363
REFERENCE   2  (bases 1 to 1177)
  AUTHORS   Debets,R., Timans,J.C., Zurawski,S., Bazan,J.F. and Kastelein,R.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-NOV-1999) Molecular Biology, DNAX Research Institute
            of Molecular and Cellular Biology, Inc., 901 California Avenue,
            Palo Alto, CA 94304-1104, USA
FEATURES             Location/Qualifiers
     source          1. .1177
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /tissue_type="airway epithelial cells induced with TNF
                     alpha and IFN"
     gene            1. .1177
                     /gene="IL1E"
     CDS             67. .576
                     /gene="IL1E"
                     /note="interleukin-1-like protein; similar to IL-1a, IL-1b
                     and IL-1ra; highly expressed in skin tissue; acts through
                     an IL-1-like receptor IL-1Rrp2 resulting in IL-1-like
                     signaling cascade; antagonized by IL-1d"
                     /codon_start=1
                     /product="interleukin-1 epsilon"
                     /protein_id="AAG35670.1"
                     /db_xref="GI:11493848"
                     /translation="MRGTPGDADGGGRAVYQSMCKPITGTINDLNQQVWTLQGQNLVA
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                     KIMDLYGQPEPVKPFLFYRAKTGRTSTLESVAFPDWFIASSKRDQPIILTSELGKSYN
                     TAFELNIND"
BASE COUNT      320 a    249 c    267 g    341 t
ORIGIN


  Query Match             45.7%;  Score 97.4;  DB 9;  Length 1177;
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  Best Local Similarity   70.9%;  Pred. No. 1.1e-19;
  Matches  144;  Conservative    0;  Mismatches   56;  Indels    3;  Gaps    1;

Qy       1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtccttttctcttctac 60
           ||  || | || |||||| ||||   |||||||||||| |||||  |||| || ||||||
Db     367 GAGCAGAAGATCATGGATCTGTATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTAC 426

Qy      61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
           |    | ||| ||| |||| ||||||| | |||||||||||| ||||| | |||||||||
Db     427 CGTGCCAAGACTGGTAGGACCTCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT- 485

Qy     121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
             || |  |||  |  ||| |   ||  |||| || ||   |||||| ||||| |  ||
Db     486 --TGCCTCCTCCAAGAGAGACCAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATAC 543

Qy     181 actactgactttgggttaactat 203
           |  |||| |||||  |||| |||
Db     544 AACACTGCCTTTGAATTAAATAT 566


RESULT  13
E54910
LOCUS       E54910                 1183 bp    DNA     linear   PAT 07-FEB-2001
DEFINITION  Interleukin-1 receptor antagonist beta (IL-1RA-beta) polypeptide.
ACCESSION   E54910
VERSION     E54910.1  GI:13019313
KEYWORDS    JP 2000032990-A/1.
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1183)
  AUTHORS   Peter,R.Y.
  TITLE     Interleukin-1 receptor antagonist beta (IL-1RA-beta) polypeptide
  JOURNAL   Patent: JP 2000032990-A 1 02-FEB-2000;
            SMITHKLINE BEECHAM CORP
COMMENT     OS   Unidentified
            PN   JP 2000032990-A/1
            PD   02-FEB-2000
            PF   14-MAY-1999 JP 1999134172
            PR   28-JAN-1997 US    08/790032
            PI   PETER R YOUNG
            PC   C12N15/09,A61K38/00,A61K39/395,A61K45/00,C07K14/545,C07K16/24,
            PC   C12P21/02,
            PC   C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53//A61K31/00, PC
              A61K31/00,
            PC   A61K31/00,A61K31/00,C12N15/00,A61K37/02
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .1183
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .1183
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                     /db_xref="taxon:32644"
BASE COUNT      329 a    249 c    269 g    336 t
ORIGIN


  Query Match             45.7%;  Score 97.4;  DB 6;  Length 1183;
  Best Local Similarity   70.9%;  Pred. No. 1.1e-19;
  Matches  144;  Conservative    0;  Mismatches   56;  Indels    3;  Gaps    1;

Qy       1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtccttttctcttctac 60
           ||  || | || |||||| ||||   |||||||||||| |||||  |||| || ||||||
Db     375 GAGCAGAAGATCATGGATCTGTATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTAC 434

Qy      61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
           |    | ||| ||| |||| ||||||| | |||||||||||| ||||| | |||||||||
Db     435 CGTGCCAAGACTGGTAGGACCTCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT- 493

Qy     121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
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Db    494 --TGCCTCCTCCAAGAGAGACCAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATAC 551

Qy    181 actactgactttgggttaactat 203
          |  ||||  |||||  ||||  |||
Db    552 AACACTGCCTTTGAATTAAATAT 574


RESULT  14
AF200492
LOCUS       AF200492               1183 bp    mRNA    linear   PRI 11-MAY-2000
DEFINITION  Homo sapiens interleukin-1 homolog 1 mRNA, complete cds.
ACCESSION   AF200492
VERSION     AF200492.1  GI:7769111
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1183)
  AUTHORS   Kumar,S., McDonnell,P.C., Lehr,R., Tierney,L., Tzimas,M.N.,
            Griswold,D.E., Capper,E.A., Tal-Singer,R., Wells,G.I., Doyle,M.L.
            and Young,P.R.
  TITLE     Identification and initial characterization of four novel members
            of the interleukin-1 family
  JOURNAL   J. Biol. Chem. 275 (14), 10308-10314 (2000)
  MEDLINE   20209405
   PUBMED   10744718
REFERENCE   2  (bases 1 to 1183)
  AUTHORS   Kumar,S., McDonnell,P.C. and Young,P.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-NOV-1999) Bone and Cartilage Biology, UW 2109,
            SmithKline Beecham Pharmaceuticals, 709 Swedeland Rd., King of
            Prussia, PA 19406, USA
FEATURES             Location/Qualifiers
     source          1. .1183
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="2"
                     /map="2q12-q21; close to IL-1 locus"
                     /cell_type="primary keratinocytes; epithelial"
     CDS             75. .584
                     /note="cytokine; IL-1H1"
                     /codon_start=1
                     /product="interleukin-1 homolog 1"
                     /protein_id="AAF69248.1"
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                     TAFELNIND"
BASE COUNT      329 a    249 c    269 g    336 t
ORIGIN


  Query Match             45.7%;  Score 97.4;  DB 9;  Length 1183;
  Best Local Similarity   70.9%;  Pred. No. 1.1e-19;
  Matches  144;  Conservative    0;  Mismatches   56;  Indels    3;  Gaps    1;

Qy      1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 60
          ||  || | || |||||| ||||   ||||||||||| |||||  |||| || ||||||
Db    375 GAGCAGAAGATCATGGATCTGTATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTAC 434

Qy     61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
          |    | ||| ||| |||| ||||||| | |||||||||||| ||||| | |||||||||
Db    435 CGTGCCAAGACTGGTAGGACCTCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT- 493

Qy    121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
            || |  |||  |  ||| |   ||  |||| || ||   |||||| |||||  |  ||
Db    494 --TGCCTCCTCCAAGAGAGACCAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATAC 551

Qy    181 actactgactttgggttaactat 203
          |  ||||  |||||  ||||  |||
Db    552 AACACTGCCTTTGAATTAAATAT 574


RESULT  15
AC096974/c
LOCUS       AC096974               184626 bp    DNA     linear   HTG 21-DEC-2001
DEFINITION  Rattus norvegicus clone CH230-58P9, *** SEQUENCING IN PROGRESS ***,
            58 unordered pieces.
ACCESSION   AC096974
VERSION     AC096974.3  GI:17975666
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 184626)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
            Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
            Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
            Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
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            Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
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            Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
            Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
            Morgan,M., Morris,S., Moser,M., Neal,D., Newtson,J., Newtson,N.,
            Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
            Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
            Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
            Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,
            Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N.,
            Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
            Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
            Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N.,
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            Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
            Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
            Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
            Weinstock,G. and Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 184626)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-OCT-2001) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Dec 21, 2001 this sequence version replaced gi:17062392.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: GGKC
                Center clone name: CH230-58P9
            -------------- Summary Statistics
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    Assembly program: Phrap; version 0.990329First call to
findPhrapList
    Consensus quality: 162978 bases at least Q40
    Consensus quality: 170371 bases at least Q30
    Consensus quality: 176254 bases at least Q20
    Estimated insert size: 168569; sum-of-contigs estimation
    Quality coverage: 0x in Q20 bases; agarose-fp estimation
    Quality coverage: 2.4x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
*   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 58 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*       1     9509: contig of 9509 bp in length
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*   20395    26560: contig of 6166 bp in length
*   26561    26660: gap of unknown length
*   26661    32468: contig of 5808 bp in length
*   32469    32568: gap of unknown length
*   32569    37161: contig of 4593 bp in length
*   37162    37261: gap of unknown length
*   37262    43622: contig of 6361 bp in length
*   43623    43722: gap of unknown length
*   43723    49522: contig of 5800 bp in length
*   49523    49622: gap of unknown length
*   49623    55011: contig of 5389 bp in length
*   55012    55111: gap of unknown length
*   55112    61121: contig of 6010 bp in length
*   61122    61221: gap of unknown length
*   61222    65846: contig of 4625 bp in length
*   65847    65946: gap of unknown length
*   65947    69741: contig of 3795 bp in length
*   69742    69841: gap of unknown length
*   69842    75397: contig of 5556 bp in length
*   75398    75497: gap of unknown length
*   75498    79915: contig of 4418 bp in length
*   79916    80015: gap of unknown length
*   80016    84077: contig of 4062 bp in length
*   84078    84177: gap of unknown length
*   84178    87893: contig of 3716 bp in length
*   87894    87993: gap of unknown length
*   87994    91910: contig of 3917 bp in length
*   91911    92010: gap of unknown length
*   92011    95678: contig of 3668 bp in length
*   95679    95778: gap of unknown length
*   95779    98303: contig of 2525 bp in length
*   98304    98403: gap of unknown length
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*  102205   102304: gap of unknown length
*  102305   105578: contig of 3274 bp in length
*  105579   105678: gap of unknown length
*  105679   108120: contig of 2442 bp in length
*  108121   108220: gap of unknown length
*  108221   111769: contig of 3549 bp in length
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*  141432   142889: contig of 1458 bp in length
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*  142990   145132: contig of 2143 bp in length
*  145133   145232: gap of unknown length
*  145233   147763: contig of 2531 bp in length
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*  147864   148869: contig of 1006 bp in length
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*  148970   150836: contig of 1867 bp in length
*  150837   150936: gap of unknown length
*  150937   152850: contig of 1914 bp in length
*  152851   152950: gap of unknown length
*  152951   155212: contig of 2262 bp in length
*  155213   155312: gap of unknown length
*  155313   157809: contig of 2497 bp in length
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*  157910   159713: contig of 1804 bp in length
*  159714   159813: gap of unknown length
*  159814   161490: contig of 1677 bp in length
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*  166944   168772: contig of 1829 bp in length
*  168773   168872: gap of unknown length
*  168873   170399: contig of 1527 bp in length
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*  170500   171818: contig of 1319 bp in length
*  171819   171918: gap of unknown length
*  171919   173015: contig of 1097 bp in length
*  173016   173115: gap of unknown length
*  173116   174590: contig of 1475 bp in length
*  174591   174690: gap of unknown length
*  174691   175976: contig of 1286 bp in length
*  175977   176076: gap of unknown length
*  176077   177770: contig of 1694 bp in length
*  177771   177870: gap of unknown length
*  177871   179038: contig of 1168 bp in length
*  179039   179138: gap of unknown length
*  179139   180545: contig of 1407 bp in length
*  180546   180645: gap of unknown length
*  180646   182147: contig of 1502 bp in length
*  182148   182247: gap of unknown length

  Query Match            35.3%;  Score 75.2;  DB 2;  Length 184626;
  Best Local Similarity  63.5%;  Pred. No. 1.3e-12;
  Matches  132;  Conservative    0;  Mismatches   73;  Indels    3;  Gaps    1;

Qy      1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtccttttctcttctac 60
          ||| || | ||  || ||||||||| |||| || |||||  |||||  | || || || |||
Db 108651 GAAGAGAAGATTTTGAATTTGTACCACCATCCTGAGCCAATGAAGCCATTCCTGTTTTAC 108592

Qy     61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
          |||| || ||  ||    |  |||||||| || || |||| |||||||||| | || ||
Db 108591 CACACCCTGACAGGTGCAACGTCCACCTTTGAATCAGTGGTTTTCCCTGGCAGCTTTAT- 108531

Qy    121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
            || |  |||  |    |||   ||  || |||| ||   | ||  |||  ||    ||
```

```
Db 108532 --TGCCTCCTCCAAGATTGGCAAACCCATCTTCCTCACATCAAAAAAGGGAGAACATTAC 108475

Qy     181 actactgactttgggttaactatgctgt 208
           |   | |.||||   | |||   |||   | |
Db 108474 AACATTCACTTCAGTTTAGATATAATTT 108447


Search completed: June 21, 2002, 11:56:00
Job time: 15373 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: June 21, 2002, 07:54:17 ; Search time 338.08 Seconds
(without alignments)
1081.705 Million cell updates/sec

Title: US-09-763-498-5
Perfect score: 213
Sequence: 1 gaaaaggatataatggattt.....ggttaactatgctgttttaa 213

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802:*
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2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	213	100.0	213	21	AAZ51246	3' exon of human I
2	213	100.0	477	21	AAZ51247	Human Interleukin-
3	213	100.0	477	21	AAZ51248	Polymorphic human
4	210	98.6	819	22	AAD06911	Human interleukin-
5	175	82.2	391	22	AAF83870	Human interleukin-
6	125	58.7	219	19	AAV71959	Rodent interleukin
7	125	58.7	746	20	AAX86455	cDNA encoding a mu
8	125	58.7	809	19	AAV71960	Rodent interleukin
9	125	58.7	838	20	AAX86460	cDNA encoding a mu
10	97.4	45.7	1073	22	AAD12296	Human interleukin-
11	97.4	45.7	1183	19	AAV42659	cDNA encoding Inte
12	97.4	45.7	1183	20	AAX90135	Human interleukin-
13	97.4	45.7	1183	22	AAS26842	Human cDNA encodin
14	97.4	45.7	1291	20	AAX86458	cDNA encoding a hu
15	97.4	45.7	1321	21	AAA96351	cDNA encoding a no
16	97.4	45.7	1321	21	AAA51595	Human IL-1 recepto
17	97.4	45.7	1377	20	AAX86459	cDNA encoding a hu
18	97	45.5	673	22	AAS26915	Human cDNA encodin
19	97	45.5	673	22	AAD16762	Human novel protei
20	65.8	30.9	520	22	AAF83869	Human interleukin-
21	65.8	30.9	585	22	AAC90487	Human IL-1 eta cDN
22	65.8	30.9	1244	22	AAD08531	Human Interleukin-
23	54.2	25.4	465	21	AAA09194	Human IL-1 homolog
24	54.2	25.4	465	21	AAA09195	Human IL-1 homolog
25	51	23.9	1710	20	AAV99953	Nucleotide sequenc
26	48.8	22.9	468	20	AAX89431	Mouse interleukin
27	48.8	22.9	468	22	AAF31373	Invention related
28	48.8	22.9	468	22	AAC81700	Murine interleukin
29	48.8	22.9	470	19	AAV71958	Rodent interleukin
30	48.8	22.9	1275	21	AAA09198	Murine IL-1 homolo
31	48.8	22.9	1284	22	AAF27924	Murine IL-IL1 codi
32	48.8	22.9	1360	21	AAZ50811	Murine TANGO-93 cD
33	48.8	22.9	1385	21	AAA51599	Murine IL-1 recept
34	48.6	22.8	531	22	AAF85156	Nucleotide sequenc
35	48.6	22.8	603	22	AAF85157	Nucleotide sequenc
36	48.6	22.8	1577	19	AAV21578	Equine interleukin
37	48.6	22.8	1614	22	AAF85155	Nucleotide sequenc
38	47.2	22.2	8032	22	AAF31372	Invention related
39	46.8	22.0	357	22	AAF31351	B2HFLS20W cDNA lib
40	46.8	22.0	358	20	AAZ30048	cDNA encoding a hu
41	46.8	22.0	468	20	AAX89432	Human interleukin
42	46.8	22.0	468	21	AAA51597	Human IL-1 recepto
43	46.8	22.0	766	21	AAA09193	Human IL-1 homolog
44	46.8	22.0	985	20	AAZ30049	cDNA encoding a hu
45	46.8	22.0	985	22	AAF31352	B2HFLS20W cDNA lib

ALIGNMENTS

RESULT 1
AAZ51246
ID AAZ51246 standard; DNA; 213 BP.
XX
AC AAZ51246;
XX
DT 06-JUN-2000 (first entry)
XX
DE 3' exon of human Interleukin-1 epsilon DNA.
XX
KW Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;
KW gene mapping; immune system; treatment; inflammatory disease;
KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
KW psoriasis; human; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..213
FT /*tag= a
FT /partial
FT /product= "Partial human IL-1 epsilon protein"
FT /note= "Homologous to mouse IL-1 epsilon protein"
XX
PN WO200011174-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US18771.
XX
PR 21-AUG-1998; 98US-0097413.

PR 31-AUG-1998; 98US-0098595.
PR 11-SEP-1998; 98US-0099974.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Sims JE, Smith DE;
XX
DR WPI; 2000-237653/20.
DR P-PSDB; AAY70216.
XX
PT Nucleotide sequences encoding human interleukin -1 epsilon, useful to
PT treat inflammatory and immune system-related diseases such as
PT rheumatoid arthritis and inflammatory bowel disease -
XX
PS Claim 1a; Fig 1; 76pp; English.
XX
CC The present sequence is the 3' exon of human Interleukin-1 (IL-1)
CC epsilon DNA. IL-1 epsilon gene is mapped to chromosome 2q and is mainly
CC expressed in spleen, lymph node, thymus, tonsil and leucocyte tissues.
CC IL-1 epsilon is a cytokine, with antiinflammatory, immunosuppressant,
CC antirheumatic, antiarthritic and antipsoriatic activity. The DNA
CC sequence can be used in chromosome identification, gene mapping and
CC study of immune system. IL-1 epsilon can be used in the treatment of
CC inflammatory or autoimmune diseases such as rheumatoid arthritis,
CC inflammatory bowel disease and psoriasis.
XX
SQ Sequence 213 BP; 51 A; 56 C; 48 G; 58 T; 0 other;

Query Match 100.0%; Score 213; DB 21; Length 213;
Best Local Similarity 100.0%; Pred. No. 7e-59;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 60

Qy     61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120

Qy    121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180

Qy    181 actactgactttgggttaactatgctgttttaa 213
          |||||||||||||||||||||||||||||||
Db    181 actactgactttgggttaactatgctgttttaa 213
```

RESULT 2
AAZ51247
ID AAZ51247 standard; DNA; 477 BP.
XX
AC AAZ51247;
XX
DT 06-JUN-2000 (first entry)
XX
DE Human Interleukin-1 epsilon DNA.
XX
KW Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;
KW gene mapping; immune system; treatment; inflammatory disease;
KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
KW psoriasis; human; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..477
FT /*tag= a
FT /product= "Interleukin-1 epsilon protein"
FT /note= "Homologous to mouse IL-1 epsilon protein"

XX
PN WO200011174-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US18771.
XX
PR 21-AUG-1998; 98US-0097413.
PR 31-AUG-1998; 98US-0098595.
PR 11-SEP-1998; 98US-0099974.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Sims JE, Smith DE;
XX
DR WPI; 2000-237653/20.
DR P-PSDB; AAY70217.
XX
PT Nucleotide sequences encoding human interleukin -1 epsilon, useful to
PT treat inflammatory and immune system-related diseases such as
PT rheumatoid arthritis and inflammatory bowel disease -
XX
PS Claim 1a; Fig 1; 76pp; English.
XX
CC The present sequence is the human Interleukin-1 (IL-1) epsilon DNA
CC encoding IL-1 epsilon protein. This gene is mapped to chromosome 2q and
CC is mainly expressed in spleen, lymph node, thymus, tonsil and leucocyte
CC tissues. IL-1 epsilon is a cytokine, with antiinflammatory,
CC immunosuppressant, antirheumatic, antiarthritic and antipsoriatic
CC activity. The DNA sequence can be used in chromosome identification,
CC gene mapping and study of immune system. IL-1 epsilon can be used in the
CC treatment of inflammatory or autoimmune diseases such as rheumatoid
CC arthritis, inflammatory bowel disease and psoriasis.
XX
SQ Sequence 477 BP; 124 A; 123 C; 117 G; 113 T; 0 other;

Query Match 100.0%; Score 213; DB 21; Length 477;
Best Local Similarity 100.0%; Pred. No. 9.6e-59;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 60
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Db    265 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 324

Qy     61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    325 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 384

Qy    121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    385 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 444

Qy    181 actactgactttgggttaactatgctgttttaa 213
          |||||||||||||||||||||||||||||||
Db    445 actactgactttgggttaactatgctgttttaa 477
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RESULT 3
AAZ51248
ID AAZ51248 standard; DNA; 477 BP.
XX
AC AAZ51248;
XX
DT 06-JUN-2000 (first entry)
XX
DE Polymorphic human Interleukin-1 epsilon DNA.
XX
KW Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;
KW gene mapping; immune system; treatment; inflammatory disease;
KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
KW psoriasis; human; ds.

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XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..477
FT                   /*tag=  a
FT                   /product= "Interleukin-1 epsilon polymorphic variant"
FT                   /note= "Homologous to mouse IL-1 epsilon protein"
FT   variation       replace (35, A)
FT                   /*tag=  b
XX
PN   WO200011174-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US18771.
XX
PR   21-AUG-1998;   98US-0097413.
PR   31-AUG-1998;   98US-0098595.
PR   11-SEP-1998;   98US-0099974.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Sims JE, Smith DE;
XX
DR   WPI; 2000-237653/20.
DR   P-PSDB; AAY70218.
XX
PT   Nucleotide sequences encoding human interleukin -1 epsilon, useful to
PT   treat inflammatory and immune system-related diseases such as
PT   rheumatoid arthritis and inflammatory bowel disease -
XX
PS   Claim 1a; Fig 1; 76pp; English.
XX
CC   The present sequence is the polymorphic human Interleukin-1 (IL-1)
CC   epsilon DNA. This gene is mapped to chromosome 2q and is mainly
CC   expressed in spleen, lymph node, thymus, tonsil and leucocyte
CC   tissues. IL-1 epsilon is a cytokine, with antiinflammatory,
CC   immunosuppressant, antirheumatic, antiarthritic and antipsoriatic
CC   activity. The DNA sequence can be used in chromosome identification,
CC   gene mapping and study of immune system. IL-1 epsilon can be used in the
CC   treatment of inflammatory or autoimmune diseases such as rheumatoid
CC   arthritis, inflammatory bowel disease and psoriasis.
XX
SQ   Sequence 477 BP; 123 A; 123 C; 118 G; 113 T; 0 other;


  Query Match             100.0%;  Score 213;  DB 21;  Length 477;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-59;
  Matches  213;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 60
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Db     265 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 324

Qy      61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     325 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 384

Qy     121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     385 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 444

Qy     181 actactgactttgggttaactatgctgttttaa 213
          |||||||||||||||||||||||||||||||||
Db     445 actactgactttgggttaactatgctgttttaa 477


RESULT   4
AAD06911
ID   AAD06911 standard; cDNA; 819 BP.
XX
AC   AAD06911;
XX
DT   03-AUG-2001  (first entry)
XX
DE   Human interleukin-1 receptor antagonist-like (IL-1ra-L) cDNA.
XX
KW   Human; interleukin-1 receptor antagonist-like protein; IL-1ra-L; therapy;
KW   rheumatoid arthritis; psoriatic arthritis; inflammatory arthritis; lupus;
KW   joint disease; autoimmune disease; multiple sclerosis; diabetes; obesity;
KW   transplant rejection; graft versus host disease; strain; sprain; leprosy;
KW   cartilage damage; hepatitis; human immunodeficiency virus; HIV; anorexia;
KW   clostridium-associated diarrhoea; pulmonary tuberculosis; septic shock;
KW   myopathy; Alzheimer's disease; Parkinson's disease; memory disorder;
KW   acute respiratory disease syndrome; cystic fibrosis; asthma; psoriasis;
KW   eczema; glomerulonephritis; osteoporosis; Paget's disease; lymphoma;
KW   hypercalcaemia; haemorrhage; ischaemia; atherosclerosis; leukaemia;
KW   infertility; endometriosis; retinal neuropathy; acute pancreatitis;
KW   Kawasaki's disease; cancer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..819
FT                   /*tag=  a
FT                   /product= "Human interleukin-1 receptor antagonist-like
FT                   (IL-1ra-L) protein"
FT                   /note= "CDS does not include stop codon"
FT                   /partial
XX
PN   WO200141792-A1.
XX
PD   14-JUN-2001.
XX
PF   04-DEC-2000; 2000WO-US32891.
XX
PR   10-DEC-1999;   99US-0170105.
PR   28-NOV-2000; 2000US-0724859.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Calzone FJ,  Luethy R,  Boedigheimer MJ,  Zhu J,  Chung Y,  Jing S;
XX
DR   WPI; 2001-381495/40.
DR   P-PSDB; AAE03417.
XX
PT   Novel Interleukin-1 Receptor Antagonist-Like nucleic acid molecule, the
PT   polypeptide encoded by the nucleic acid is useful diagnosis, treatment,
PT   and prevention of diseases such as arthritis, diabetes, transplant
PT   rejection  -
XX
PS   Claim 1; Fig 1A; 127pp; English.
XX
CC   The present sequence is human interleukin-1 receptor antagonist-like
CC   (IL-1ra-L) cDNA. IL-1ra-L is useful for treating, preventing or
CC   ameliorating IL-1ra-L polypeptide-related disease, condition or disorder
CC   which include rheumatoid arthritis, psoriatic arthritis, inflammatory
CC   arthritis, osteoarthritis, autoimmune disease, multiple sclerosis,
CC   lupus, diabetes, transplant rejection, inflammatory joint disease, graft
CC   versus host disease and inflammatory conditions resulting from strain,
CC   sprain, cartilage damage, trauma, orthopaedic surgery, hepatitis, human
CC   immunodeficiency virus (HIV) infection, clostridium-associated
CC   diarrhoea, leprosy, pulmonary tuberculosis, septic shock, obesity,
CC   anorexia, myopathies, Alzheimer's disease, Parkinson's disease, memory
CC   disorders, acute respiratory disease syndrome, cystic fibrosis, asthma,
CC   psoriasis, eczema, acute and chronic glomerulonephritis, osteoporosis,
CC   Paget's disease, hypercalcaemia, haemorrhage, ischaemia, atherosclerosis,
CC   lymphomas, lung and breast cancer, leukaemias, infertility,
CC   endometriosis, retinal degeneration, retinal neuropathy, acute
CC   pancreatitis and Kawasaki's disease.
XX
SQ   Sequence 819 BP; 202 A; 196 C; 204 G; 217 T; 0 other;

  Query Match             98.6%;  Score 210;  DB 22;  Length 819;
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  Best Local Similarity   100.0%;  Pred. No. 1.1e-57;
  Matches  210;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    670 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 729

Qy    121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    730 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 789

Qy    181 actactgactttgggttaactatgctgttt 210
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Db    790 actactgactttgggttaactatgctgttt 819


RESULT   5
AAF83870
ID   AAF83870 standard; cDNA; 391 BP.
XX
AC   AAF83870;
XX
DT   06-AUG-2001  (first entry)
XX
DE   Human interleukin-1 receptor antagonist (NOVINTRA C) encoding cDNA.
XX
KW   NOVX; transmembrane protein; NOVTRAN; neuromedin peptide; NOVNEUR;
KW   gonadotropin-like protein; NOVGON; interleukin-1; NOVINTRA; human;
KW   cytostatic; neuroprotective; reproductive; antiinflammatory; cancer;
KW   antibacterial; cerebroprotective; antidiabetic; antiarthritic;
KW   antiasthmatic; antiallergic; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..391
FT                   /*tag=  a
FT                   /product= "NOVINTRA C"
XX
PN   WO200140291-A2.
XX
PD   07-JUN-2001.
XX
PF   06-DEC-2000; 2000WO-US33029.
XX
PR   06-DEC-1999;   99US-0169056.
PR   09-DEC-1999;   99US-0169866.
PR   09-DEC-1999;   99US-0169886.
PR   10-DEC-1999;   99US-0170252.
PR   12-JAN-2000; 2000US-0175740.
PR   05-DEC-2000; 2000US-0170252.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Burgess CE,  Prayaga SK,  Shimkets RA,  Rastelli L,  Zerhusen BD;
PI   Mezes PS;
XX
DR   WPI; 2001-374790/39.
DR   P-PSDB; AAB85001.
XX
PT   Novel isolated human transmembrane, neuromedin peptide
PT   gonadotropin-like protein and interleukin-1 receptor antagonist
PT   proteins, useful for treating cancer, immune response disorder,
PT   metabolic function disorders  -
XX
PS   Claim 50; Fig 15A; 138pp; English.
XX
CC   The invention provides novel polypeptides (NOVX) selected from human
CC   transmembrane protein (NOVTRAN), neuromedin peptide (NOVNEUR),
CC   gonadotropin-like protein (NOVGON) and two interleukin-1 receptor
CC   antagonist proteins (NOVINTRA A and B). The invention also provides
CC   methods in which a NOVX polypeptide, polynucleotide  and antibody are
CC   used in the detection, prevention and treatment of a broad range of
CC   pathological states. NOVTRAN can be used to treat is a cell signaling
CC   disorder such as cancer, immune  response disorder, hematopoietic
CC   disorder, neurodegenerative disorder. NOVNEUR can be used to treat
CC   endocrine disorder, muscle disorder, neurologic disorder, cancers of
CC   central nervous system, breast, colon, ovary, kidney, prostate and
CC   thyroid. NOVGON can be used to treat reproductive development disorder,
CC   metabolic function disorder and melanoma. NOVINTRA A and B can be used
CC   to treat bone metabolism or structure disorder, inflammatory response
CC   disorder, immune regulation disorder, septic shock, stroke, diabetes,
CC   arthritis and cancer. The present sequence represents a cDNA encoding
CC   the NOVINTRA C polypeptide.
XX
SQ   Sequence 391 BP; 94 A; 106 C; 99 G; 92 T; 0 other;


  Query Match             82.2%;  Score 175;  DB 22;  Length 391;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-46;
  Matches  175;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    217 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 276

Qy     61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    277 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 336

Qy    121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaag 175
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    337 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaag 391


RESULT   6
AAV71959
ID   AAV71959 standard; cDNA; 219 BP.
XX
AC   AAV71959;
XX
DT   19-FEB-1999  (first entry)
XX
DE   Rodent interleukin (IL)-1 epsilon partial polypeptide encoding cDNA.
XX
KW   Interleukin; IL-1 delta; polyclonal antibody; IL-1 epsilon; cytokine;
KW   inflammatory response; immune system; diagnosis; agonist; antagonist;
KW   chemokine; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..219
FT                   /*tag=  a
FT                   /product= "IL-1 eppsilon polypeptide partial sequence"
FT                   /note= "the start codon is not indicated"
XX
PN   WO9847921-A1.
XX
PD   29-OCT-1998.
XX
PF   17-APR-1998;   98WO-US06879.
XX
PR   06-AUG-1997;   97US-0055111.
PR   21-APR-1997;   97US-0837627.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Bazan JF,  Hedrick JA,  Kastelein RA,  Sana TR;
XX
DR   WPI; 1998-609976/51.
DR   P-PSDB; AAW86285.
```

XX
PT Mammalian interleukin 1-delta and 1-epsilon - useful for, e.g.
PT regulating the immune system and inflammatory responses
XX
PS Claim 14; Page 91; 113pp; English.
XX
CC This represents a partial cDNA sequence encoding a rodent interleukin
CC (IL)-1 epsilon partial polypeptide. The invention relates to a
CC recombinant polypeptide that specifically binds polyclonal antibodies
CC (Abs) generated against a 12 consecutive amino acid segment of IL-1 delta
CC or IL-1 epsilon. Agonists or antagonists of these IL polypeptides are
CC used to regulate a cell involved in an inflammatory response. The IL-1
CC delta or IL-1 epsilon polypeptides and peptides are used to produce Abs
CC and antigen-Ab complexes. The polypeptides, Abs and the corresponding
CC nucleic acids regulate development and/or the immune system, and can be
CC used to diagnose and treat conditions associated with abnormal expression
CC of IL. Agonists or antagonists of IL-1 delta or IL-1 epsilon polypeptides
CC are used with agonists or antagonists of IL-1 alpha, IL-1RA, IL-1 beta,
CC IL-1 gamma, IL-2 and/or IL-12. The IL-1 delta or IL-1 epsilon
CC polypeptides may be used as a soluble polypeptide or as a fusion protein
CC with another cytokine or chemokine.
XX
SQ Sequence 219 BP; 64 A; 51 C; 47 G; 57 T; 0 other;

```
  Query Match           58.7%;  Score 125;  DB 19;  Length 219;
  Best Local Similarity  74.2%;  Pred. No. 1.6e-30;
  Matches  158;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy       1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 60
           |||  | | ||||||||  ||||||||  ||   || |||||  ||  ||| |||||||||
Db       7 gaagggaacataatggaaatgtacaacaaaaaggaacctgtaaaagcctctctcttctat 66

Qy      61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
           ||||   ||||||| |  | ||| || || |||||||  || |||||||| |||||||||
Db      67 cacaagaagagtggtacaacctctacatttgagtctgcagccttccctggttggttcatc 126

Qy     121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
           |||||| ||||| ||||  |||| || ||||| || ||||||||||||||| ||  |  |
Db     127 gctgtctgctctaaagggagctgcccactcattctgacccaagaactgggggaaatcttc 186

Qy     181 actactgactttgggttaactatgctgttttaa 213
           |  |||||||| | | | | || |   ||||
Db     187 atcactgacttcgagatgattgtggtacattaa 219
```

RESULT 7
AAX86455
ID AAX86455 standard; cDNA; 746 BP.
XX
AC AAX86455;
XX
DT 30-SEP-1999 (first entry)
XX
DE cDNA encoding a murine SPOIL-I protein.
XX
KW SPOIL-I; interleukin-1 receptor antagonist; IL-1ra; modulating agent;
KW bone metabolism disorder; proinflammatory disorder; immune disorder;
KW inflammatory disease; septic shock; stroke; diabetes; arthritis;
KW intercolitis; pneumonitis; epithelial cell; skin disease;
KW proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;
KW epithelial cancer; squamous cell carcinoma; bone resorption disorder;
KW osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;
KW osteogenesis imperfecta; fibrous displasia; hypophosphatasia;
KW bone sarcoma; myeloma bone disorder; osteolytic bone lesion;
KW hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;
KW bone fracture; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 135..431
FT /*tag= a
FT /product= SPOIL-1
XX
PN WO9937662-A1.
XX
PD 29-JUL-1999.
XX
PF 26-JAN-1999; 99WO-US01575.
XX
PR 27-JAN-1998; 98US-0013810.
XX
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI Busfield SJ;
XX
DR WPI; 1999-458675/38.
DR P-PSDB; AAY24040.
XX
PT New isolated SPOIL proteins, used to develop products for treating,
PT e.g. inflammatory and immune disorders
XX
PS Claim 1; Fig 1; 126pp; English.
XX
CC The present sequence encodes a SPOIL-I protein. The SPOIL proteins have
CC homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.
CC The SPOIL proteins are used as modulating agents in regulating a variety
CC of cellular processes. The products can be used for treating disorders
CC characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone
CC metabolism disorder, a proinflammatory disorder or an immune disorder.
CC They can be used for treating e.g. inflammatory diseases and disorders
CC e.g. inflammation, septic shock, stroke, diabetes, arthritis,
CC intercolitis and pneumonitis, epithelial cell and/or skin diseases and
CC disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma
CC and Kaposi's sarcoma and other epithelial cancers including squamous cell
CC carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and
CC bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's
CC disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,
CC fibrous displasia, hypophosphatasia, bone sarcoma, myeloma bone disorder
CC (e.g. osteolytic bone lesions) and hypercalcemia. SPOIL molecules and
CC SPOIL modulators are useful for regulation of bone mass (e.g. increase in
CC bone mass and/or inhibit bone loss), management of bone fragility (e.g.
CC decrease bone fragility); and prevention and/or treatment of bone pain,
CC bone deformities and/or bone fractures. The products can also be used for
CC detection, diagnosis and screening assays.
XX
SQ Sequence 746 BP; 275 A; 150 C; 142 G; 179 T; 0 other;

```
  Query Match           58.7%;  Score 125;  DB 20;  Length 746;
  Best Local Similarity  74.2%;  Pred. No. 2.6e-30;
  Matches  158;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy       1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 60
           |||  | | ||||||||  ||||||||  ||   || |||||  ||  ||| |||||||||
Db     219 gaagggaacataatggaaatgtacaacaaaaaggaacctgtaaaagcctctctcttctat 278

Qy      61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
           ||||   ||||||| |  | ||| || || |||||||  || |||||||| |||||||||
Db     279 cacaagaagagtggtacaacctctacatttgagtctgcagccttccctggttggttcatc 338

Qy     121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
           |||||| ||||| ||||  |||| || ||||| || ||||||||||||||| ||  |  |
Db     339 gctgtctgctctaaagggagctgcccactcattctgacccaagaactgggggaaatcttc 398

Qy     181 actactgactttgggttaactatgctgttttaa 213
           |  |||||||| | | | | || |   ||||
Db     399 atcactgacttcgagatgattgtggtacattaa 431
```

RESULT 8
AAV71960
ID AAV71960 standard; cDNA; 809 BP.
XX
AC AAV71960;

```
XX
DT   19-FEB-1999  (first entry)
XX
DE   Rodent interleukin (IL)-1 epsilon polypeptide encoding cDNA.
XX
KW   Interleukin; IL-1 delta; polyclonal antibody; IL-1 epsilon; cytokine;
KW   inflammatory response; immune system; diagnosis; agonist; antagonist;
KW   chemokine; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             90..572
FT                   /*tag= a
FT                   /product= "IL-1 epsilon polypeptide"
XX
PN   WO9847921-A1.
XX
PD   29-OCT-1998.
XX
PF   17-APR-1998;    98WO-US06879.
XX
PR   06-AUG-1997;    97US-0055111.
PR   21-APR-1997;    97US-0837627.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Bazan JF,  Hedrick JA,  Kastelein RA,  Sana TR;
XX
DR   WPI; 1998-609976/51.
DR   P-PSDB; AAW86286.
XX
PT   Mammalian interleukin 1-delta and 1-epsilon - useful for, e.g.
PT   regulating the immune system and inflammatory responses
XX
PS   Claim 14; Pages 92-93; 113pp; English.
XX
CC   This cDNA encodes a rodent interleukin (IL)-1 epsilon polypeptide. The
CC   invention relates to a recombinant polypeptide that specifically binds
CC   polyclonal antibodies (Abs) generated against a 12 consecutive amino acid
CC   segment of IL-1 delta or IL-1 epsilon. Agonists or antagonists of these
CC   IL polypeptides are used to regulate a cell involved in an inflammatory
CC   response. The IL-1 delta or IL-1 epsilon polypeptides and peptides are
CC   used to produce Abs and antigen-Ab complexes. The polypeptides, Abs and
CC   the corresponding nucleic acids regulate development and/or the immune
CC   system, and can be used to diagnose and treat conditions associated with
CC   abnormal expression of IL. Agonists or antagonists of IL-1 delta or IL-1
CC   epsilon polypeptides are used with agonists or antagonists of IL-1 alpha,
CC   IL-1RA, IL-1 beta, IL-1 gamma, IL-2 and/or IL-12. The IL-1 delta or IL-1
CC   epsilon polypeptides may be used as a soluble polypeptide or as a fusion
CC   protein with another cytokine or chemokine.
XX
SQ   Sequence 809 BP; 241 A; 180 C; 179 G; 209 T; 0 other;


  Query Match             58.7%;  Score 125;  DB 19;  Length 809;
  Best Local Similarity   74.2%;  Pred. No. 2.7e-30;
  Matches  158;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy       1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtccttttctcttctac 60
           |||  | | ||||||||  |||||||| ||   || ||||| ||  ||| |||||||||
Db     360 gaagggaacataatggaaatgtacaacaaaaaggaacctgtaaaagcctctctcttctat 419

Qy      61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
           ||||   ||||||| |  | ||| || || |||||||  || ||||||||  |||||||||
Db     420 cacaagaagagtggtacaacctctacatttgagtctgcagccttccctggttggttcatc 479

Qy     121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
           |||||| ||||| ||||  |||| || ||||| || ||||||||||||||  ||  |  |
Db     480 gctgtctgctctaaagggagctgcccactcattctgacccaagaactgggggaaatcttc 539

Qy     181 actactgactttgggttaactatgctgttttaa 213
           |  |||||||| | | | | | || |   ||||
Db     540 atcactgacttcgagatgattgtggtacattaa 572


RESULT   9
AAX86460
ID   AAX86460 standard; cDNA; 838 BP.
XX
AC   AAX86460;
XX
DT   30-SEP-1999  (first entry)
XX
DE   cDNA encoding a murine SPOIL-II protein.
XX
KW   SPOIL-II; interleukin-1 receptor antagonist; IL-1ra; modulating agent;
KW   bone metabolism disorder; proinflammatory disorder; immune disorder;
KW   inflammatory disease; septic shock; stroke; diabetes; arthritis;
KW   intercolitis; pneumonitis; epithelial cell; skin disease;
KW   proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;
KW   epithelial cancer; squamous cell carcinoma; bone resorption disorder;
KW   osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;
KW   osteogenesis imperfecta; fibrous displasia; hypophosphatasia;
KW   bone sarcoma; myeloma bone disorder; osteolytic bone lesion;
KW   hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;
KW   bone fracture; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             96..578
FT                   /*tag= a
FT                   /product= SPOIL-II
XX
PN   WO9937662-A1.
XX
PD   29-JUL-1999.
XX
PF   26-JAN-1999;    99WO-US01575.
XX
PR   27-JAN-1998;    98US-0013810.
XX
PA   (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI   Busfield SJ;
XX
DR   WPI; 1999-458675/38.
DR   P-PSDB; AAY24049.
XX
PT   New isolated SPOIL proteins, used to develop products for treating,
PT   e.g. inflammatory and immune disorders
XX
PS   Claim 1; Fig 6; 126pp; English.
XX
CC   The present sequence encodes a SPOIL-II protein. The SPOIL proteins have
CC   homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.
CC   The SPOIL proteins are used as modulating agents in regulating a variety
CC   of cellular processes. The products can be used for treating disorders
CC   characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone
CC   metabolism disorder, a proinflammatory disorder or an immune disorder.
CC   They can be used for treating e.g. inflammatory diseases and disorders
CC   e.g. inflammation, septic shock, stroke, diabetes, arthritis,
CC   intercolitis and pneumonitis, epithelial cell and/or skin diseases and
CC   disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma
CC   and Kaposi's sarcoma and other epithelial cancers including squamous cell
CC   carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and
CC   bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's
CC   disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,
CC   fibrous displasia, hypophosphatasia, bone sarcoma, myeloma bone disorder
CC   (e.g. osteolytic bone lesions) and hypercalcemia. SPOIL molecules and
CC   SPOIL modulators are useful for regulation of bone mass (e.g. increase in
CC   bone mass and/or inhibit bone loss), management of bone fragility (e.g.
CC   decrease bone fragility); and prevention and/or treatment of bone pain,
CC   bone deformities and/or bone fractures. The products can also be used for
CC   detection, diagnosis and screening assays.
```

```
XX
SQ   Sequence 838 BP; 256 A; 188 C; 184 G; 210 T; 0 other;


  Query Match             58.7%;  Score 125;  DB 20;  Length 838;
  Best Local Similarity   74.2%;  Pred. No. 2.7e-30;
  Matches  158;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy       1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 60
           |||  | | ||||||||  |||||||| ||   || ||||| ||  ||| |||||||||
Db     366 gaagggaacataatggaaatgtacaacaaaaaggaacctgtaaaagcctctctcttctat 425

Qy      61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
           ||||  |||||||  |  | ||| || || |||||||  || ||||||||  |||||||||
Db     426 cacaagaagagtggtacaacctctacatttgagtctgcagccttccctggttggttcatc 485

Qy     121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
           ||||||  |||||  ||||  ||||  || ||||| || ||||||||||||||| ||  |  |
Db     486 gctgtctgctctaaagggagctgcccactcattctgacccaagaactgggggaaatcttc 545

Qy     181 actactgactttgggttaactatgctgttttaa 213
           |  |||||||| | | | | | || |   ||||
Db     546 atcactgacttcgagatgattgtggtacattaa 578


RESULT  10
AAD12296
ID   AAD12296 standard; DNA; 1073 BP.
XX
AC   AAD12296;
XX
DT   16-OCT-2001  (first entry)
XX
DE   Human interleukin-1epsilon (IL-1epsilon) protein DNA.
XX
KW   Human; interleukin-1epsilon; IL-1epsilon; virucide; hepatotropic; fever;
KW   immunological disorder; tumour; inflammatory disorder; hypoglycaemia;
KW   autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;
KW   psoriasis; viral infection; allergy; cytokine; HIV; drug screening; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             67..576
FT                   /*tag=  a
FT                   /product= "Human interleukin-1epsilon (IL-1epsilon)
FT                   protein"
XX
PN   WO200157219-A2.
XX
PD   09-AUG-2001.
XX
PF   01-FEB-2001; 2001WO-US03285.
XX
PR   02-FEB-2000; 2000US-0179638.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Debets JEMA,  Timans JC,  Bazan JF,  Kastelein RA;
XX
DR   WPI; 2001-488886/53.
DR   P-PSDB; AAE06656.
XX
PT   Novel isolated or recombinant antigenic interleukin-1 delta or epsilon
PT   polypeptide useful for treating conditions exhibiting abnormal
PT   expression of interleukin such as immunological disorders, tumor and
PT   allergy  -
XX
PS   Claim 18; Page 86-87; 103pp; English.
XX
CC   The invention relates to recombinant antigenic interleukin-1 like
CC   molecules and their corresponding nucleic acid sequences, designated
CC   as interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon).
CC   IL-1delta and IL-1epsilon are useful for treating conditions exhibiting
CC   abnormal expression of the interleukin such as immunological disorders,
CC   tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis,
CC   allergy, autoimmune diseases and infectious diseases (e.g., pulmonary
CC   tuberculosis, leprosy, fulminant hepatitis, and viral infections such as
CC   HIV). The invention also relates to methods of using the composition
CC   containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic
CC   utilities. IL-1delta is used as an immunogen for the production of
CC   antisera or antibodies specific, e.g., capable of distinguishing between
CC   IL-1 family members and an IL-1delta, for the interleukin or its
CC   fragment. The purified interleukin is used as a reagent to detect any
CC   antibodies generated in response to the presence of elevated levels of
CC   expression, or immunological disorders which lead to antibody production
CC   to the endogenous cytokine. The invention also contemplates the use of
CC   competitive drug screening assays. The present DNA sequence encodes human
CC   interleukin-1epsilon (IL-1epsilon) protein.
XX
SQ   Sequence 1073 BP; 281 A; 241 C; 255 G; 296 T; 0 other;


  Query Match             45.7%;  Score 97.4;  DB 22;  Length 1073;
  Best Local Similarity   70.9%;  Pred. No. 2.3e-21;
  Matches  144;  Conservative    0;  Mismatches   56;  Indels    3;  Gaps    1;

Qy       1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 60
             ||  || | || |||||| ||||   |||||||||||| |||||  |||| || ||||||
Db     367 gagcagaagatcatggatctgtatggccaacccgagcccgtgaaacccttcctttttctac 426

Qy      61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
           |    | ||| ||| |||| ||||||| | |||||||||||| ||||| | |||||||||
Db     427 cgtgccaagactggtaggacctccacccttgagtctgtggccttcccggactggttcat- 485

Qy     121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
             || |  |||  |  ||| |   ||  |||| || ||   |||||| |||||  |  ||
Db     486 --tgcctcctccaagagagaccagcccatcattctgacttcagaacttgggaagtcatac 543

Qy     181 actactgactttgggttaactat 203
           |  |||| |||||  |||| |||
Db     544 aacactgcctttgaattaaatat 566


RESULT  11
AAV42659
ID   AAV42659 standard; cDNA; 1183 BP.
XX
AC   AAV42659;
XX
DT   14-OCT-1998  (first entry)
XX
DE   cDNA encoding Interleukin-1 receptor antagonist beta (IL-1ra-beta).
XX
KW   Interleukin-1 receptor antagonist beta; IL-1ra-beta; IL-1 alpha;
KW   IL-1 beta; inflammatory response; treatment; inflammation; septicaemia;
KW   cancer; anaemia; arthritis; inflammatory bowel disease;
KW   graft vs. host rejection; autoimmunity; stroke; cardiac ischaemia;
KW   acute respiratory disease syndrome; psoriasis; restenosis;
KW   traumatic brain injury; acquired immune deficiency syndrome;
KW   cachexia; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             75..584
FT                   /*tag=  a
FT                   /product= IL-1ra-beta
XX
PN   EP855404-A1.
XX
PD   29-JUL-1998.
XX
PF   27-JAN-1998;   98EP-0300572.
XX
PR   28-JAN-1997;   97US-0790032.
```

XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Young PR;
XX
DR WPI; 1998-389778/34.
DR P-PSDB; AAW63136.
XX
PT New nucleic acid encoding human interleukin-1 receptor antagonist
PT beta polypeptides - and related expression systems, transformed
PT cells, proteins, antibodies, agonists and antagonists, useful for
PT treatment, prevention and diagnosis of inflammation, septicaemia,
PT cancer etc
XX
PS Claim 3; Fig 1; 20pp; English.
XX
CC The present sequence encodes human Interleukin-1 receptor antagonist
CC beta (IL-ra-beta). IL-1 alpha and IL-1 beta play key roles in
CC inflammatory responses, and are produced as zymogens which are cleaved
CC upon secretion to yield mature carboxyl terminal 17 kD fragments.
CC IL-1ra-beta polypeptides and polynucleotides are useful in treatment of
CC chronic and acute inflammation, septicaemia, cancer, anaemia, arthritis,
CC inflammatory bowel disease, graft vs. host rejection, autoimmunity,
CC stroke, cardiac ischaemia, acute respiratory disease syndrome (ARDS),
CC psoriasis, restenosis, traumatic brain injury, acquired immune
CC deficiency syndrome (AIDS) and cachexia. These conditions (or
CC susceptibility to them) may be diagnosed by detecting mutations in the
CC IL-1ra-beta coding sequence analysing a sample for presence or amount
CC of IL-1ra-beta.
XX
SQ Sequence 1183 BP; 329 A; 249 C; 269 G; 336 T; 0 other;

Query Match 45.7%; Score 97.4; DB 19; Length 1183;
Best Local Similarity 70.9%; Pred. No. 2.4e-21;
Matches 144; Conservative 0; Mismatches 56; Indels 3; Gaps 1;

```
Qy       1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtccttttctcttctac 60
          ||  || | || |||||| ||||   |||||||||||| |||||  |||| || ||||||
Db     375 gagcagaagatcatggatctgtatggccaacccgagcccgtgaaacccttcctttttctac 434

Qy      61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
           |    | ||| ||| |||| ||||||| | |||||||||||| ||||| | |||||||||
Db     435 cgtgccaagactggtaggacctccacccttgagtctgtggccttcccggactggttcat- 493

Qy     121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
             || |  |||  |  ||| |   ||  |||| || ||   |||||| |||||  |  ||
Db     494 --tgcctcctccaagagagaccagcccatcattctgacttcagaacttgggaagtcatac 551

Qy     181 actactgactttgggttaactat 203
           |  |||| |||||  |||| |||
Db     552 aacactgcctttgaattaaatat 574
```

RESULT 12
AAX90135
ID AAX90135 standard; cDNA; 1183 BP.
XX
AC AAX90135;
XX
DT 20-SEP-1999 (first entry)
XX
DE Human interleukin-1 receptor antagonist beta encoding cDNA.
XX
KW Human; interleukin-1 receptor antagonist beta; IL-1RA beta; septicemia;
KW chronic inflammation; acute inflammation; arthritis; autoimmunity;
KW inflammatory bowel disease; graft vs. host disease; stroke; psoriasis;
KW cardiac ischaemia; acute respiratory disease syndrome; ARDS; restenosis;
KW traumatic brain injury; AIDS; cachexia; allergy; parasite infection;
KW allergic rhinitis; allergic asthma; atopic dermatitis; gene therapy;
KW allergic inflammatory disease; delayed hypersensitivity; vaccine; ss.
XX
OS Homo sapiens.

XX
PN WO9936541-A1.
XX
PD 22-JUL-1999.
XX
PF 14-JAN-1999; 99WO-US00847.
XX
PR 29-APR-1998; 98US-0069619.
PR 14-JAN-1998; 98US-0007464.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Marshall L, Young PR;
XX
DR WPI; 1999-430615/36.
DR P-PSDB; AAY24395.
XX
PT New interleukin-1 receptor antagonist beta, useful for treating
PT inflammation and autoimmune diseases
XX
PS Claim 5; Fig 1; 34pp; English.
XX
CC The present sequence encodes human interleukin-1 receptor antagonist
CC beta (IL-1RA beta). IL-1RA beta polypeptides and polynucleotides are
CC useful for diagnosing diseases (or susceptibility to diseases) related
CC to the expression or activity of IL-1RA beta, by determining mutations
CC in the IL-1RA beta nucleic acid sequences and/or analysing for the
CC presence or amount of IL-1RA beta polypeptide. IL-1RA beta polypeptides
CC are also useful for screening for compounds which affect activity of the
CC protein. These can be used in treatment to inhibit (antagonist) or
CC enhance (agonist) IL-1RA beta activity, in addition to direct
CC administration of IL-1RA beta polypeptides to treat conditions, or
CC direct administration of antisense sequences to prevent expression.
CC IL-1RA beta polypeptides (administered directly, in a vector i.e. gene
CC therapy, and as a vaccine) and antibodies induce an immune response to
CC immunise and prevent disease. Diseases diagnosed, prevented or treated
CC include chronic and acute inflammation, septicemia, arthritis,
CC inflammatory bowel disease, graft vs. host disease, autoimmunity,
CC stroke, cardiac ischaemia, acute respiratory disease syndrome (ARDS),
CC psoriasis, restenosis, traumatic brain injury, AIDS, cachexia, allergy,
CC parasite infection, allergic rhinitis, allergic asthma, atopic
CC dermatitis, allergic inflammatory diseases and delayed hypersensitivity.
XX
SQ Sequence 1183 BP; 329 A; 249 C; 269 G; 336 T; 0 other;

Query Match 45.7%; Score 97.4; DB 20; Length 1183;
Best Local Similarity 70.9%; Pred. No. 2.4e-21;
Matches 144; Conservative 0; Mismatches 56; Indels 3; Gaps 1;

```
Qy       1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtccttttctcttctac 60
          ||  || | || |||||| ||||   |||||||||||| |||||  |||| || ||||||
Db     375 gagcagaagatcatggatctgtatggccaacccgagcccgtgaaacccttcctttttctac 434

Qy      61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
           |    | ||| ||| |||| ||||||| | |||||||||||| ||||| | |||||||||
Db     435 cgtgccaagactggtaggacctccacccttgagtctgtggccttcccggactggttcat- 493

Qy     121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
             || |  |||  |  ||| |   ||  |||| || ||   |||||| |||||  |  ||
Db     494 --tgcctcctccaagagagaccagcccatcattctgacttcagaacttgggaagtcatac 551

Qy     181 actactgactttgggttaactat 203
           |  |||| |||||  |||| |||
Db     552 aacactgcctttgaattaaatat 574
```

RESULT 13
AAS26842
ID AAS26842 standard; cDNA; 1183 BP.
XX
AC AAS26842;
XX

DT 07-NOV-2001 (first entry)
XX
DE Human cDNA encoding a novel secreted protein, SEQ ID 34.
XX
KW Human; immunosuppressive; antiarthritic; ss; antirheumatic;
KW cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;
KW neuroprotective; antibacterial; virucide; fungicide; opthalmalogical;
KW vulnerary; secreted protein; rheumatoid arthritis;
KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;
KW corneal infection; wound healing; epithelial cell proliferation;
KW skin ageing; food additive; preservative; antiproliferative.
XX
OS Homo sapiens.
XX
PN WO200155441-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01320.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.

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PR   01-DEC-2000; 2000US-0250391.
PR   05-DEC-2000; 2000US-0251030.
PR   05-DEC-2000; 2000US-0251988.
PR   05-DEC-2000; 2000US-0256719.
PR   06-DEC-2000; 2000US-0251479.
PR   08-DEC-2000; 2000US-0251856.
PR   08-DEC-2000; 2000US-0251868.
PR   08-DEC-2000; 2000US-0251869.
PR   08-DEC-2000; 2000US-0251989.
PR   08-DEC-2000; 2000US-0251990.
PR   11-DEC-2000; 2000US-0254097.
PR   05-JAN-2001; 2001US-0259678.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-476222/51.
DR   P-PSDB; AAU16937.
XX
PT   Novel polypeptides and polynucleotides useful as diagnostic reagents to
PT   diagnose diseases or disorders associated with aberrant expression or
PT   activity of polypeptides, for treating blood clotting disorder,
PT   haemophilia  -
XX
PS   Claim 1; SEQ ID No 34; 601pp; English.
XX
CC   The invention relates to isolated nucleic acid molecules and their
CC   encoded secreted proteins. The nucleic acids and proteins are used to
CC   prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC   rabbits, goats, horses, cats, dogs, chickens or sheep. They
CC   are also used in diagnosing a pathological condition or susceptibility
CC   to a pathological condition. Antibodies to the proteins can also
CC   be used in alleviating symptoms associated with the disorders and in
CC   diagnostic immunoassays e.g. radioimmunoassays or enzyme linked
CC   immunosorbant assays (ELISA). Disorders which are diagnosed or treated
CC   include autoimmune diseases e.g. rheumatoid arthritis,
CC   hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC   cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC   e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
CC   Alzheimer's disease, infections caused by bacteria, viruses and fungi
CC   and ocular disorders e.g. corneal infection, and many other
CC   disorders listed in the specification. The polypeptides can also
CC   be used to aid wound healing and epithelial cell proliferation, to
CC   prevent skin aging due to sunburn, to maintain organs before
CC   transplantation, for supporting cell culture of primary tissues, to
CC   regenerate tissues and in chemotaxis. The polypeptides can also be used
CC   as a food additive or preservative to increase or decrease storage
CC   capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC   minerals, cofactors and other nutritional components. The present

  Query Match             45.7%;  Score 97.4;  DB 22;  Length 1183;
  Best Local Similarity   70.9%;  Pred. No. 2.4e-21;
  Matches  144;  Conservative    0;  Mismatches   56;  Indels    3;  Gaps    1;

Qy       1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtccttttctcttctac 60
           ||  || | || |||||| ||||   |||||||||||| |||||  |||| || ||||||
Db     375 gagcagaagatcatggatctgtatggccaacccgagcccgtgaaacccttcctttttctac 434

Qy      61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
           |    | ||| ||| |||| ||||||| | |||||||||||| ||||| | |||||||||
Db     435 cgtgccaagactggtaggacctccaccttgagtctgtggccttcccggactggttcat- 493

Qy     121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
             || |  |||  |  ||| |   ||  |||| || ||   |||||| |||||  |  ||
Db     494 --tgcctcctccaagagagaccagcccatcattctgacttcagaacttgggaagtcatac 551

Qy     181 actactgactttgggttaactat 203
           |  |||| |||||  |||| |||
Db     552 aacactgcctttgaattaaatat 574


RESULT  14
```

```
AAX86458
ID   AAX86458 standard; DNA; 1291 BP.
XX
AC   AAX86458;
XX
DT   30-SEP-1999  (first entry)
XX
DE   cDNA encoding a human SPOIL-I protein (also known as hTANGO 080-I).
XX
KW   SPOIL-I; interleukin-1 receptor antagonist; IL-1ra; modulating agent;
KW   bone metabolism disorder; proinflammatory disorder; immune disorder;
KW   inflammatory disease; septic shock; stroke; diabetes; arthritis;
KW   intercolitis; pneumonitis; epithelial cell; skin disease;
KW   proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;
KW   epithelial cancer; squamous cell carcinoma; bone resorption disorder;
KW   osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;
KW   osteogenesis imperfecta; fibrous displasia; hypophosphatasia;
KW   bone sarcoma; myeloma bone disorder; osteolytic bone lesion;
KW   hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;
KW   bone fracture; hTANGO 80-I; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             124..633
FT                   /*tag=  a
FT                   /product= SPOIL-1
XX
PN   WO9937662-A1.
XX
PD   29-JUL-1999.
XX
PF   26-JAN-1999;   99WO-US01575.
XX
PR   27-JAN-1998;   98US-0013810.
XX
PA   (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI   Busfield SJ;
XX
DR   WPI; 1999-458675/38.
DR   P-PSDB; AAY24043.
XX
PT   New isolated SPOIL proteins, used to develop products for treating,
PT   e.g. inflammatory and immune disorders.
XX
PS   Example 1; Fig 4A-B; 126pp; English.
XX
CC   The present sequence encodes a SPOIL-I protein. The SPOIL proteins have
CC   homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.
CC   The SPOIL proteins are used as modulating agents in regulating a variety
CC   of cellular processes. The products can be used for treating disorders
CC   characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone
CC   metabolism disorder, a proinflammatory disorder or an immune disorder.
CC   They can be used for treating e.g. inflammatory diseases and disorders
CC   e.g. inflammation, septic shock, stroke, diabetes, arthritis,
CC   intercolitis and pneumonitis, epithelial cell and/or skin diseases and
CC   disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma
CC   and Kaposi's sarcoma and other epithelial cancers including squamous cell
CC   carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and
CC   bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's
CC   disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,
CC   fibrous displasia, hypophosphatasia, bone sarcoma, myeloma bone disorder
CC   (e.g. osteolytic bone lesions) and hypercalcemia. SPOIL molecules and
CC   SPOIL modulators are useful for regulation of bone mass (e.g. increase in
CC   bone mass and/or inhibit bone loss), management of bone fragility (e.g.
CC   decrease bone fragility); and prevention and/or treatment of bone pain,
CC   bone deformities and/or bone fractures. The products can also be used for
CC   detection, diagnosis and screening assays.
XX
SQ   Sequence 1291 BP; 375 A; 271 C; 291 G; 354 T; 0 other;
```

```
  Query Match             45.7%;  Score 97.4;  DB 20;  Length 1291;
  Best Local Similarity   70.9%;  Pred. No. 2.5e-21;
  Matches  144;  Conservative    0;  Mismatches   56;  Indels    3;  Gaps    1;

Qy       1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 60
           ||  || | || |||||| ||||   ||||||||||| |||||  |||| || ||||||
Db     424 gagcagaagatcatggatctgtatggccaacccgagcccgtgaaacccttccttttctac 483

Qy      61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
           |    | ||| ||| |||| ||||||| | |||||||||||| ||||| | |||||||||
Db     484 cgtgccaagactggtaggacctccaccttgagtctgtggccttcccggactggttcat- 542

Qy     121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
             || |  |||  |  ||| |   ||  |||| || ||   |||||| |||||  |  ||
Db     543 --tgcctcctccaagagagaccagcccatcattctgacttcagaacttgggaagtcatac 600

Qy     181 actactgactttgggttaactat 203
           |  |||| |||||  |||| |||
Db     601 aacactgcctttgaattaaatat 623


RESULT  15
AAA96351
ID   AAA96351 standard; cDNA; 1321 BP.
XX
AC   AAA96351;
XX
DT   08-FEB-2001  (first entry)
XX
DE   cDNA encoding a novel polypeptide designated PRO5737.
XX
KW   Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122;
KW   PRO1889; PRO1890; PRO1887; PRO1785; PRO4353; PRO4357; PRO4405; PRO4356;
KW   PRO4352; PRO4380; PRO4354; PRO4408; PRO5737; PRO4425; PRO5990; PRO6030;
KW   PRO4424; PRO4422; PRO4430; PRO4499; tumour; obesity; diabetes;
KW   insulinemia; kidney disorder; Bergers disease; nephropathy;
KW   Schonlein-Henoch purpura; celiac disease; dermatitis herpetiformis;
KW   Crohns disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             96..500
FT                   /*tag=  a
FT   sig_peptide     96..146
FT                   /*tag=  b
XX
PN   WO200056889-A2.
XX
PD   28-SEP-2000.
XX
PF   01-MAR-2000; 2000WO-US05601.
XX
PR   23-MAR-1999;   99US-0125774.
PR   23-MAR-1999;   99US-0125778.
PR   24-MAR-1999;   99US-0125826.
PR   31-MAR-1999;   99US-0127035.
PR   05-APR-1999;   99US-0127706.
PR   21-APR-1999;   99US-0130359.
PR   27-APR-1999;   99US-0131270.
PR   27-APR-1999;   99US-0131272.
PR   27-APR-1999;   99US-0131291.
PR   04-MAY-1999;   99US-0132371.
PR   04-MAY-1999;   99US-0132379.
PR   04-MAY-1999;   99US-0132383.
PR   25-MAY-1999;   99US-0135750.
PR   08-JUN-1999;   99US-0138166.
PR   20-JUL-1999;   99US-0144791.
PR   03-AUG-1999;   99US-0146970.
PR   09-DEC-1999;   99US-0170262.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI   Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX
DR   WPI; 2000-628263/60.
DR   P-PSDB; AAB18924.
XX
PT   Novel secreted and transmembrane polypeptides useful for diagnosing
PT   tumour in a mammal, for identifying agonists and antagonists of the
PT   polypeptide and for therapeutic use  -
XX
PS   Claim 2; Fig 31; 222pp; English.
XX
CC   The present sequence encodes a secreted or transmembrane polypeptide.
CC   The specification describes polypeptides designated PRO1484, PRO4334,
CC   PRO1122, PRO1889, PRO1890, PRO1887, PRO1785, PRO4353, PRO4357, PRO4405,
CC   PRO4356, PRO4352, PRO4380, PRO4354, PRO4408, PRO5737, PRO4425, PRO5990,
CC   PRO6030, PRO4424, PRO4422, PRO4430 and PRO4499. PRO1889 polypeptide is
CC   useful for diagnosing tumour in a mammal. The polypeptides, their
CC   agonists and antagonists are useful treating a condition associated with
CC   expression or activity of the polypeptide. Conditions treated include
CC   obesity, diabetes or hyper-or hypo-insulinemia. The polypeptides are
CC   capable of inducing proliferation of mammalian kidney mesangial cells
CC   and are therefore useful for treating kidney disorders associated with
CC   decreased mesangial cell function such as Bergers disease or other
CC   nephropathies associated with Schonlein-Henoch purpura, celiac disease,
CC   dermatitis herpetiformis or Crohns disease. The nucleic acids may be used
CC   to generate transgenic animals for use in development and screening of
CC   therapeutically useful reagents and also for chromosome identification
CC   and tissue typing.
XX
SQ   Sequence 1321 BP; 362 A; 278 C; 293 G; 388 T; 0 other;


  Query Match             45.7%;  Score 97.4;  DB 21;  Length 1321;
  Best Local Similarity   70.9%;  Pred. No. 2.5e-21;
  Matches  144;  Conservative    0;  Mismatches   56;  Indels    3;  Gaps    1;

Qy       1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 60
           ||  || | || |||||| ||||   ||||||||||| |||||  |||| || ||||||
Db     291 gagcagaagatcatggatctgtatggccaacccgagcccgtgaaacccttccttttctac 350

Qy      61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
           |    | ||| ||| |||| ||||||| | |||||||||||| ||||| | |||||||||
Db     351 cgtgccaagactggtaggacctccaccttgagtctgtggccttcccggactggttcat- 409

Qy     121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
             || |  |||  |  ||| |   ||  |||| || ||   |||||| |||||  |  ||
Db     410 --tgcctcctccaagagagaccagcccatcattctgacttcagaacttgggaagtcatac 467

Qy     181 actactgactttgggttaactat 203
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Db     468 aacactgcctttgaattaaatat 490


Search completed: June 21, 2002, 12:02:57
Job time: 14920 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: June 21, 2002, 06:14:52 ; Search time 2828.95 Seconds
(without alignments)
1016.226 Million cell updates/sec

Title: US-09-763-498-5
Perfect score: 213
Sequence: 1 gaaaaggatataatggattt.....ggttaactatgctgttttaa 213

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	125	58.7	479	9	AA030324	AA030324 mi08c10.r
	2	125	58.7	883	11	AK004061	AK004061 Mus muscu
c	3	97.4	45.7	539	9	AW368430	AW368430 CM3-HT019
	4	97.4	45.7	555	9	AW361172	AW361172 RC1-CT025
c	5	97.4	45.7	555	10	BE695960	BE695960 RC1-CT025
c	6	97.4	45.7	557	9	AW368437	AW368437 CM3-HT019
c	7	97.4	45.7	559	9	AW578451	AW578451 RC1-CT025
c	8	95.8	45.0	436	9	AW361164	AW361164 RC1-CT025
	9	95.8	45.0	536	9	AW853610	AW853610 RC1-CT025
c	10	93.8	44.0	434	9	AW753217	AW753217 RC1-CT025
	11	91	42.7	560	9	AW361245	AW361245 RC1-CT025
	12	65.8	30.9	870	10	BF244205	BF244205 601863146
c	13	65.6	30.8	612	10	BM386666	BM386666 UI-R-CN1-
	14	62.6	29.4	393	9	AV011778	AV011778 AV011778
	15	56.6	26.6	1219	11	AK009787	AK009787 Mus muscu
	16	48.8	22.9	1051	11	AK009741	AK009741 Mus muscu
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	18	48.8	22.9	1531	11	AK010020	AK010020 Mus muscu
	19	48.8	22.9	2843	11	AK014576	AK014576 Mus muscu
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	21	46.8	22.0	726	10	BI089828	BI089828 602855071
	22	46.8	22.0	858	10	BI090567	BI090567 602855674
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	27	41.4	19.4	356	10	BE477245	BE477245 160853 BA
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	39	39.6	18.6	864	10	BI489807	BI489807 603031536
	40	38.8	18.2	281	10	R50241	R50241 yj58a03.r1
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c	42	38.6	18.1	350	10	BI020732	BI020732 CM4-MT021
c	43	37.2	17.5	421	10	BI289899	BI289899 UI-R-DK0-
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c	45	34.2	16.1	458	9	AW636636	AW636636 bl49a05.w

ALIGNMENTS

RESULT 1
AA030324
LOCUS AA030324 479 bp mRNA linear EST 21-JAN-1997
DEFINITION mi08c10.r1 Soares mouse placenta 4NbMP13.5 14.5 Mus musculus cDNA clone IMAGE:459858 5', mRNA sequence.
ACCESSION AA030324
VERSION AA030324.1 GI:1497479
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 479)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:276746
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 467.
FEATURES Location/Qualifiers
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:459858"
/clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
/sex="unknown"

/tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGGAAATTTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 148 a 108 c 102 g 121 t
ORIGIN

Query Match 58.7%; Score 125; DB 9; Length 479;
Best Local Similarity 74.2%; Pred. No. 3.2e-27;
Matches 158; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

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Db    204 GAAGGGAACATAATGGAAATGTACAACAAAAAGGAACCTGTAAAAGCCTCTCTCTTCTAT 263

Qy     61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
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Db    264 CACAAGAAGAGTGGTACAACCTCTACATTTGAGTCTGCAGCCTTCCCTGGTTGGTTCATC 323

Qy    121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
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Db    324 GCTGTCTGCTCTAAAGGGAGCTGCCCACTCATTCTGACCCAAGAACTGGGGGAAATCTTC 383

Qy    181 actactgactttgggttaactatgctgttttaa 213
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Db    384 ATCACTGACTTCGAGATGATTGTGGTACATTAA 416
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RESULT 2
AK004061
LOCUS AK004061 883 bp mRNA linear HTC 19-JAN-2002
DEFINITION Mus musculus 18 days embryo whole body cDNA, RIKEN full-length enriched library, clone:1110033G16:interleukin 1 family, member 6 (epsilon), full insert sequence.
ACCESSION AK004061
VERSION AK004061.1 GI:12835089
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (strain:C57BL/6J) 18 days embryo cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:1110033G16.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2 (sites)
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3 (sites)
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4 (sites)
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5 (bases 1 to 883)
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0. Second strand cDNA was prepared with the primer adapter of sequence[5' GAGAGAGAGAAGGATCCAAGAGCTCAATTAATTTAATTAAACCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.
FEATURES Location/Qualifiers
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/strain="C57BL/6J"
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/db_xref="taxon:10090"
/clone="1110033G16"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="18 days embryo"
gene 162. .644
/gene="Il1f6"
CDS 162. .644
/gene="Il1f6"
/note="data source:MGD, source key:MGI:1859324, evidence:ISS
interleukin 1 family, member 6 (epsilon)
putative"
/codon_start=1
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/db_xref="GI:12835090"
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TITLLPCQYLDTLETNRGDPTYMGVQRPMSCLFCTKDGEQPVLQLGEGNIMEMYNKKE
PVKASLFYHKKSGTTSTFESAAFPGWFIAVCSKGSCPLILTQELGEIFITDFEMIVVH

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     polyA_site      883
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  Best Local Similarity   74.2%;  Pred. No. 4.2e-27;
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Qy      61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
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Db     492 CACAAGAAGAGTGGTACAACCTCTACATTTGAGTCTGCAGCCTTCCCTGGTTGGTTCATC 551

Qy     121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
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Db     552 GCTGTCTGCTCTAAAGGGAGCTGCCCACTCATTCTGACCCAAGAACTGGGGGAAATCTTC 611

Qy     181 actactgactttgggttaactatgctgttttaa 213
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RESULT   3
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LOCUS       AW368430                539 bp    mRNA    linear   EST 04-FEB-2000
DEFINITION  CM3-HT0192-071099-022-e12 HT0192 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW368430
VERSION     AW368430.1  GI:6873080
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 539)
  AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
  TITLE     The FAPESP/LICR Human Cancer Genome Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM3&t2=CM3-HT0192-
            071099-022-e12&t3=1999-10-07&t4=1)
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                     /db_xref="taxon:9606"
                     /clone_lib="HT0192"
                     /dev_stage="Adult"
                     /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT      145 a    131 c    123 g    140 t
ORIGIN


  Query Match             45.7%;  Score 97.4;  DB 9;  Length 539;
  Best Local Similarity   70.9%;  Pred. No. 7.2e-19;
  Matches  144;  Conservative    0;  Mismatches   56;  Indels    3;  Gaps    1;

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Qy      61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
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Db     437 CGTGCCAAGACTGGTAGGACCTCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT- 377

Qy     121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
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Db     378 --TGCCTCCTCCAAGAGAGACCAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATAC 321

Qy     181 actactgactttgggttaactat 203
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Db     320 AACACTGCCTTTGAATTAAATAT 298


RESULT   4
AW361172
LOCUS       AW361172                555 bp    mRNA    linear   EST 04-FEB-2000
DEFINITION  RC1-CT0251-141099-012-h04 CT0251 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW361172
VERSION     AW361172.1  GI:6865822
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 555)
  AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
  TITLE     The FAPESP/LICR Human Cancer Genome Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC1&t2=RC1-CT0251-
            141099-012-h04&t3=1999-10-14&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 555.
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                     /dev_stage="Adult"
                     /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT      148 a    129 c    130 g    147 t      1 others
ORIGIN


  Query Match             45.7%;  Score 97.4;  DB 9;  Length 555;
  Best Local Similarity   70.9%;  Pred. No. 7.3e-19;
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Db     43 GAGCAGAAGATCATGGATCTGTATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTAC 102

Qy     61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
          |    | ||| ||| |||| ||||||| | |||||||||||| ||||| | |||||||||
Db    103 CGTGCCAAGACTGGTAGGACCTCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT- 161

Qy    121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
          || |  |||  |  ||| |   ||  |||| || ||   |||||| |||||  |  ||
Db    162 --TGCCTCCTCCAAGAGAGACCAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATAC 219

Qy    181 actactgactttgggttaactat 203
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Db    220 AACACTGCCTTTGAATTAAATAT 242


RESULT   5
BE695960/c
LOCUS       BE695960                555 bp    mRNA    linear   EST 11-SEP-2000
DEFINITION  RC1-CT0252-150600-028-h05 CT0252 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE695960
VERSION     BE695960.1  GI:10083120
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 555)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=RC1-CT0252-150
            600-028-h05&t3=2000-06-15&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 9
            High quality sequence stop: 555.
FEATURES             Location/Qualifiers
     source          1. .555
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="CT0252"
                     /dev_stage="Adult"
                     /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT      147 a    131 c    129 g    148 t
ORIGIN
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  Query Match           45.7%;  Score 97.4;  DB 10;  Length 555;
  Best Local Similarity  70.9%;  Pred. No. 7.3e-19;
  Matches  144;  Conservative    0;  Mismatches   56;  Indels    3;  Gaps    1;

Qy      1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 60
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Db    517 GAGCAGAAGATCATGGATCTGTATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTAC 458

Qy     61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
          |    | ||| ||| |||| ||||||| | |||||||||||| ||||| | |||||||||
Db    457 CGTGCCAAGACTGGTAGGACCTCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT- 397

Qy    121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
          || |  |||  |  ||| |   ||  |||| || ||   |||||| |||||  |  ||
Db    398 --TGCCTCCTCCAAGAGAGACCAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATAC 341

Qy    181 actactgactttgggttaactat 203
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Db    340 AACACTGCCTTTGAATTAAATAT 318


RESULT   6
AW368437/c
LOCUS       AW368437                557 bp    mRNA    linear   EST 04-FEB-2000
DEFINITION  CM3-HT0192-071099-022-h06 HT0192 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW368437
VERSION     AW368437.1  GI:6873087
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 557)
  AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
  TITLE     The FAPESP/LICR Human Cancer Genome Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM3&t2=CM3-HT0192-
            071099-022-h06&t3=1999-10-07&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 43
            High quality sequence stop: 557.
FEATURES             Location/Qualifiers
     source          1. .557
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="HT0192"
                     /dev_stage="Adult"
                     /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT      149 a    130 c    130 g    147 t      1 others
ORIGIN


  Query Match           45.7%;  Score 97.4;  DB 9;  Length 557;
  Best Local Similarity  70.9%;  Pred. No. 7.3e-19;
  Matches  144;  Conservative    0;  Mismatches   56;  Indels    3;  Gaps    1;

Qy      1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 60
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          ||  || | || |||||| ||||   |||||||||||| |||||  |||| || ||||||
Db    515 GAGCAGAAGATCATGGATCTGTATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTAC 456

Qy     61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
          |    | ||| ||| |||| ||||||| | |||||||||||| ||||| | |||||||||
Db    455 CGTGCCAAGACTGGTAGGACCTCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT- 395

Qy    121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
            || |  |||  |  ||| |   ||  |||| || ||   |||||| |||||  |  ||
Db    396 --TGCCTCCTCCAAGAGAGACCAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATAC 339

Qy    181 actactgactttgggttaactat 203
            |  |||| |||||  |||| |||
Db    338 AACACTGCCTTTGAATTAAATAT 316
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RESULT 7
AW578451/c
LOCUS AW578451 559 bp mRNA linear EST 16-MAR-2000
DEFINITION RC1-CT0252-030100-023-b06 CT0252 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW578451
VERSION AW578451.1 GI:7253500
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 559)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC1&t2=RC1-CT0252-030100-023-b06&t3=2000-01-03&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 37
High quality sequence stop: 559.
FEATURES Location/Qualifiers
source 1. .559
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0252"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 148 a 130 c 132 g 149 t
ORIGIN

Query Match 45.7%; Score 97.4; DB 9; Length 559;
Best Local Similarity 70.9%; Pred. No. 7.3e-19;
Matches 144; Conservative 0; Mismatches 56; Indels 3; Gaps 1;

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Qy      1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 60
          ||  || | || |||||| ||||   |||||||||||| |||||  |||| || ||||||
Db    517 GAGCAGAAGATCATGGATCTGTATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTAC 458

Qy     61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
          |    | ||| ||| |||| ||||||| | |||||||||||| ||||| | |||||||||
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Db    457 CGTGCCAAGACTGGTAGGACCTCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT- 397

Qy    121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
            || |  |||  |  ||| |   ||  |||| || ||   |||||| |||||  |  ||
Db    398 --TGCCTCCTCCAAGAGAGACCAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATAC 341

Qy    181 actactgactttgggttaactat 203
            |  |||| |||||  |||| |||
Db    340 AACACTGCCTTTGACTTAAATAT 318
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RESULT 8
AW361164/c
LOCUS AW361164 436 bp mRNA linear EST 04-FEB-2000
DEFINITION RC1-CT0251-141099-012-c02 CT0251 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW361164
VERSION AW361164.1 GI:6865814
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 436)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC1&t2=RC1-CT0251-141099-012-c02&t3=1999-10-14&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 35
High quality sequence stop: 436.
FEATURES Location/Qualifiers
source 1. .436
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0251"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 123 a 96 c 103 g 114 t
ORIGIN

Query Match 45.0%; Score 95.8; DB 9; Length 436;
Best Local Similarity 70.4%; Pred. No. 2e-18;
Matches 143; Conservative 0; Mismatches 57; Indels 3; Gaps 1;

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Qy      1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 60
          ||  || | || |||||| ||||   |||||||||||| |||||  |||| || ||||||
Db    394 GAGCAGAAGATCATGGATCTGTATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTAC 335

Qy     61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
          |    | ||| ||| |||| ||||||| | |||||||||||| ||||| | |||||||||
Db    334 CGTGCCAAGACTGGTAGGACCTCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT- 274

Qy    121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
            || |  |||  |  ||| |   ||  |||| || ||   |||||| |||||  |  ||
Db    275 --TGCCTCCTCCAAGAGAGACCAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATAC 218
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Qy    181 actactgactttgggttaactat 203
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Db    217 AACACTGCCTTTGCAGTAAATAT 195
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RESULT   9
AW853610
LOCUS       AW853610                536 bp    mRNA    linear   EST 19-MAY-2000
DEFINITION  RC1-CT0252-170200-025-c06 CT0252 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW853610
VERSION     AW853610.1  GI:7949212
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 536)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=RC1-CT0252-170
            200-025-c06&t3=2000-02-17&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 15
            High quality sequence stop: 535.
FEATURES             Location/Qualifiers
     source          1. .536
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="CT0252"
                     /dev_stage="Adult"
                     /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT      140 a    123 c    129 g    144 t
ORIGIN
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  Query Match             45.0%;  Score 95.8;  DB 9;  Length 536;
  Best Local Similarity   70.4%;  Pred. No. 2.2e-18;
  Matches  143;  Conservative    0;  Mismatches   57;  Indels    3;  Gaps    1;

Qy      1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtccttttctcttctac 60
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Db     43 GAGCAGAAGATCATGGATCTGTATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTAC 102

Qy     61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
          |    | ||| ||| |||| ||||||| | |||||||||| ||||| | |||||||||
Db    103 CGTGCCAAGACTGGTAGGACCTCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT- 161

Qy    121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
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          || |  | |  |  ||| |   ||  |||| || ||   |||||| |||||  |  ||
Db    162 --TGCCTCCACCAAGAGAGACCAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATAC 219

Qy    181 actactgactttgggttaactat 203
          |  |||| |||||  |||| |||
Db    220 AACACTGCCTTTGACTTAAATAT 242
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RESULT  10
AW753217/c
LOCUS       AW753217                434 bp    mRNA    linear   EST 28-APR-2000
DEFINITION  RC1-CT0251-081099-011-a04 CT0251 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW753217
VERSION     AW753217.1  GI:7668149
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 434)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC1&t2=RC1-CT0251-
            081099-011-a04&t3=1999-10-08&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 42
            High quality sequence stop: 67.
FEATURES             Location/Qualifiers
     source          1. .434
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="CT0251"
                     /dev_stage="Adult"
                     /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT      125 a     94 c    101 g    114 t
ORIGIN
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  Query Match             44.0%;  Score 93.8;  DB 9;  Length 434;
  Best Local Similarity   71.5%;  Pred. No. 8.1e-18;
  Matches  138;  Conservative    0;  Mismatches   52;  Indels    3;  Gaps    1;

Qy     11 taatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctaccacagccaga 70
          | |||||| ||||   |||||||||||| |||||  |||| || |||||||    | |||
Db    381 TCATGGATCTGTATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGA 322

Qy     71 gtggcaggaactccaccttcgagtctgtggctttccctggctggttcatcgctgtcagct 130
            ||| |||| ||||||| | |||||||||| ||||| | |||||||||   || |  ||
Db    321 CTGGTAGGACCTCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT---TGCCTCCT 265
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Qy    131 ctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaacactactgact 190
          |  |  ||| |   ||  |||| || ||   |||||| |||||  |  |||  |||| ||
Db    264 CCAAGAGAGACCAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCT 205

Qy    191 ttgggttaactat 203
          |||  |||| |||
Db    204 TTGAATTAAATAT 192
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RESULT 11
AW361245
LOCUS AW361245 560 bp mRNA linear EST 04-FEB-2000
DEFINITION RC1-CT0252-181299-022-e08 CT0252 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW361245
VERSION AW361245.1 GI:6865895
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 560)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC1&t2=RC1-CT0252-181299-022-e08&t3=1999-12-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 13
High quality sequence stop: 551.

FEATURES Location/Qualifiers
source 1. .560
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0252"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 143 a 131 c 141 g 145 t
ORIGIN

Query Match 42.7%; Score 91; DB 9; Length 560;
Best Local Similarity 69.0%; Pred. No. 6.3e-17;
Matches 140; Conservative 0; Mismatches 60; Indels 3; Gaps 1;

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Qy      1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 60
          ||  ||   || |||||| ||||    |  | ||||||| |||||  |||| ||  |||||
Db     61 GAGCAGACGATCATGGATCTGTATGGCACAACCGAGCCCGTGAAACCCTTCCTTGTCTAC 120

Qy     61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
          |    | ||| ||| |||| ||||||| | |||||||||| ||||| | ||||||||||
Db    121 CGGGCCAAGACTGGTAGGACCTCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCATC 180

Qy    121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
          ||   |  |||  | ||| |   ||  |||| || ||   |||||| |||||  |  ||
Db    181 GC---CTCCTCCAAGAGAGACCAGCCCATCATTCTGACTTCAGAACTCGGGAAGTCATAC 237

Qy    181 actactgactttgggttaactat 203
          |  |||| |||||  |||| |||
Db    238 AACACTGCCTTTGAATTAAATAT 260
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RESULT 12
BF244205
LOCUS BF244205 870 bp mRNA linear EST 14-NOV-2000
DEFINITION 601863146F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4080899 5', mRNA sequence.
ACCESSION BF244205
VERSION BF244205.1 GI:11158135
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 870)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM941 row: k column: 12
High quality sequence stop: 582.

FEATURES Location/Qualifiers
source 1. .870
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4080899"
/clone_lib="NIH_MGC_57"
/tissue_type="glioblastoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

BASE COUNT 256 a 216 c 171 g 227 t
ORIGIN

Query Match 30.9%; Score 65.8; DB 10; Length 870;
Best Local Similarity 56.8%; Pred. No. 3e-09;
Matches 121; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

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Db    134 GAAAAAAATATCATGGACCTGTATGTGGAGAAGAAAGCACAGAAGCCCTTTCTCTTTTTC 193

Qy     61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
          ||||   |    |||   |  ||   |||  |||| ||  ||| ||||||||||||||
Db    194 CACAATAAAGAAGGCTCCACTTCTGTCTTTCAGTCAGTCTCTTACCCTGGCTGGTTCATA 253

Qy    121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
          ||   |  | |   |  |||    ||  || | || ||| | ||    || | | | ||
Db    254 GCCACCTCCACCACATCAGGACAGCCCATCTTTCTCACCAAGGAGAGAGGCATAACTAAT 313

Qy    181 actactgactttgggttaactatgctgttttaa 213
          |  ||| ||||    |||  |    ||   |||
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Db 314 AACACTAACTTCTACTTAGATTCTGTGGAATAA 346

RESULT 13
BM386666/c
LOCUS BM386666 612 bp mRNA linear EST 17-JAN-2002
DEFINITION UI-R-CN1-cjg-l-09-0-UI.s1 UI-R-CN1 Rattus norvegicus cDNA clone UI-R-CN1-cjg-l-09-0-UI 3', mRNA sequence.
ACCESSION BM386666
VERSION BM386666.1 GI:18186719
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 612)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized fundus library cDNA Library Preparation: M.B. Soares Lab.
Clone distribution: clones will be available through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.
FEATURES Location/Qualifiers
source 1. .612
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CN1-cjg-l-09-0-UI"
/clone_lib="UI-R-CN1"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CN1 library is a subtracted library derived from the following pool of seven normalized rat libraries: normalized rat seminal vesicles, normalized rat penis, normalized rat bladder, normalized rat cervix, normalized rat brown adipose, normalized rat fundus, and normalized rat salivary gland. It was constructed according to the procedure described by Bonaldo, Lennon & Soares (Genome Research Genome 6: 791-806, 1996). For construction of the CN1 library, plasmid DNA from the pool of normalized libraries was electroporated into competent bacteria for the production of single-stranded circular DNA. This was then used as a tracer in a subtractive hybridization with a driver (PCR amplified inserts from a plamid DNA template preparation) comprising: a) a pool of about 34,000 clones from the Rat Unigene Set corresponding to plates R-5-AA-NN excluding plates R-5-MM and MN. This pool represented 40% of the final driver population. b) a pool of about 29,000 clones from subtracted libraries CA0 and CA1 corresponding to plates R-CA0-AWV through R-CA0-AXS, R-CA0-AZX through R-CA0-BAZ, R-CA0-BFE through R-CA0-BHY, R-CA0-BJS, R-CA0-BKE, R-CA0-BKG-H, R-CA0-BKJ-K, R-CA0-BKP through R-CA0-BKS, R-CA0-BKU-V, R-CA0-BLY through R-CA0-BMA, R-CA0-BMC through R-CA0-BME, R-CA0-BNS, R-CA0-BOB through R-CA0-BOJ, R-CA0-BPA through R-CA0-BPG, R-CA1-BBA through R-CA1-BDA, R-CA1-BHZ through R-CA1-BJF, R-CA1-BJR, R-CA1-BJT through R-CA1-BKB, R-CA1-BKD, R-CA1-BKF, R-CA1-BKI, R-CA1-BKT, R-CA1-BLF, R-CA1-BLH through R-CA1-BLN, R-CA1-BLS, R-CA1-BLU-V, R-CA1-BNR, and R-CA1-BLE. The resulting pool represented 20% of the final driver population. c) a pool of about 15,000 clones from non-normalized libraries CS0s, CT0s, CU0s, CW0s, CX0s and normalized libaries CS0, CT0, CU0, CW0, and CX0 corresponding to plates R-CS0s-CBD through R-CS0s-CBO, R-CT0s-CAM through R-CT0s-CAX, R-CU0s-CBP through R-CU0s-CCA, R-CW0s-CCB through R-CW0s-CCM, R-CX0s-CCN through R-CX0s-CCX, R-CS0-BSD, R-CS0-BTD through R-CS0-BTV, R-CS0-BVM, R-CT0-BTW through R-CT0-BUP, R-CT0-BVN, R-CU0-BUQ through R-CU0-BVL, R-CW0-BVV through R-CW0-BWP, R-CW0-BXN through R-CW0-BXO, R-CX0-BWQ through R-CX0-BXM. The resulting pool represented 5% of the final driver population. d) a pool of about 5,000 clones (1,000 from non-normalized eye library CV0 and 4,000 from normalized eye library CV1) corresponding to plates R-CV0-BRH through R-CV0-BRR, R-CV1-BRS through R-CV1-BSC, R-CV1-BSE through R-CV1-BTC, and R-CV1-BVO through R-CV1-BVU. This pool represented about 5% of the final driver population. e) A pool of about 10,000 clones from subtracted library BS2, BV0 and BV0p (7-9.5 kb cDNA library fraction from rat whole embryo), and BX0 (0.5-7kb cDNA library fraction from rat whole embryo) corresponding to plates R-BS2-BDB through R-BS2-BFB, R-BV0-ANK through R-BV0-ANR, R-BV0p-AOI through R-BV0p-AOX, and R-BX0-AQY through R-BX0-ASH. The resulting pool represented 5% of the final driver population. f) a pool of about 7,000 clones from the seven non-normalized libraries that make up the tracer including CY0, CZ0, DA0, DB0, DC0, DD0, and DE0 corresponding to plates R-CY0-BXP through R-CY0-BXZ, R-CZ0-BYA through R-CZ0-BYI, R-CZ0-BZB-C, R-DA0-BYJ through R-DA0-BYP, R-DA0-BZD through R-DA0-BZH, R-DB0-BYQ through R-DB0-BZA, R-DC0-BZI through R-DC0-BZQ, R-DC0-CAY through R-DC0-CBA, R-DD0-BZR through R-DD0-CAA, R-DD0-CBB-C, and R-DE0-CAB through R-DE0-CAL. The resulting pool represented about 10% of the final driver population. g) a pool of about 2,000 clones from the pool of normalized libraries, CN0, that makes up the tracer. The corresponding plates are R-CN0-BKW through R-CN0-BLD, R-CN0-BLG, R-CN0-BLP through R-CNO-BLR, R-CN0-BLT, R-CN0-BLW-X, R-CN0-BMB, and R-CN0-BMF through R-CN0-BML. This pool represented 5% of the final driver population. h) a pool of the 28 most abundant clones in the CN0 pool corresponding to the following addresses: bkw-a-09-0-UI, bkw-b-09-0-UI, bkw-b-11-0-UI, bkx-b-10-0-UI, bkx-d-01-0-UI, bkx-d-06-0-UI, bkx-g-08-0-UI, bkx-h-12-0-UI, bky-a-05-0-UI, bkz-a-06-0-UI, bkz-a-11-0-UI, bkz-c-06-0-UI, bkz-c-09-0-UI, bkz-d-10-0-UI, bla-a-01-0-UI, bla-a-02-0-UI, bla-f-04-0-UI, bla-g-07-0-UI, bla-g-12-0-UI, blb-a-12-0-UI, blb-f-02-0-UI, blc-a-11-0-UI, blc-e-95-0-UI, bld-1-08-0-UI, bld-f-02-0-UI, blq-h-04-0-UI, blr-a-05-0-UI, blt-f-08-0-UI. This pool represented 5% of the final driver population. i) One abundant CN0 clone (corresponding to the address bkz-a-11-0-UI) was digested with Not I and Eco RI and the resulting insert was gel purified. This purified insert was added directly to the driver so that it represented 5% of the final driver population.
TAG_LIB=UI-R-CN1
TAG_TISSUE=fundus
TAG_SEQ=TTCGG"
BASE COUNT 160 a 130 c 124 g 198 t
ORIGIN

Query Match 30.8%; Score 65.6; DB 10; Length 612;
Best Local Similarity 58.9%; Pred. No. 3e-09;
Matches 113; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

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           || || ||||||||||||||  |     |  |   |||  ||||||||||||||||  ||
Db     397 GACATCATGGATTTGTACAATGAGAAAAAAGCACAGAAAGCCTTTCTCTTCTACCATGGC 338

Qy      67 cagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatcgctgtc 126
             ||    |  ||   |||  |||| ||    |  ||||||||||| || ||   |
Db     337 ATAGAGGGATCTACTTCTGTCTTTCAGTCAGTCTTGTATCCTGGCTGGTTTATAGCCACC 278

Qy     127 agctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaacactact 186
             ||   || | |     |  |||| ||||| || ||   |||  |||| || |  |||
Db     277 TCTTCCACAGCAAGACAAACAATCATTCTTACACAGGAGAGGGGTGAAGCTAATAACACT 218

Qy     187 gactttgggtta 198
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Db     217 AACTTCTACTTA 206
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RESULT  14
AV011778
LOCUS       AV011778                393 bp    mRNA    linear   EST 25-AUG-1999
DEFINITION  AV011778 Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA
            clone 1110033G16, mRNA sequence.
ACCESSION   AV011778
VERSION     AV011778.1  GI:4788765
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 393)
  AUTHORS   Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
            Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
            ,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
            Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
            Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
            ,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N.,
            Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
            Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Chie Owa
            Genome Science Laboratory
            RIKEN
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-9145
            Fax: 81-298-36-9098
            Email: genome-res@rtc.riken.go.jp
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length cDNA
            (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .393
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                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="1110033G16"
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ORIGIN
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Qy      73 ggcaggaactccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctct 132
           | ||  | ||| || ||  | |||   || |||  | | ||||||||||||  |   || |
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Db      14 GACATAACCTCAACATTTAATTCTACAGCCTTCTATAGATGGTTCATCGCTATTTTCTAT 73

Qy     133 gaaggaggctgtcctctcatccttacccaagaactggggaaagccaacactactgacttt 192
             | ||  |||| || |||||  | ||||||||||||||| ||  |  ||  |||||||
Db      74 AATGGGAGCTGCCCACTCATTTTGACCCAAGAACTGGGGGAAATCTTCATCACTGACTTC 133

Qy     193 gggttaactatgctgttttaa 213
           | | | | | ||    ||||
Db     134 GAGATGATTGTGGAACATTAA 154
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```
RESULT  15
AK009787
LOCUS       AK009787                1219 bp    mRNA    linear   HTC 19-JAN-2002
DEFINITION  Mus musculus adult male tongue cDNA, RIKEN full-length enriched
            library, clone:2310043N20:homolog to FIL1 ETA, full insert
            sequence.
ACCESSION   AK009787
VERSION     AK009787.1  GI:12844799
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA,
            clone_lib:RIKEN full-length enriched mouse cDNA library
            clone:2310043N20.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (sites)
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2  (sites)
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3  (sites)
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4  (sites)
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5  (bases 1 to 1219)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
            Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
            Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
            Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
            Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
            Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,
            Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
            Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
```

```
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Gemomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. cDNA went
            through one round of normalization to Rot = 5.0 and subtraction to
            Rot = 25.0. Second strand cDNA was prepared with the primer adapter
            of sequence [5'
            GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved
            with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
            Host: SOLR.
FEATURES              Location/Qualifiers
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                      EMEGKPTLQLKEVDIMNLYKERKAQKAFLFYHGIEGSTSVFQSVLYPGWFIATSSIER
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ORIGIN
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Job time: 17648 sec

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  Matches  107;  Conservative    0;  Mismatches   84;  Indels    0;  Gaps    0;

Qy       1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 60
           |||   || || ||| ||||||||||  |     |  |    ||  ||||||| |||||
Db     417 GAAGTAGACATCATGAATTTGTACAAAGAGAGAAAAGCACAAAAAGCCTTTCTGTTCTAT 476

Qy      61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120
           ||  ||      |||   |  ||   |||  |||| ||    |  |||||||||| ||
Db     477 CATGGCATAGAGGGCTCCACTTCTGTCTTTCAGTCAGTCCTCTATCCTGGCTGGTTTATA 536

Qy     121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180
           ||   |   ||   || | |     |  ||||||| || ||  | | ||| |||
Db     537 GCCACCTCTTCCATAGAAAGACAGACAATCATCCTCACACATCAGCGGGGTAAATTGGTT 596

Qy     181 actactgactt 191
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Db     597 AACACTAACTT 607
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 20, 2002, 15:01:09 ; Search time 73.84 Seconds
(without alignments)
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Perfect score: 371
Sequence: 1 EKDIMDLYNQPEPVKSFLFY.....ILTQELGKANTTDFGLTMLF 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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4: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:*
6: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*
7: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*
8: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*
9: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1988.DAT:*
10: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*
11: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
12: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
13: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:*
14: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*
15: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1994.DAT:*
16: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
17: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT:*
18: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1997.DAT:*
19: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	371	100.0	70	21	AAY70216	Partial human Inte
2	371	100.0	158	21	AAY70217	Human Interleukin-
3	371	100.0	158	21	AAY70218	Human Interleukin-
4	371	100.0	273	22	AAE03417	Human interleukin-
5	309	83.3	130	22	AAB85001	Human interleukin-
6	238	64.2	72	19	AAW86285	Rodent interleukin
7	238	64.2	98	20	AAY24040	Amino acid sequenc
8	238	64.2	157	22	AAE06662	Mouse interleukin-
9	238	64.2	160	19	AAW86286	Rodent interleukin
10	238	64.2	160	20	AAY24049	Amino acid sequenc
11	208.5	56.2	134	21	AAB18924	A novel polypeptid
12	208.5	56.2	134	21	AAY96935	Human IL-1 recepto
13	208.5	56.2	169	19	AAW63136	Interleukin-1 rece
14	208.5	56.2	169	20	AAY24043	A human SPOIL-I pr
15	208.5	56.2	169	20	AAY24395	Human interleukin-
16	208.5	56.2	169	22	AAE06656	Human interleukin-
17	208.5	56.2	169	22	AAB83008	Human IL-1ra prote
18	208.5	56.2	173	22	AAU16937	Human novel secret
19	208.5	56.2	208	20	AAY24044	A human SPOIL-II p
20	201.5	54.3	172	22	AAU17010	Human novel secret
21	201.5	54.3	172	22	AAE09702	Human gene 13 enco
22	184	49.6	157	22	AAE04299	Human Interleukin-
23	184	49.6	157	22	AAB50444	Human IL-1 eta. H
24	184	49.6	170	22	AAB85000	Human interleukin-
25	147	39.6	68	20	AAY24047	SPOIL protein cons
26	127	34.2	154	22	AAE06663	Mouse interleukin-
27	127	34.2	155	21	AAY96937	Murine IL-1 recept
28	127	34.2	155	22	AAB35261	Murine IL-IL1. Mu
29	127	34.2	155	22	AAB66672	Invention related
30	127	34.2	155	22	AAB48828	Murine interleukin
31	127	34.2	156	19	AAW86284	Rodent interleukin
32	127	34.2	156	20	AAY28407	Mouse interleukin
33	127	34.2	156	21	AAY92260	Murine IL-1 homolo
34	127	34.2	156	21	AAY45061	Murine TANGO-93 pr
35	125	33.7	258	22	ABG22711	Novel human diagno
36	124	33.4	80	20	AAY43525	A human interleuki
37	124	33.4	80	22	AAB66663	Protein encoded by
38	124	33.4	154	22	AAB35263	Interleukin-IL1 re
39	124	33.4	155	20	AAY28408	Human interleukin
40	124	33.4	155	21	AAY96936	Human IL-1 recepto
41	124	33.4	155	21	AAY92254	Hhuman IL-1 homolo
42	124	33.4	155	21	AAY92257	Human IL-1 homolog
43	124	33.4	155	21	AAY45062	Human TANGO-93 pro
44	124	33.4	155	22	AAE06655	Human interleukin-
45	124	33.4	155	22	AAB87601	Human PRO4342. Ho

ALIGNMENTS

RESULT 1
AAY70216
ID AAY70216 standard; Protein; 70 AA.
XX
AC AAY70216;
XX
DT 06-JUN-2000 (first entry)
XX
DE Partial human Interleukin-1 epsilon protein.
XX
KW Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;
KW gene mapping; immune system; treatment; inflammatory disease;
KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
KW psoriasis; human.
XX
OS Homo sapiens.
XX
PN WO200011174-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US18771.
XX
PR 21-AUG-1998; 98US-0097413.
PR 31-AUG-1998; 98US-0098595.
PR 11-SEP-1998; 98US-0099974.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Sims JE, Smith DE;
XX
DR WPI; 2000-237653/20.
DR N-PSDB; AAZ51246.

```
XX
PT   Nucleotide sequences encoding human interleukin -1 epsilon, useful to
PT   treat inflammatory and immune system-related diseases such as
PT   rheumatoid arthritis and inflammatory bowel disease -
XX
PS   Claim 1b; Fig 2; 76pp; English.
XX
CC   The present sequence is the partial Interleukin-1 (IL-1) epsilon
CC   protein encoded by the 3' exon of IL-1 epsilon DNA. IL-1 epsilon
CC   gene is mapped to chromosome 2q and is mainly expressed in spleen,
CC   lymph node, thymus, tonsil and leucocyte tissues. IL-1 epsilon is
CC   a cytokine, with antiinflammatory, immunosuppressant,
CC   antirheumatic, antiarthritic and antipsoriatic activity. The DNA
CC   sequence can be used in chromosome identification, gene mapping and
CC   study of immune system. IL-1 epsilon can be used in the treatment of
CC   inflammatory or autoimmune diseases such as rheumatoid arthritis,
CC   inflammatory bowel disease and psoriasis.
XX
SQ   Sequence   70 AA;


  Query Match             100.0%;  Score 371;  DB 21;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-38;
  Matches   70;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 EKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKAN 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ekdimdlynqpepvksflfyhsqsgrnstfesvafpgwfiavsseggcpliltqelgkan 60

Qy     61 TTDFGLTMLF 70
          ||||||||||
Db     61 ttdfgltmlf 70


RESULT   2
AAY70217
ID   AAY70217 standard; Protein; 158 AA.
XX
AC   AAY70217;
XX
DT   06-JUN-2000  (first entry)
XX
DE   Human Interleukin-1 epsilon protein.
XX
KW   Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
KW   immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;
KW   gene mapping; immune system; treatment; inflammatory disease;
KW   autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
KW   psoriasis; human.
XX
OS   Homo sapiens.
XX
PN   WO200011174-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US18771.
XX
PR   21-AUG-1998;   98US-0097413.
PR   31-AUG-1998;   98US-0098595.
PR   11-SEP-1998;   98US-0099974.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Sims JE,  Smith DE;
XX
DR   WPI; 2000-237653/20.
DR   N-PSDB; AAZ51247.
XX
PT   Nucleotide sequences encoding human interleukin -1 epsilon, useful to
PT   treat inflammatory and immune system-related diseases such as
PT   rheumatoid arthritis and inflammatory bowel disease -
XX
PS   Claim 1b; Fig 2; 76pp; English.
XX
CC   The present sequence is that of human Interleukin-1 (IL-1) epsilon
CC   protein. IL-1 epsilon gene is mapped to chromosome 2q and is mainly
CC   expressed in spleen, lymph node, thymus, tonsil and leucocyte
CC   tissues. IL-1 epsilon is a cytokine, with antiinflammatory,
CC   immunosuppressant, antirheumatic, antiarthritic and antipsoriatic
CC   activity. It can be used in the treatment of inflammatory or autoimmune
CC   diseases such as rheumatoid arthritis, inflammatory bowel disease and
CC   psoriasis. The DNA sequence can be used in chromosome identification,
CC   gene mapping and study of immune system.
XX
SQ   Sequence   158 AA;


  Query Match             100.0%;  Score 371;  DB 21;  Length 158;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-37;
  Matches   70;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 EKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKAN 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     89 ekdimdlynqpepvksflfyhsqsgrnstfesvafpgwfiavsseggcpliltqelgkan 148

Qy     61 TTDFGLTMLF 70
          ||||||||||
Db    149 ttdfgltmlf 158


RESULT   3
AAY70218
ID   AAY70218 standard; Protein; 158 AA.
XX
AC   AAY70218;
XX
DT   06-JUN-2000  (first entry)
XX
DE   Human Interleukin-1 epsilon polymorphic variant.
XX
KW   Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
KW   immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;
KW   gene mapping; immune system; treatment; inflammatory disease;
KW   autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
KW   psoriasis; polymorphic variant; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 12
FT                   /note= "Wild type Gln replaced with Arg"
XX
PN   WO200011174-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US18771.
XX
PR   21-AUG-1998;   98US-0097413.
PR   31-AUG-1998;   98US-0098595.
PR   11-SEP-1998;   98US-0099974.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Sims JE,  Smith DE;
XX
DR   WPI; 2000-237653/20.
DR   N-PSDB; AAZ51248.
XX
PT   Nucleotide sequences encoding human interleukin -1 epsilon, useful to
PT   treat inflammatory and immune system-related diseases such as
PT   rheumatoid arthritis and inflammatory bowel disease -
XX
PS   Claim 1b; Fig 2; 76pp; English.
XX
```

CC The present protein sequence is that of human Interleukin-1 (IL-1)
CC epsilon polymorphic variant. IL-1 epsilon gene is mapped to chromosome 2q
CC and is mainly expressed in spleen, lymph node, thymus, tonsil and
CC leucocyte tissues. IL-1 epsilon is a cytokine, with antiinflammatory,
CC immunosuppressant, antirheumatic, antiarthritic and antipsoriatic
CC activity. It can be used in the treatment of inflammatory or autoimmune
CC diseases such as rheumatoid arthritis, inflammatory bowel disease and
CC psoriasis. The DNA sequence can be used in chromosome identification,
CC gene mapping and study of immune system.
XX
SQ Sequence 158 AA;

Query Match 100.0%; Score 371; DB 21; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.8e-37;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKAN 60
Db 89 ekdimdlynqpepvksflfyhsqsgrnstfesvafpgwfiavsseggcpliltqelgkan 148

Qy 61 TTDFGLTMLF 70
Db 149 ttdfgltmlf 158

RESULT 4
AAE03417
ID AAE03417 standard; Protein; 273 AA.
XX
AC AAE03417;
XX
DT 03-AUG-2001 (first entry)
XX
DE Human interleukin-1 receptor antagonist-like (IL-1ra-L).
XX
KW Human; interleukin-1 receptor antagonist-like protein; IL-1ra-L; therapy;
KW rheumatoid arthritis; psoriatic arthritis; inflammatory arthritis; lupus;
KW joint disease; autoimmune disease; multiple sclerosis; diabetes; obesity;
KW transplant rejection; graft versus host disease; strain; sprain; leprosy;
KW cartilage damage; hepatitis; human immunodeficiency virus; HIV; anorexia;
KW clostridium-associated diarrhoea; pulmonary tuberculosis; septic shock;
KW myopathy; Alzheimer's disease; Parkinson's disease; memory disorder;
KW acute respiratory disease syndrome; cystic fibrosis; asthma; psoriasis;
KW eczema; glomerulonephritis; osteoporosis; Paget's disease; lymphoma;
KW hypercalcaemia; haemorrhage; ischaemia; atherosclerosis; leukaemia;
KW infertility; endometriosis; retinal neuropathy; acute pancreatitis;
KW Kawasaki's disease; cancer.
XX
OS Homo sapiens.
XX
PN WO200141792-A1.
XX
PD 14-JUN-2001.
XX
PF 04-DEC-2000; 2000WO-US32891.
XX
PR 10-DEC-1999; 99US-0170105.
PR 28-NOV-2000; 2000US-0724859.
XX
PA (AMGE-) AMGEN INC.
XX
PI Calzone FJ, Luethy R, Boedigheimer MJ, Zhu J, Chung Y, Jing S;
XX
DR WPI; 2001-381495/40.
DR N-PSDB; AAD06911.
XX
PT Novel Interleukin-1 Receptor Antagonist-Like nucleic acid molecule, the
PT polypeptide encoded by the nucleic acid is useful diagnosis, treatment,
PT and prevention of diseases such as arthritis, diabetes, transplant
PT rejection -
XX
PS Claim 13; Fig 1A; 127pp; English.

XX
CC The present sequence is human interleukin-1 receptor antagonist-like
CC (IL-1ra-L) protein. IL-1ra-L is useful for treating, preventing or
CC ameliorating IL-1ra-L polypeptide-related disease, condition or disorder
CC which include rheumatoid arthritis, psoriatic arthritis, inflammatory
CC arthritis, osteoarthritis, autoimmune disease, multiple sclerosis,
CC lupus, diabetes, transplant rejection, inflammatory joint disease, graft
CC versus host disease and inflammatory conditions resulting from strain,
CC sprain, cartilage damage, trauma, orthopaedic surgery, hepatitis, human
CC immunodeficiency virus (HIV) infection, clostridium-associated
CC diarrhoea, leprosy, pulmonary tuberculosis, septic shock, obesity,
CC anorexia, myopathies, Alzheimer's disease, Parkinson's disease, memory
CC disorders, acute respiratory disease syndrome, cystic fibrosis, asthma,
CC psoriasis, eczema, acute and chronic glomerulonephritis, osteoporosis,
CC Paget's disease, hypercalcaemia, haemorrhage, ischaemia, atherosclerosis,
CC lymphomas, lung and breast cancer, leukaemias, infertility,
CC endometriosis, retinal degeneration, retinal neuropathy, acute
CC pancreatitis and Kawasaki's disease.
XX
SQ Sequence 273 AA;

Query Match 100.0%; Score 371; DB 22; Length 273;
Best Local Similarity 100.0%; Pred. No. 3.4e-37;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKAN 60
Db 204 ekdimdlynqpepvksflfyhsqsgrnstfesvafpgwfiavsseggcpliltqelgkan 263

Qy 61 TTDFGLTMLF 70
Db 264 ttdfgltmlf 273

RESULT 5
AAB85001
ID AAB85001 standard; Protein; 130 AA.
XX
AC AAB85001;
XX
DT 06-AUG-2001 (first entry)
XX
DE Human interleukin-1 receptor antagonist (NOVINTRA C) polypeptide.
XX
KW NOVX; transmembrane protein; NOVTRAN; neuromedin peptide; NOVNEUR;
KW gonadotropin-like protein; NOVGON; interleukin-1; NOVINTRA; human;
KW cytostatic; neuroprotective; reproductive; antiinflammatory; cancer;
KW antibacterial; cerebroprotective; antidiabetic; antiarthritic;
KW antiasthmatic; antiallergic.
XX
OS Homo sapiens.
XX
PN WO200140291-A2.
XX
PD 07-JUN-2001.
XX
PF 06-DEC-2000; 2000WO-US33029.
XX
PR 06-DEC-1999; 99US-0169056.
PR 09-DEC-1999; 99US-0169866.
PR 09-DEC-1999; 99US-0169886.
PR 10-DEC-1999; 99US-0170252.
PR 12-JAN-2000; 2000US-0175740.
PR 05-DEC-2000; 2000US-0170252.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Burgess CE, Prayaga SK, Shimkets RA, Rastelli L, Zerhusen BD;
PI Mezes PS;
XX
DR WPI; 2001-374790/39.
DR N-PSDB; AAF83870.

XX
PT Novel isolated human transmembrane, neuromedin peptide
PT gonadotropin-like protein and interleukin-1 receptor antagonist
PT proteins, useful for treating cancer, immune response disorder,
PT metabolic function disorders -
XX
PS Claim 53; Fig 15B; 138pp; English.
XX
CC The invention provides novel polypeptides (NOVX) selected from human
CC transmembrane protein (NOVTRAN), neuromedin peptide (NOVNEUR),
CC gonadotropin-like protein (NOVGON) and two interleukin-1 receptor
CC antagonist proteins (NOVINTRA A and B). The invention also provides
CC methods in which a NOVX polypeptide, polynucleotide and antibody are
CC used in the detection, prevention and treatment of a broad range of
CC pathological states. NOVTRAN can be used to treat is a cell signaling
CC disorder such as cancer, immune response disorder, hematopoietic
CC disorder, neurodegenerative disorder. NOVNEUR can be used to treat
CC endocrine disorder, muscle disorder, neurologic disorder, cancers of
CC central nervous system, breast, colon, ovary, kidney, prostate and
CC thyroid. NOVGON can be used to treat reproductive development disorder,
CC metabolic function disorder and melanoma. NOVINTRA A and B can be used
CC to treat bone metabolism or structure disorder, inflammatory response
CC disorder, immune regulation disorder, septic shock, stroke, diabetes,
CC arthritis and cancer. The present sequence represents the NOVINTRA C
CC polypeptide.
XX
SQ Sequence 130 AA;

Query Match 83.3%; Score 309; DB 22; Length 130;
Best Local Similarity 100.0%; Pred. No. 5.4e-30;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGK 58
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 73 ekdimdlynqpepvksflfyhsqsgrnstfesvafpgwfiavsseggcpliltqelgk 130

RESULT 6
AAW86285
ID AAW86285 standard; Protein; 72 AA.
XX
AC AAW86285;
XX
DT 19-FEB-1999 (first entry)
XX
DE Rodent interleukin (IL)-1 epsilon partial polypeptide.
XX
KW Interleukin; IL-1 delta; polyclonal antibody; IL-1 epsilon; cytokine;
KW inflammatory response; immune system; diagnosis; agonist; antagonist;
KW chemokine.
XX
OS Mus sp.
XX
PN WO9847921-A1.
XX
PD 29-OCT-1998.
XX
PF 17-APR-1998; 98WO-US06879.
XX
PR 06-AUG-1997; 97US-0055111.
PR 21-APR-1997; 97US-0837627.
XX
PA (SCHE) SCHERING CORP.
XX
PI Bazan JF, Hedrick JA, Kastelein RA, Sana TR;
XX
DR WPI; 1998-609976/51.
DR N-PSDB; AAV71959.
XX
PT Mammalian interleukin 1-delta and 1-epsilon - useful for, e.g.
PT regulating the immune system and inflammatory responses
XX
PS Disclosure; Page 91; 113pp; English.
XX
CC This represents a partial amino acid sequence of a rodent interleukin
CC (IL)-1 epsilon polypeptide. The invention relates to a recombinant
CC polypeptide that specifically binds polyclonal antibodies (Abs)
CC generated against a 12 consecutive amino acid segment of IL-1 delta
CC or IL-1 epsilon. Agonists or antagonists of these IL polypeptides are
CC used to regulate a cell involved in an inflammatory response. The IL-1
CC delta or IL-1 epsilon polypeptides and peptides are used to produce Abs
CC and antigen-Ab complexes. The polypeptides, Abs and the corresponding
CC nucleic acids regulate development and/or the immune system, and can be
CC used to diagnose and treat conditions associated with abnormal expression
CC of IL. Agonists or antagonists of IL-1 delta or IL-1 epsilon polypeptides
CC are used with agonists or antagonists of IL-1 alpha, IL-1RA, IL-1 beta,
CC IL-1 gamma, IL-2 and/or IL-12. The IL-1 delta or IL-1 epsilon
CC polypeptides may be used as a soluble polypeptide or as a fusion protein
CC with another cytokine or chemokine.
XX
SQ Sequence 72 AA;

Query Match 64.2%; Score 238; DB 19; Length 72;
Best Local Similarity 63.8%; Pred. No. 1.3e-21;
Matches 44; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

Qy 1 EKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKAN 60
| :||::||: |||| |||| :|| ||||| ||||||||| |:| ||||||||||:
Db 3 egnimemynkkepvkaslfyhkksgttstfesaafpgwfiavcskgscpliltqelgeif 62

Qy 61 TTDFGLTML 69
||| : ::
Db 63 itdfemivv 71

RESULT 7
AAY24040
ID AAY24040 standard; Protein; 98 AA.
XX
AC AAY24040;
XX
DT 30-SEP-1999 (first entry)
XX
DE Amino acid sequence of a murine SPOIL-I protein.
XX
KW SPOIL-I; interleukin-1 receptor antagonist; IL-1ra; modulating agent;
KW bone metabolism disorder; proinflammatory disorder; immune disorder;
KW inflammatory disease; septic shock; stroke; diabetes; arthritis;
KW intercolitis; pneumonitis; epithelial cell; skin disease;
KW proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;
KW epithelial cancer; squamous cell carcinoma; bone resorption disorder;
KW osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;
KW osteogenesis imperfecta; fibrous displasia; hypophosphatasia;
KW bone sarcoma; myeloma bone disorder; osteolytic bone lesion;
KW hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;
KW bone fracture; ss.
XX
OS Mus sp.
XX
PN WO9937662-A1.
XX
PD 29-JUL-1999.
XX
PF 26-JAN-1999; 99WO-US01575.
XX
PR 27-JAN-1998; 98US-0013810.
XX
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI Busfield SJ;
XX
DR WPI; 1999-458675/38.
DR N-PSDB; AAX86455.
XX

PT New isolated SPOIL proteins, used to develop products for treating,
PT e.g. inflammatory and immune disorders
XX
PS Claim 8; Fig 1; 126pp; English.
XX
CC The present sequence represents a SPOIL-I protein. SPOIL proteins have
CC homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.
CC The SPOIL proteins are used as modulating agents in regulating a variety
CC of cellular processes. The products can be used for treating disorders
CC characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone
CC metabolism disorder, a proinflammatory disorder or an immune disorder.
CC They can be used for treating e.g. inflammatory diseases and disorders
CC e.g. inflammation, septic shock, stroke, diabetes, arthritis,
CC intercolitis and pneumonitis, epithelial cell and/or skin diseases and
CC disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma
CC and Kaposi's sarcoma and other epithelial cancers including squamous cell
CC carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and
CC bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's
CC disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,
CC fibrous displasia, hypophosphatasia, bone sarcoma, myeloma bone disorder
CC (e.g. osteolytic bone lesions) and hypercalcemia. SPOIL molecules and
CC SPOIL modulators are useful for regulation of bone mass (e.g. increase in
CC bone mass and/or inhibit bone loss), management of bone fragility (e.g.
CC decrease bone fragility); and prevention and/or treatment of bone pain,
CC bone deformities and/or bone fractures. The products can also be used for
CC detection, diagnosis and screening assays.
XX
SQ Sequence 98 AA;

Query Match 64.2%; Score 238; DB 20; Length 98;
Best Local Similarity 63.8%; Pred. No. 1.8e-21;
Matches 44; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

```
Qy       1 EKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKAN 60
           | :||::||: ||||: |||| :|| ||||| ||||||||| |:| ||||||||||:
Db      29 egnimemynkkepvkaslfyhkksgttstfesaafpgwfiavcskgscpliltqelgeif 88

Qy      61 TTDFGLTML 69
             ||| : ::
Db      89 itdfemivv 97
```

RESULT 8
AAE06662
ID AAE06662 standard; Protein; 157 AA.
XX
AC AAE06662;
XX
DT 16-OCT-2001 (first entry)
XX
DE Mouse interleukin-1epsilon (IL-1epsilon) protein.
XX
KW Mouse; interleukin-1epsilon; IL-1epsilon; virucide; hepatotropic; fever;
KW immunological disorder; tumour; inflammatory disorder; hypoglycaemia;
KW autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;
KW psoriasis; viral infection; allergy; cytokine; HIV; drug screening.
XX
OS Mus sp.
XX
PN WO200157219-A2.
XX
PD 09-AUG-2001.
XX
PF 01-FEB-2001; 2001WO-US03285.
XX
PR 02-FEB-2000; 2000US-0179638.
XX
PA (SCHE) SCHERING CORP.
XX
PI Debets JEMA, Timans JC, Bazan JF, Kastelein RA;
XX
DR WPI; 2001-488886/53.
XX
PT Novel isolated or recombinant antigenic interleukin-1 delta or epsilon
PT polypeptide useful for treating conditions exhibiting abnormal
PT expression of interleukin such as immunological disorders, tumor and
PT allergy -
XX
PS Disclosure; Fig 1; 103pp; English.
XX
CC The invention relates to recombinant antigenic interleukin-1 like
CC molecules and their corresponding nucleic acid sequences, designated
CC as interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon).
CC IL-1delta and IL-1epsilon are useful for treating conditions exhibiting
CC abnormal expression of the interleukin such as immunological disorders,
CC tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis,
CC allergy, autoimmune diseases and infectious diseases (e.g., pulmonary
CC tuberculosis, leprosy, fulminant hepatitis, and viral infections such as
CC HIV). The invention also relates to methods of using the composition
CC containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic
CC utilities. IL-1delta is used as an immunogen for the production of
CC antisera or antibodies specific, e.g., capable of distinguishing between
CC IL-1 family members and an IL-1delta, for the interleukin or its
CC fragment. The purified interleukin is used as a reagent to detect any
CC antibodies generated in response to the presence of elevated levels of
CC expression, or immunological disorders which lead to antibody production
CC to the endogenous cytokine. The invention also contemplates the use of
CC competitive drug screening assays. The present sequence is mouse
CC interleukin-1epsilon (IL-1epsilon) protein related to the invention.
XX
SQ Sequence 157 AA;

Query Match 64.2%; Score 238; DB 22; Length 157;
Best Local Similarity 63.8%; Pred. No. 3.1e-21;
Matches 44; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

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Db      88 egnimemynkkepvkaslfyhkksgttstfesaafpgwfiavcskgscpliltqelgeif 147

Qy      61 TTDFGLTML 69
             ||| : ::
Db     148 itdfemivv 156
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RESULT 9
AAW86286
ID AAW86286 standard; Protein; 160 AA.
XX
AC AAW86286;
XX
DT 19-FEB-1999 (first entry)
XX
DE Rodent interleukin (IL)-1 epsilon polypeptide.
XX
KW Interleukin; IL-1 delta; polyclonal antibody; IL-1 epsilon; cytokine;
KW inflammatory response; immune system; diagnosis; agonist; antagonist;
KW chemokine.
XX
OS Mus sp.
XX
PN WO9847921-A1.
XX
PD 29-OCT-1998.
XX
PF 17-APR-1998; 98WO-US06879.
XX
PR 06-AUG-1997; 97US-0055111.
PR 21-APR-1997; 97US-0837627.
XX
PA (SCHE) SCHERING CORP.
XX
PI Bazan JF, Hedrick JA, Kastelein RA, Sana TR;
XX

DR WPI; 1998-609976/51.
DR N-PSDB; AAV71960.
XX
PT Mammalian interleukin 1-delta and 1-epsilon - useful for, e.g.
PT regulating the immune system and inflammatory responses
XX
PS Claim 1; Pages 92-93; 113pp; English.
XX
CC This represents a rodent interleukin (IL)-1 epsilon polypeptide. The
CC invention relates to a recombinant polypeptide that specifically binds
CC polyclonal antibodies (Abs) generated against a 12 consecutive amino acid
CC segment of IL-1 delta or IL-1 epsilon. Agonists or antagonists of these
CC IL polypeptides are used to regulate a cell involved in an inflammatory
CC response. The IL-1 delta or IL-1 epsilon polypeptides and peptides are
CC used to produce Abs and antigen-Ab complexes. The polypeptides, Abs and
CC the corresponding nucleic acids regulate development and/or the immune
CC system, and can be used to diagnose and treat conditions associated with
CC abnormal expression of IL. Agonists or antagonists of IL-1 delta or IL-1
CC epsilon polypeptides are used with agonists or antagonists of IL-1 alpha,
CC IL-1RA, IL-1 beta, IL-1 gamma, IL-2 and/or IL-12. The IL-1 delta or IL-1
CC epsilon polypeptides may be used as a soluble polypeptide or as a fusion
CC protein with another cytokine or chemokine.
XX
SQ Sequence 160 AA;

Query Match 64.2%; Score 238; DB 19; Length 160;
Best Local Similarity 63.8%; Pred. No. 3.2e-21;
Matches 44; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

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           | :||::||: ||||: |||| :||  ||||| ||||||||| |:| ||||||||||:
Db      91 egnimemynkkepvkaslfyhkksgttstfesaafpgwfiavcskgscpliltqelgeif 150

Qy      61 TTDFGLTML 69
              ||| : ::
Db     151 itdfemivv 159
```

RESULT 10
AAY24049
ID AAY24049 standard; Protein; 160 AA.
XX
AC AAY24049;
XX
DT 30-SEP-1999 (first entry)
XX
DE Amino acid sequence of a murine SPOIL-II protein.
XX
KW SPOIL-II; interleukin-1 receptor antagonist; IL-1ra; modulating agent;
KW bone metabolism disorder; proinflammatory disorder; immune disorder;
KW inflammatory disease; septic shock; stroke; diabetes; arthritis;
KW intercolitis; pneumonitis; epithelial cell; skin disease;
KW proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;
KW epithelial cancer; squamous cell carcinoma; bone resorption disorder;
KW osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;
KW osteogenesis imperfecta; fibrous displasia; hypophosphatasia;
KW bone sarcoma; myeloma bone disorder; osteolytic bone lesion;
KW hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;
KW bone fracture.
XX
OS Mus sp.
XX
PN WO9937662-A1.
XX
PD 29-JUL-1999.
XX
PF 26-JAN-1999; 99WO-US01575.
XX
PR 27-JAN-1998; 98US-0013810.
XX
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX

PI Busfield SJ;
XX
DR WPI; 1999-458675/38.
DR N-PSDB; AAX86460.
XX
PT New isolated SPOIL proteins, used to develop products for treating,
PT e.g. inflammatory and immune disorders
XX
PS Claim 8; Fig 6; 126pp; English.
XX
CC The present sequence represents a SPOIL-II protein. SPOIL proteins have
CC homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.
CC The SPOIL proteins are used as modulating agents in regulating a variety
CC of cellular processes. The products can be used for treating disorders
CC characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone
CC metabolism disorder, a proinflammatory disorder or an immune disorder.
CC They can be used for treating e.g. inflammatory diseases and disorders
CC e.g. inflammation, septic shock, stroke, diabetes, arthritis,
CC intercolitis and pneumonitis, epithelial cell and/or skin diseases and
CC disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma
CC and Kaposi's sarcoma and other epithelial cancers including squamous cell
CC carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and
CC bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's
CC disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,
CC fibrous displasia, hypophosphatasia, bone sarcoma, myeloma bone disorder
CC (e.g. osteolytic bone lesions) and hypercalcemia. SPOIL molecules and
CC SPOIL modulators are useful for regulation of bone mass (e.g. increase in
CC bone mass and/or inhibit bone loss), management of bone fragility (e.g.
CC decrease bone fragility); and prevention and/or treatment of bone pain,
CC bone deformities and/or bone fractures. The products can also be used for
CC detection, diagnosis and screening assays.
XX
SQ Sequence 160 AA;

Query Match 64.2%; Score 238; DB 20; Length 160;
Best Local Similarity 63.8%; Pred. No. 3.2e-21;
Matches 44; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

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Db      91 egnimemynkkepvkaslfyhkksgttstfesaafpgwfiavcskgscpliltqelgeif 150

Qy      61 TTDFGLTML 69
              ||| : ::
Db     151 itdfemivv 159
```

RESULT 11
AAB18924
ID AAB18924 standard; Protein; 134 AA.
XX
AC AAB18924;
XX
DT 08-FEB-2001 (first entry)
XX
DE A novel polypeptide designated PRO5737.
XX
KW Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122;
KW PRO1889; PRO1890; PRO1887; PRO1785; PRO4353; PRO4357; PRO4405; PRO4356;
KW PRO4352; PRO4380; PRO4354; PRO4408; PRO5737; PRO4425; PRO5990; PRO6030;
KW PRO4424; PRO4422; PRO4430; PRO4499; tumour; obesity; diabetes;
KW insulinemia; kidney disorder; Bergers disease; nephropathy;
KW Schonlein-Henoch purpura; celiac disease; dermatitis herpetiformis;
KW Crohns disease.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1..17
FT		/note= "signal sequence"
FT	Modified-site	10..16
FT		/note= "N-myristoylation site"

XX
PN WO200056889-A2.
XX
PD 28-SEP-2000.
XX
PF 01-MAR-2000; 2000WO-US05601.
XX
PR 23-MAR-1999; 99US-0125774.
PR 23-MAR-1999; 99US-0125778.
PR 24-MAR-1999; 99US-0125826.
PR 31-MAR-1999; 99US-0127035.
PR 05-APR-1999; 99US-0127706.
PR 21-APR-1999; 99US-0130359.
PR 27-APR-1999; 99US-0131270.
PR 27-APR-1999; 99US-0131272.
PR 27-APR-1999; 99US-0131291.
PR 04-MAY-1999; 99US-0132371.
PR 04-MAY-1999; 99US-0132379.
PR 04-MAY-1999; 99US-0132383.
PR 25-MAY-1999; 99US-0135750.
PR 08-JUN-1999; 99US-0138166.
PR 20-JUL-1999; 99US-0144791.
PR 03-AUG-1999; 99US-0146970.
PR 09-DEC-1999; 99US-0170262.
XX
PA (GETH) GENENTECH INC.
XX
PI Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2000-628263/60.
DR N-PSDB; AAA96351.
XX
PT Novel secreted and transmembrane polypeptides useful for diagnosing
PT tumour in a mammal, for identifying agonists and antagonists of the
PT polypeptide and for therapeutic use -
XX
PS Claim 12; Fig 32; 222pp; English.
XX
CC The present sequence represents a secreted or transmembrane polypeptide.
CC The specification describes polypeptides designated PRO1484, PRO4334,
CC PRO1122, PRO1889, PRO1890, PRO1887, PRO1785, PRO4353, PRO4357, PRO4405,
CC PRO4356, PRO4352, PRO4380, PRO4354, PRO4408, PRO5737, PRO4425, PRO5990,
CC PRO6030, PRO4424, PRO4422, PRO4430 and PRO4499. PRO1889 polypeptide is
CC useful for diagnosing tumour in a mammal. The polypeptides, their
CC agonists and antagonists are useful treating a condition associated with
CC expression or activity of the polypeptide. Conditions treated include
CC obesity, diabetes or hyper-or hypo-insulinemia. The polypeptides are
CC capable of inducing proliferation of mammalian kidney mesangial cells
CC and are therefore useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Bergers disease or other
CC nephropathies associated with Schonlein-Henoch purpura, celiac disease,
CC dermatitis herpetiformis or Crohns disease. The nucleic acids may be used
CC to generate transgenic animals for use in development and screening of
CC therapeutically useful reagents and also for chromosome identification
CC and tissue typing.
XX
SQ Sequence 134 AA;

Query Match 56.2%; Score 208.5; DB 21; Length 134;
Best Local Similarity 63.2%; Pred. No. 1e-17;
Matches 43; Conservative 8; Mismatches 16; Indels 1; Gaps 1;

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Db      66 eqkimdlygqpepvkpflfyraktgrtstlesvafpdwfia-sskrdqpiiltselgksy 124

Qy      61 TTDFGLTM 68
             | | | :
Db     125 ntafelni 132
```

RESULT 12
AAY96935
ID AAY96935 standard; Protein; 134 AA.
XX
AC AAY96935;
XX
DT 31-OCT-2000 (first entry)
XX
DE Human IL-1 receptor antagonist 2.
XX
KW hIL-1Ra2; human interleukin-1 receptor antagonist-2; IL-1lp; osteopathic;
KW interleukin-1-like polypeptide; anti-inflammatory; anti-asthmatic;
KW anti-arthritic; antimicrobial; respiratory; anti-ischemic; vaccine;
KW dermatalogical; immunomodulatory; gastrointestinal; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200039297-A2.
XX
PD 06-JUL-2000.
XX
PF 22-DEC-1999; 99WO-US30720.
XX
PR 23-DEC-1998; 98US-0113430.
PR 22-JAN-1999; 99US-0116843.
PR 13-APR-1999; 99US-0129122.
XX
PA (GETH) GENENTECH INC.
XX
PI Goddard A, Pan J;
XX
DR WPI; 2000-452395/39.
DR N-PSDB; AAA51595.
XX
PT Nucleic acids encoding interleukin-1-like polypeptides, useful for
PT preventing and treating e.g. inflammation, asthma and psoriasis
XX
PS Claim 22; Fig 5A-B; 143pp; English.
XX
CC An isolated nucleic acid molecule encoding an interleukin-1-like
CC polypeptide (IL-1lp) that retains one or more activities of the peptide
CC from which it is derived, such as the IL-18R binding activity of a human
CC interleukin-1 receptor antagonist-1 (hIL-1Ra1) polypeptide, is new. The
CC nucleic acids may be used in molecular engineering applications, e.g.
CC hybridization assays and chromosome and gene mapping studies, for
CC recombinantly producing the IL-1lp polypeptide or for producing gene
CC knock out animals to study the role of the protein in metabolism and
CC disease processes (conversely, gene therapy protocols may be used to
CC supplement a patients production of the polypeptide or to rectify
CC mutations that lead to the production of in active peptides). The
CC peptides produced may be used to screen for and produce modulators (e.g.
CC antibodies) of IL-1lp protein expression and activity which may be use
CC to treat disorders associated with inappropriate IL-1lp expression and
CC activity, such as inflammatory disorders, asthma, arthritis,
CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress
CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
CC psoriasis, graft versus host disease and/or inflammatory bowel disease.
XX
SQ Sequence 134 AA;

Query Match 56.2%; Score 208.5; DB 21; Length 134;
Best Local Similarity 63.2%; Pred. No. 1e-17;
Matches 43; Conservative 8; Mismatches 16; Indels 1; Gaps 1;

```
Qy       1 EKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKAN 60
           |: ||||| |||||| |||| :::|| || |||||| |||| ||:   |:||| ||||:
Db      66 eqkimdlygqpepvkpflfyraktgrtstlesvafpdwfia-sskrdqpiiltselgksy 124

Qy      61 TTDFGLTM 68
             | | | :
Db     125 ntafelni 132
```

RESULT 13
AAW63136
ID AAW63136 standard; Protein; 169 AA.
XX
AC AAW63136;
XX
DT 14-OCT-1998 (first entry)
XX
DE Interleukin-1 receptor antagonist beta (IL-1ra-beta).
XX
KW Interleukin-1 receptor antagonist beta; IL-1ra-beta; IL-1 alpha;
KW IL-1 beta; inflammatory response; treatment; inflammation; septicaemia;
KW cancer; anaemia; arthritis; inflammatory bowel disease;
KW graft vs. host rejection; autoimmunity; stroke; cardiac ischaemia;
KW acute respiratory disease syndrome; psoriasis; restenosis;
KW traumatic brain injury; acquired immune deficiency syndrome;
KW cachexia.
XX
OS Homo sapiens.
XX
PN EP855404-A1.
XX
PD 29-JUL-1998.
XX
PF 27-JAN-1998; 98EP-0300572.
XX
PR 28-JAN-1997; 97US-0790032.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Young PR;
XX
DR WPI; 1998-389778/34.
DR N-PSDB; AAV42659.
XX
PT New nucleic acid encoding human interleukin-1 receptor antagonist
PT beta polypeptides - and related expression systems, transformed
PT cells, proteins, antibodies, agonists and antagonists, useful for
PT treatment, prevention and diagnosis of inflammation, septicaemia,
PT cancer etc
XX
PS Claim 13; Fig 2; 20pp; English.
XX
CC The present sequence represents human Interleukin-1 receptor antagonist
CC beta (IL-ra-beta). IL-1 alpha and IL-1 beta play key roles in
CC inflammatory responses, and are produced as zymogens which are cleaved
CC upon secretion to yield mature carboxyl terminal 17 kD fragments.
CC IL-1ra-beta polypeptides and polynucleotides are useful in treatment of
CC chronic and acute inflammation, septicaemia, cancer, anaemia, arthritis,
CC inflammatory bowel disease, graft vs. host rejection, autoimmunity,
CC stroke, cardiac ischaemia, acute respiratory disease syndrome (ARDS),
CC psoriasis, restenosis, traumatic brain injury, acquired immune
CC deficiency syndrome (AIDS) and cachexia. These conditions (or
CC susceptibility to them) may be diagnosed by detecting mutations in the
CC IL-1ra-beta coding sequence analysing a sample for presence or amount
CC of IL-1ra-beta.
XX
SQ Sequence 169 AA;

Query Match 56.2%; Score 208.5; DB 19; Length 169;
Best Local Similarity 63.2%; Pred. No. 1.4e-17;
Matches 43; Conservative 8; Mismatches 16; Indels 1; Gaps 1;

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Qy     61 TTDFGLTM 68
            | | | :
Db    160 ntafelni 167
```

RESULT 14
AAY24043
ID AAY24043 standard; Protein; 169 AA.
XX
AC AAY24043;
XX
DT 30-SEP-1999 (first entry)
XX
DE A human SPOIL-I protein (also known as hTANGO 080-I).
XX
KW SPOIL-I; interleukin-1 receptor antagonist; IL-1ra; modulating agent;
KW bone metabolism disorder; proinflammatory disorder; immune disorder;
KW inflammatory disease; septic shock; stroke; diabetes; arthritis;
KW intercolitis; pneumonitis; epithelial cell; skin disease;
KW proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;
KW epithelial cancer; squamous cell carcinoma; bone resorption disorder;
KW osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;
KW osteogenesis imperfecta; fibrous displasia; hypophosphatasia;
KW bone sarcoma; myeloma bone disorder; osteolytic bone lesion;
KW hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;
KW bone fracture; hTANGO 80-I.
XX
OS Homo sapiens.
XX
PN WO9937662-A1.
XX
PD 29-JUL-1999.
XX
PF 26-JAN-1999; 99WO-US01575.
XX
PR 27-JAN-1998; 98US-0013810.
XX
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI Busfield SJ;
XX
DR WPI; 1999-458675/38.
DR N-PSDB; AAX86458.
XX
PT New isolated SPOIL proteins, used to develop products for treating,
PT e.g. inflammatory and immune disorders
XX
PS Example 1; Fig 4A-B; 126pp; English.
XX
CC The present sequence represents a SPOIL-I protein. SPOIL proteins have
CC homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.
CC The SPOIL proteins are used as modulating agents in regulating a variety
CC of cellular processes. The products can be used for treating disorders
CC characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone
CC metabolism disorder, a proinflammatory disorder or an immune disorder.
CC They can be used for treating e.g. inflammatory diseases and disorders
CC e.g. inflammation, septic shock, stroke, diabetes, arthritis,
CC intercolitis and pneumonitis, epithelial cell and/or skin diseases and
CC disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma
CC and Kaposi's sarcoma and other epithelial cancers including squamous cell
CC carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and
CC bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's
CC disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,
CC fibrous displasia, hypophosphatasia, bone sarcoma, myeloma bone disorder
CC (e.g. osteolytic bone lesions) and hypercalcemia. SPOIL molecules and
CC SPOIL modulators are useful for regulation of bone mass (e.g. increase in
CC bone mass and/or inhibit bone loss), management of bone fragility (e.g.
CC decrease bone fragility); and prevention and/or treatment of bone pain,
CC bone deformities and/or bone fractures. The products can also be used for
CC detection, diagnosis and screening assays.
XX
SQ Sequence 169 AA;

Query Match 56.2%; Score 208.5; DB 20; Length 169;
Best Local Similarity 63.2%; Pred. No. 1.4e-17;
Matches 43; Conservative 8; Mismatches 16; Indels 1; Gaps 1;

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Db    101 eqkimdlygqpepvkpflfyraktgrtstlesvafpdwfia-sskrdqpiiltselgksy 159

Qy     61 TTDFGLTM 68
            | | | :
Db    160 ntafelni 167
```

RESULT 15
AAY24395
ID AAY24395 standard; Protein; 169 AA.
XX
AC AAY24395;
XX
DT 20-SEP-1999 (first entry)
XX
DE Human interleukin-1 receptor antagonist beta.
XX
KW Human; interleukin-1 receptor antagonist beta; IL-1RA beta; septicemia;
KW chronic inflammation; acute inflammation; arthritis; autoimmunity;
KW inflammatory bowel disease; graft vs. host disease; stroke; psoriasis;
KW cardiac ischaemia; acute respiratory disease syndrome; ARDS; restenosis;
KW traumatic brain injury; AIDS; cachexia; allergy; parasite infection;
KW allergic rhinitis; allergic asthma; atopic dermatitis; gene therapy;
KW allergic inflammatory disease; delayed hypersensitivity; vaccine.
XX
OS Homo sapiens.
XX
PN WO9936541-A1.
XX
PD 22-JUL-1999.
XX
PF 14-JAN-1999; 99WO-US00847.
XX
PR 29-APR-1998; 98US-0069619.
PR 14-JAN-1998; 98US-0007464.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Marshall L, Young PR;
XX
DR WPI; 1999-430615/36.
DR N-PSDB; AAX90135.
XX
PT New interleukin-1 receptor antagonist beta, useful for treating
PT inflammation and autoimmune diseases
XX
PS Claim 15; Fig 1; 34pp; English.
XX
CC The present sequence represents human interleukin-1 receptor antagonist
CC beta (IL-1RA beta). IL-1RA beta polypeptides and polynucleotides are
CC useful for diagnosing diseases (or susceptibility to diseases) related
CC to the expression or activity of IL-1RA beta, by determining mutations
CC in the IL-1RA beta nucleic acid sequences and/or analysing for the
CC presence or amount of IL-1RA beta polypeptide. IL-1RA beta polypeptides
CC are also useful for screening for compounds which affect activity of the
CC protein. These can be used in treatment to inhibit (antagonist) or
CC enhance (agonist) IL-1RA beta activity, in addition to direct
CC administration of IL-1RA beta polypeptides to treat conditions, or
CC direct administration of antisense sequences to prevent expression.
CC IL-1RA beta polypeptides (administered directly, in a vector i.e. gene
CC therapy, and as a vaccine) and antibodies induce an immune response to
CC immunise and prevent disease. Diseases diagnosed, prevented or treated
CC include chronic and acute inflammation, septicemia, arthritis,
CC inflammatory bowel disease, graft vs. host disease, autoimmunity,
CC stroke, cardiac ischaemia, acute respiratory disease syndrome (ARDS),
CC psoriasis, restenosis, traumatic brain injury, AIDS, cachexia, allergy,
CC parasite infection, allergic rhinitis, allergic asthma, atopic
CC dermatitis, allergic inflammatory diseases and delayed hypersensitivity.
XX
SQ Sequence 169 AA;

Query Match 56.2%; Score 208.5; DB 20; Length 169;
Best Local Similarity 63.2%; Pred. No. 1.4e-17;
Matches 43; Conservative 8; Mismatches 16; Indels 1; Gaps 1;

```
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Db    101 eqkimdlygqpepvkpflfyraktgrtstlesvafpdwfia-sskrdqpiiltselgksy 159

Qy     61 TTDFGLTM 68
            | | | :
Db    160 ntafelni 167
```

Search completed: June 20, 2002, 15:03:07
Job time: 118 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 20, 2002, 15:01:10 ; Search time 36.86 Seconds
(without alignments)
182.481 Million cell updates/sec

Title: US-09-763-498-6
Perfect score: 371
Sequence: 1 EKDIMDLYNQPEPVKSFLFY.....ILTQELGKANTTDFGLTMLF 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	124	33.4	155	2	JC7104	interleukin-1 rece
2	107	28.8	177	2	A54377	interleukin-1 rece
3	107	28.8	178	2	C40956	interleukin-1 rece
4	105	28.3	178	2	A44610	interleukin-1 rece
5	101	27.2	177	2	A30368	interleukin-1 rece
6	101	27.2	180	2	A39386	interleukin-1 rece
7	96	25.9	267	1	JN0724	interleukin-1 beta
8	96	25.9	267	2	S38373	interleukin-1 beta
9	89	24.0	266	1	S23010	interleukin-1 beta
10	88	23.7	266	1	ICBO1B	interleukin-1 beta
11	85	22.9	269	1	ICHU1B	interleukin-1 beta
12	81	21.8	214	2	JC5646	interleukin-1 beta
13	74	19.9	268	1	A30584	interleukin-1 beta
14	65.5	17.7	269	1	I55969	interleukin-1 beta
15	64.5	17.4	541	2	S56653	thioglucosidase (E
16	63	17.0	364	1	S77360	cbiD protein - Syn
17	62.5	16.8	268	1	ICBO1A	interleukin-1 alph
18	62.5	16.8	268	1	A61246	interleukin-1 alph
19	62.5	16.8	270	1	S10532	interleukin-1 alph
20	62.5	16.8	533	2	T19416	hypothetical prote
21	62	16.7	939	2	E82121	peptidase, insulin
22	61.5	16.6	325	2	E87125	ribonucleotide red
23	61	16.4	255	2	C95997	probable glucose-1
24	61	16.4	273	2	AB2150	hypothetical prote
25	61	16.4	522	2	C90073	hypothetical prote
26	61	16.4	1161	1	S31213	nidogen precursor
27	60.5	16.3	1558	2	C89114	protein C37C3.6a [
28	60.5	16.3	2167	2	T34395	hypothetical prote
29	60	16.2	407	2	T22554	hypothetical prote
30	60	16.2	458	2	A75504	maltose ABC transp
31	59.5	16.0	256	2	F86463	hypothetical prote
32	59.5	16.0	374	2	F87596	hypothetical prote
33	59.5	16.0	634	2	T25425	hypothetical prote
34	59.5	16.0	823	2	H72282	maltose ABC transp
35	58.5	15.8	271	1	ICHU1A	interleukin-1 alph
36	58	15.6	268	1	B24073	interleukin-1 alph
37	58	15.6	343	2	AG0278	conserved hypothet
38	58	15.6	453	2	T00724	presenilin homolog
39	58	15.6	566	2	D84611	probable cytochrom
40	58	15.6	1617	2	T28153	complement C4 - ch
41	57.5	15.5	270	2	I46620	interleukin-1 alph
42	57.5	15.5	343	2	AH1802	oxidoreductases ho
43	57	15.4	452	2	G72770	hypothetical prote
44	57	15.4	605	2	S36592	E1 protein - human
45	56.5	15.2	324	2	C70861	probable nrdG prot

ALIGNMENTS

RESULT 1
JC7104
interleukin-1 receptor antagonist - human
C;Species: Homo sapiens (man)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C;Accession: JC7104
R;Mulero, J.J.; Pace, A.M.; Nelken, S.T.; Loeb, D.B.; Correa, T.R.; Drmanac, R.; Ford
Biochem. Biophys. Res. Commun. 263, 702-706, 1999
A;Title: IL1HY1: A novel interleukin-1 receptor antagonist gene.
A;Reference number: JC7104; MUID:99443727
A;Accession: JC7104
A;Molecule type: mRNA
A;Residues: 1-155 <MUL>
A;Cross-references: GB:AF186094; NID:g6049804; PIDN:AAF02757.1; PID:g6049805
C;Genetics:
A;Gene: il1hy1
A;Map position: 2q14
C;Keywords: macrophage

Query Match 33.4%; Score 124; DB 2; Length 155;
Best Local Similarity 45.5%; Pred. No. 1.2e-07;
Matches 30; Conservative 7; Mismatches 25; Indels 4; Gaps 2;

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Qy       3 DIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQ--ELG--K 58
           :||:||   :  ||| ||    |  |:||| |:||||:    |   |: |||  | |
Db      84 NIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQPVRLTQLPENGGWN 143

Qy      59 ANTTDF 64
             |  |||
Db     144 APITDF 149
```

RESULT 2
A54377
interleukin-1 receptor antagonist secreted form precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C;Accession: A54377; I46729
R;Cominelli, F.; Bortolami, M.; Pizarro, T.T.; Monsacchi, L.; Ferretti, M.; Brewer, M
J. Biol. Chem. 269, 6962-6971, 1994
A;Title: Rabbit interleukin-1 receptor antagonist. Cloning, expression, functional ch
A;Reference number: A54377; MUID:94165101
A;Accession: A54377
A;Molecule type: mRNA
A;Residues: 1-177 <COM>
A;Cross-references: GB:S68977; NID:g545740; PIDN:AAB30093.1; PID:g545741
A;Experimental source: colon tissue
A;Note: sequence extracted from NCBI backbone (NCBIN:144168, NCBIP:144169)
R;Goto, F.; Goto, K.; Miyata, T.; Ohkawara, S.; Takao, T.; Mori, S.; Furukawa, S.; Ma
Immunology 77, 235-244, 1992
A;Title: Interleukin-1 recetor antagonist in inflammatory exudate cells of rabbits. P

A;Reference number: I46729; MUID:93052512
A;Accession: I46729
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-177 <GOT>
A;Cross-references: GB:D21832; NID:g425787; PIDN:BAA04860.1; PID:g452205
C;Superfamily: interleukin-1
C;Keywords: cytokine receptor; extracellular protein; glycoprotein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;109/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 28.8%; Score 107; DB 2; Length 177;
Best Local Similarity 41.0%; Pred. No. 1.6e-05;
Matches 25; Conservative 6; Mismatches 24; Indels 6; Gaps 1;

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Qy       3 DIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTT 62
           :| ||    |  | | |  | ||  :|||| : ||||:  : |   |: ||      ||
Db     109 NITDLGKNKEQDKRFTFIRSNSGPTTTFESASCPGWFLCTALEADQPVSLT------NTP 162

Qy      63 D 63
           |
Db     163 D 163
```

RESULT 3
C40956
interleukin-1 receptor antagonist precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 16-Jul-1999
C;Accession: C40956
R;Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson,
Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A;Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family:
A;Reference number: A40956; MUID:91271363
A;Accession: C40956
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-178 <EIS>
A;Cross-references: GB:M63101; NID:g204928; PIDN:AAA41434.1; PID:g204929
C;Superfamily: interleukin-1
C;Keywords: cytokine receptor

Query Match 28.8%; Score 107; DB 2; Length 178;
Best Local Similarity 41.5%; Pred. No. 1.6e-05;
Matches 22; Conservative 9; Mismatches 22; Indels 0; Gaps 0;

```
Qy       1 EKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILT 53
           | :| ||    |  | | |  |::|  ::|||:| ||||:  : |   |: ||
Db     108 EVNITDLNKNKEEDKRFTFIRSETGPTTSFESLACPGWFLCTTLEADHPVSLT 160
```

RESULT 4
A44610
interleukin-1 receptor antagonist precursor - mouse
N;Alternate names: IL-1Ra
C;Species: Mus musculus (house mouse)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 16-Jul-1999
C;Accession: A44610; B40956; A49031; I56106; I52970
R;Matsushime, H.; Roussel, M.F.; Matsushima, K.; Hishinuma, A.; Sherr, C.J.
Blood 78, 616-623, 1991
A;Title: Cloning and expression of murine interleukin-1 receptor antagonist in macrophag
A;Reference number: A44610; MUID:91316273
A;Accession: A44610
A;Molecule type: mRNA
A;Residues: 1-178 <MAT>
A;Cross-references: GB:M64404; NID:g198296; PIDN:AAA39277.1; PID:g198297
R;Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson,
Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A;Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family:
A;Reference number: A40956; MUID:91271363
A;Accession: B40956
A;Molecule type: DNA
A;Residues: 7-178 <EIS>
A;Cross-references: GB:M63100; NID:g198389; PIDN:AAA39310.1; PID:g198390
R;Shuck, M.E.; Eessalu, T.E.; Tracey, D.E.; Bienkowski, M.J.
Eur. J. Immunol. 21, 2775-2780, 1991
A;Title: Cloning, heterologous expression and characterization of murine interleukin
A;Reference number: A49031; MUID:92037824
A;Accession: A49031
A;Molecule type: mRNA
A;Residues: 23-178 <SHU>
A;Cross-references: GB:S64082; NID:g238584; PIDN:AAB20265.1; PID:g238585
A;Experimental source: peritoneal macrophages, ICR strain
A;Note: sequence extracted from NCBI backbone (NCBIN:64082, NCBIP:64085)
R;Zahedi, K.; Seldin, M.F.; Rits, M.; Ezekowitz, R.B.; Whitehead, A.S.
J. Immunol. 146, 4228-4233, 1991
A;Title: Mouse IL-1 receptor antagonist protein: Molecular characterization, gene map
A;Reference number: I56106; MUID:91250712
A;Accession: I56106
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-178 <RES>
A;Cross-references: GB:M74294; NID:g198387; PIDN:AAA39309.1; PID:g198388
R;Zahedi, K.A.; Uhlar, C.M.; Rits, M.; Prada, A.E.; Whitehead, A.S.
Cytokine 6, 1-9, 1994
A;Title: The mouse interleukin 1 receptor antagonist protein: gene structure and regu
A;Reference number: I52970; MUID:94271931
A;Accession: I52970
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-178 <RE2>
A;Cross-references: GB:L32838; NID:g487864; PIDN:AAA20576.1; PID:g528978
C;Genetics:
A;Gene: IL-1rn
A;Introns: 40/2; 70/1; 107/3
C;Superfamily: interleukin-1
C;Keywords: cytokine receptor
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-178/Product: interleukin-1 receptor antagonist #status predicted <MA2>

Query Match 28.3%; Score 105; DB 2; Length 178;
Best Local Similarity 41.5%; Pred. No. 2.9e-05;
Matches 22; Conservative 7; Mismatches 24; Indels 0; Gaps 0;

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Qy       1 EKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILT 53
           | :| ||    |  | | |  |: |  ::||| | ||||:  : |   |: ||
Db     108 EVNITDLSKNKEEDKRFTFIRSEKGPTTSFESAACPGWFLCTTLEADRPVSLT 160
```

RESULT 5
A30368
interleukin-1 receptor antagonist secreted form precursor - human
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-May-2000
C;Accession: A40956; I37894; A30368; S08160; S08159; A37822
R;Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thomps
Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A;Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene fami
A;Reference number: A40956; MUID:91271363
A;Accession: A40956
A;Molecule type: DNA
A;Residues: 1-177 <EIS>
A;Cross-references: GB:M63099; NID:g186385; PIDN:AAB41943.1; PID:g186386
R;Lennard, A.; Gorman, P.; Carrier, M.; Griffiths, S.; Scotney, H.; Sheer, D.; Solari
Cytokine 4, 83-89, 1992
A;Title: Cloning and chromosome mapping of the human interleukin-1 receptor antagonis
A;Reference number: I37894; MUID:92338323
A;Accession: I37894
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-177 <LEN>
A;Cross-references: EMBL:X64532; NID:g33798; PIDN:CAA45832.1; PID:g33799
R;Carter, D.B.; Deibel Jr., M.R.; Dunn, C.J.; Tomich, C.S.C.; Laborde, A.L.; Slightom

J.G.; Sieu, L.C.; Hardee, M.M.; Zurcher-Neely, H.A.; Reardon, I.M.; Heinrikson, R.L.; Tr
Nature 344, 633-638, 1990
A;Title: Purification, cloning, expression and biological characterization of an interle
A;Reference number: A30368; MUID:90220867
A;Accession: A30368
A;Molecule type: mRNA
A;Residues: 1-177 <CAR>
A;Cross-references: GB:X53296; NID:g32578; PIDN:CAA37386.1; PID:g32579
A;Note: parts of this sequence, including the amino end of the mature protein, were conf
R;Eisenberg, S.P.; Evans, R.J.; Arend, W.P.; Verderber, E.; Brewer, M.T.; Hannum, C.H.;
Nature 343, 341-346, 1990
A;Title: Primary structure and functional expression from complementary DNA of a human i
A;Reference number: S08160; MUID:90136921
A;Accession: S08160
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-177 <EI2>
A;Cross-references: GB:X52015; NID:g32576; PIDN:CAA36262.1; PID:g32577
R;Hannum, C.H.; Wilcox, C.J.; Arend, W.P.; Joslin, F.G.; Dripps, D.J.; Heimdal, P.L.; Ar
Nature 343, 336-340, 1990
A;Title: Interleukin-1 receptor antagonist activity of a human interleukin-1 inhibitor.
A;Reference number: S08159; MUID:90136920
A;Accession: S08159
A;Molecule type: protein
A;Residues: 26-75;97-108;110-116;120-131;163-176 <HAN>
R;Bienkowski, M.J.; Eessalu, T.E.; Berger, A.E.; Truesdell, S.E.; Shelly, J.A.; Laborde,
J. Biol. Chem. 265, 14505-14511, 1990
A;Title: Purification and characterization of interleukin 1 receptor level antagonist pr
A;Reference number: A37822; MUID:90354444
A;Accession: A37822
A;Molecule type: protein
A;Residues: 26-52;70-77;122-127;170-175 <BIE>
A;Experimental source: culture medium, PMA-stimulated THP-1 cells
C;Comment: For an alternative splice form, see PIR:A39386
C;Genetics:
A;Gene: GDB:IL1RN
A;Cross-references: GDB:125897; OMIM:147679
A;Map position: 2q14.2-2q14.2
A;Introns: 39/2; 69/1; 106/3
C;Superfamily: interleukin-1
C;Keywords: alternative splicing; cytokine receptor; extracellular protein; glycoprotein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-177/Product: interleukin-1 receptor antagonist #status experimental <MAT>
F;109/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 27.2%; Score 101; DB 2; Length 177;
Best Local Similarity 37.5%; Pred. No. 8.7e-05;
Matches 24; Conservative 8; Mismatches 26; Indels 6; Gaps 1;

```
Qy       3 DIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTT 62
           :| ||    :  | | |  | ||  ::|||  | ||||:  : |   |: ||      |
Db     109 NITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWFLCTAMEADQPVSLT------NMP 162

Qy      63 DFGL 66
           | |:
Db     163 DEGV 166
```

RESULT 6
A39386
interleukin-1 receptor antagonist, long intracellular splice form - human
N;Contains: interleukin-1 receptor antagonist, short intracellular splice form
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1992 #sequence_revision 11-Apr-1997 #text_change 26-May-2000
C;Accession: I37893; A39386
R;Muzio, M.; Polentarutti, N.; Sironi, M.; Poli, G.; De Gioia, L.; Introna, M.; Mantovan
J. Exp. Med. 182, 623-628, 1995
A;Title: Cloning and characterization of a new isoform of the interleukin 1 receptor ant
A;Reference number: I37893; MUID:95355865
A;Accession: I37893
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-180 <RES>
A;Cross-references: EMBL:X84348; NID:g1008970; PIDN:CAA59087.1; PID:g1008971
R;Haskill, S.; Martin, G.; Van Le, L.; Morris, J.; Peace, A.; Bigler, C.F.; Jaffe, G.
Proc. Natl. Acad. Sci. U.S.A. 88, 3681-3685, 1991
A;Title: cDNA cloning of an intracellular form of the human interleukin 1 receptor an
A;Reference number: A39386; MUID:91219436
A;Accession: A39386
A;Molecule type: mRNA
A;Residues: 1-3,25-180 <HAS>
A;Cross-references: GB:M55646; NID:g186291; PIDN:AAA59138.1; PID:g186292
C;Comment: For an alternative splice form, see PIR:A30368
C;Genetics:
A;Gene: GDB:IL1RN
A;Cross-references: GDB:125897; OMIM:147679
A;Map position: 2q14.2-2q14.2
C;Superfamily: interleukin-1
C;Keywords: alternative splicing; cytokine receptor
F;1-180/Product: interleukin-1 receptor antagonist, long intracellular splice form #s
F;1-3,25-180/Product: interleukin-1 receptor antagonist, short intracellular splice f

Query Match 27.2%; Score 101; DB 2; Length 180;
Best Local Similarity 37.5%; Pred. No. 8.9e-05;
Matches 24; Conservative 8; Mismatches 26; Indels 6; Gaps 1;

```
Qy       3 DIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTT 62
           :| ||    :  | | |  | ||  ::|||  | ||||:  : |   |: ||      |
Db     112 NITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWFLCTAMEADQPVSLT------NMP 165

Qy      63 DFGL 66
           | |:
Db     166 DEGV 169
```

RESULT 7
JN0724
interleukin-1 beta precursor - pig
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 14-Jul-1994 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999
C;Accession: JN0724
R;Huether, M.J.; Lin, G.; Smith, D.M.; Murtaugh, M.P.; Molitor, T.W.
Gene 129, 285-289, 1993
A;Title: Cloning, sequencing and regulation of an mRNA encoding porcine interleukin-1
A;Reference number: JN0724; MUID:93314975
A;Accession: JN0724
A;Molecule type: mRNA
A;Residues: 1-267 <HUE>
A;Cross-references: GB:M86725; NID:g164607; PIDN:AAA02584.1; PID:g164608
A;Experimental source: alveolar macrophage
C;Comment: This protein is a pleiotropic cytokine that mediates a variety of processe
C;Comment: This protein lacks a conventional signal sequence for protein export. Clea
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrop
F;115-267/Product: interleukin-1 beta #status predicted <IL1>
F;77/Binding site: myristate (Lys) (covalent) #status predicted

Query Match 25.9%; Score 96; DB 1; Length 267;
Best Local Similarity 30.6%; Pred. No. 0.00057;
Matches 19; Conservative 13; Mismatches 30; Indels 0; Gaps 0;

```
Qy       8 YNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLT 67
           | : :  | |:|| ::      |||  :| |:|: |     |: |    |: : ||| :
Db     204 YPKRDMEKRFVFYKTEIKNRVEFESALYPNWYISTSQAEQKPVFLGNSKGRQDITDFTME 263

Qy      68 ML 69
           :|
Db     264 VL 265
```

```
RESULT   8
S38373
interleukin-1 beta precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 20-May-1994 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999
C;Accession: S38373
R;Vandenbroeck, K.; Fiten, P.; Beuken, E.; Martens, E.; Janssen, A.; van Damme, J.; Opde
Eur. J. Biochem. 217, 45-52, 1993
A;Title: Gene sequence, cDNA construction, expression in Escherichia coli and geneticall
A;Reference number: S38373; MUID:94039070
A;Accession: S38373
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-267 <VAN>
A;Cross-references: EMBL:X74568; NID:g407899; PIDN:CAA52660.1; PID:g407900
C;Genetics:
A;Introns: 16/2; 33/3; 99/1; 154/1; 197/3
C;Superfamily: interleukin-1


  Query Match             25.9%;  Score 96;  DB 2;  Length 267;
  Best Local Similarity   30.6%;  Pred. No. 0.00057;
  Matches   19;  Conservative   13;  Mismatches   30;  Indels    0;  Gaps    0;

Qy       8 YNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLT 67
           |  :  :  | |:|| ::      |||  :| |:|: |     |: |    |: : ||| :
Db     204 YPKRDMEKRFVFYKTEIKNRVEFESALYPNWYISTSQAEQKPVFLGNSKGRQDITDFTME 263

Qy      68 ML 69
           :|
Db     264 VL 265


RESULT   9
S23010
interleukin-1 beta precursor - sheep
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 08-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 15-Oct-1999
C;Accession: S23010; S43047; S13092; B61246
R;Seow, H.F.; Rothel, J.S.; David, M.J.; Wood, P.R.
DNA Seq. 1, 423-426, 1991
A;Title: Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.
A;Reference number: S23010; MUID:92119335
A;Accession: S23010
A;Molecule type: mRNA
A;Residues: 1-266 <SEO>
A;Cross-references: EMBL:X56972; NID:g1808; PIDN:CAA40293.1; PID:g1809
A;Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in having an addi
R;Sargan, D.R.
submitted to the EMBL Data Library, May 1992
A;Reference number: S43047
A;Accession: S43047
A;Molecule type: mRNA
A;Residues: 1-13,'C',15-54,'K',56-63,'A',65-144,'L',146-266 <SAR>
A;Cross-references: EMBL:X54796; NID:g1273; PIDN:CAA38566.1; PID:g1274
R;Fiskerstrand, C.; Sargan, D.
Nucleic Acids Res. 18, 7165, 1990
A;Title: Nucleotide sequence of ovine interleukin-1 beta.
A;Reference number: S13092; MUID:91088326
A;Accession: S13092
A;Molecule type: mRNA
A;Residues: 1-13,'C',15-54,'K',56-61,'S',63,'A',65-144,'L',146-266 <FIS>
A;Cross-references: EMBL:X54796
A;Note: the authors translated the codon AGT for residue 62 as Arg
R;Andrews, A.E.; Barcham, G.J.; Brandon, M.R.; Nash, A.D.
Immunology 74, 453-460, 1991
A;Title: Molecular cloning and characterization of ovine IL-1alpha and IL-1beta.
A;Reference number: A61246; MUID:92120716
A;Accession: B61246
A;Molecule type: mRNA
A;Residues: 1-144,'L',146-266 <AND>
C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavag
```

```
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin
C;Genetics:
A;Gene: IL-1-beta
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;114-266/Product: interleukin-1 beta #status predicted <MAT>


  Query Match             24.0%;  Score 89;  DB 1;  Length 266;
  Best Local Similarity   31.7%;  Pred. No. 0.004;
  Matches   20;  Conservative   12;  Mismatches   31;  Indels    0;  Gaps    0;

Qy       7 LYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGL 66
           :| :    | |:|| ::      |||| :| |:|: |     |: | :  |  : ||| :
Db     202 VYPKRNMEKRFVFYKTEIKNTVEFESVLYPNWYISTSQIEEKPVFLGRFRGGQDITDFRM 261

Qy      67 TML 69
             |
Db     262 ETL 264


RESULT  10
ICBO1B
interleukin-1 beta precursor - bovine
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
C;Accession: JL0010; S01380
R;Maliszewski, C.R.; Baker, P.E.; Schoenborn, M.A.; Davis, B.S.; Cosman, D.; Gillis,
Mol. Immunol. 25, 429-437, 1988
A;Title: Cloning, sequence and expression of bovine interleukin 1-alpha and interleuk
A;Reference number: A94695; MUID:88318652
A;Accession: JL0010
A;Molecule type: mRNA
A;Residues: 1-266 <MAL>
A;Cross-references: GB:M37211; NID:g163200; PIDN:AAA30584.1; PID:g163201
R;Leong, S.R.; Flaggs, G.M.; Lawman, M.; Gray, P.W.
Nucleic Acids Res. 16, 9054, 1988
A;Title: The nucleotide sequence for the cDNA of bovine interleukin-1 beta.
A;Reference number: S01380; MUID:89016591
A;Accession: S01380
A;Molecule type: mRNA
A;Residues: 1-251,'A',253-266 <LEO>
A;Cross-references: EMBL:X12498; NID:g448; PIDN:CAA31018.1; PID:g449
C;Comment: This protein is a cytokine that mediates a variety of immunoregulatory and
C;Comment: This protein lacks a conventional signal sequence for protein export. Clea
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;114-266/Product: interleukin-1 beta #status predicted <MAT>


  Query Match             23.7%;  Score 88;  DB 1;  Length 266;
  Best Local Similarity   31.7%;  Pred. No. 0.0053;
  Matches   20;  Conservative   11;  Mismatches   32;  Indels    0;  Gaps    0;

Qy       7 LYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGL 66
           :| :    | |:|| ::      |||| :| |:|: |     |: |    |  : ||| :
Db     202 VYPKRNMEKRFVFYKTEIKNTVEFESVLYPNWYISTSQIEERPVFLGHFRGGQDITDFRM 261

Qy      67 TML 69
             |
Db     262 ETL 264


RESULT  11
ICHU1B
interleukin-1 beta precursor [validated] - human
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1986 #sequence_revision 15-May-1998 #text_change 15-Sep-2000
```

C;Accession: A25542; A29019; A94023; A93361; I51852; I65200; I38132; B27616; A01848; S19
R;Clark, B.D.; Collins, K.L.; Gandy, M.S.; Webb, A.C.; Auron, P.E.
Nucleic Acids Res. 14, 7897-7914, 1986
A;Title: Genomic sequence for human prointerleukin 1 beta: possible evolution from a rev
A;Reference number: A25542; MUID:87040762
A;Accession: A25542
A;Molecule type: DNA; mRNA
A;Residues: 1-5,'K',7-269 <CLA>
A;Cross-references: GB:X04500; NID:g33788
A;Note: the mRNA sequence had codon AAG for 6-Lys, the DNA sequence had GAG for 6-Glu
R;Bensi, G.; Raugei, G.; Palla, E.; Carinci, V.; Buonamassa, D.T.; Melli, M.
Gene 52, 95-101, 1987
A;Title: Human interleukin-1 beta gene.
A;Reference number: A29019; MUID:87248099
A;Accession: A29019
A;Molecule type: DNA
A;Residues: 1-269 <BEN>
A;Cross-references: GB:M15840; NID:g186281; PIDN:AAA74137.1; PID:g386816
R;Auron, P.E.; Webb, A.C.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Dinare
Proc. Natl. Acad. Sci. U.S.A. 81, 7907-7911, 1984
A;Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
A;Reference number: A94023; MUID:85088517
A;Accession: A94023
A;Molecule type: mRNA
A;Residues: 1-5,'K',7-269 <AUR>
A;Cross-references: GB:K02770; NID:g186268; PIDN:AAA36106.1; PID:g307043
R;March, C.J.; Mosley, B.; Larsen, A.; Cerretti, D.P.; Braedt, G.; Price, V.; Gillis, S.
Nature 315, 641-647, 1985
A;Title: Cloning, sequence and expression of two distinct human interleukin-1 complement
A;Reference number: A93361; MUID:85240547
A;Accession: A93361
A;Molecule type: mRNA
A;Residues: 1-269 <MAR>
A;Cross-references: GB:X02532; NID:g33789; PIDN:CAA26372.1; PID:g33790
A;Note: parts of this sequence, including the amino end of the mature form, were confirm
R;Webb, A.C.; Dinarello, C.A.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Au
Adv. Gene Technol. 22, 339-340, 1985
A;Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
A;Reference number: I51852
A;Accession: I51852
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-5,'K',7-19,'H',21-110,'Q',112-176,'A',178-213,'P',215-269 <WEB>
A;Cross-references: GB:M54933; NID:g186287; PIDN:AAA59136.1; PID:g186288
R;Nishida, T.; Nishino, N.; Takano, M.; Kawai, K.; Bando, K.; Masui, Y.; Nakai, S.; Hira
Biochem. Biophys. Res. Commun. 143, 345-352, 1987
A;Title: cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell line.
A;Reference number: I52217; MUID:87156769
A;Accession: I65200
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-269 <NIS>
A;Cross-references: GB:M15330; NID:g186283; PIDN:AAA59135.1; PID:g307045
R;Kotenko, S.V.; Bulenkov, M.T.; Veiko, V.P.; Epishin, S.M.; Lomakin, I.B.; Emel'yanov,
ii, S.A.; Vinetskii, Y.P.
Dokl. Akad. Nauk SSSR 309, 1005-1008, 1989
A;Title: [Cloning of the cDNA coding for human prointerleukin-1 alpha and prointerleukin
A;Reference number: I38131; MUID:90249285
A;Accession: I38132
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-269 <KOT>
A;Cross-references: EMBL:X56087; NID:g35662; PIDN:CAA39567.1; PID:g35663
R;Zsebo, K.M.; Wypych, J.; Yuschenkoff, V.N.; Lu, H.; Hunt, P.; Dukes, P.P.; Langley, K.
Blood 71, 962-968, 1988
A;Title: Effects of hematopoietin-1 and interleukin 1 activities on early hematopoietic
A;Reference number: A90732; MUID:88184226
A;Accession: B27616
A;Molecule type: protein
A;Residues: 117-123,'X',125-126,'X',128 <ZSE>
R;Stevenson, F.T.; Bursten, S.L.; Fanton, C.; Locksley, R.M.; Lovett, D.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 7245-7249, 1993
A;Title: The 31-kDa precursor of interleukin lalpha is myristoylated on specific lysines
A;Reference number: A48293; MUID:93348250
A;Contents: annotation; myristylation of lysines
R;Nanduri, V.B.; Hulmes, J.D.; Pan, Y.C.E.; Kilian, P.L.; Stern, A.S.
Biochim. Biophys. Acta 1118, 25-35, 1991
A;Title: The role of arginine residues in interleukin 1 receptor binding.
A;Reference number: S19608; MUID:92110334
A;Contents: annotation; type 1 IL-1 receptor interaction site
A;Note: modification of Arg-120 by phenylglyoxal blocks receptor binding
R;Clore, G.M.; Gronenborn, A.M.
submitted to the Brookhaven Protein Data Bank, January 1991
A;Reference number: A50049; PDB:6I1B
A;Contents: annotation; conformation by (13)C- and (1)H-NMR, residues 117-269
R;Clore, G.M.; Wingfield, P.T.; Gronenborn, A.M.
Biochemistry 30, 2315-2323, 1991
A;Title: High-resolution three-dimensional structure of interleukin 1beta in solution
A;Reference number: A44675; MUID:91159409
A;Contents: annotation; (1)H-NMR structural determination
R;Hazuda, D.J.; Strickler, J.; Simon, P.; Young, P.R.
J. Biol. Chem. 266, 7081-7086, 1991
A;Title: Structure-function mapping of interleukin 1 precursors. Cleavage leads to a
A;Reference number: A39774; MUID:91201363
A;Contents: annotation
R;Finzel, B.C.; Watenpaugh, K.D.; Einspahr, H.M.
submitted to the Brookhaven Protein Data Bank, December 1989
A;Reference number: A50016; PDB:1I1B
A;Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 119-269
R;Finzel, B.C.; Clancy, L.L.; Holland, D.R.; Muchmore, S.W.; Watenpaugh, K.D.; Einspa
J. Mol. Biol. 209, 779-791, 1989
A;Title: Crystal structure of recombinant human interleukin-1beta at 2.0 angstrom res
A;Reference number: A44666; MUID:90064532
A;Contents: annotation; X-ray crystallography, 2.0 angstroms
C;Comment: This protein lacks a conventional signal sequence for protein export. Clea
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin
C;Genetics:
A;Gene: GDB:IL1B
A;Cross-references: GDB:120094; OMIM:147720
A;Map position: 2q13-2q21
A;Introns: 16/2; 33/3; 101/1; 156/1; 199/3
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrop
F;117-269/Product: interleukin-1 beta #status experimental <IL1>
F;76/Binding site: myristate (Lys) (covalent) (partial) #status experimental
F;123/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 22.9%; Score 85; DB 1; Length 269;
Best Local Similarity 33.3%; Pred. No. 0.012;
Matches 21; Conservative 8; Mismatches 32; Indels 2; Gaps 1;

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Qy       8 YNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLT 67
          | : :  | |:|   :      |||  || |:|: |     |: |    |  : |||  |
Db     206 YPKKKMEKRFVFNKIEINNKLEFESAQFPNWYISTSQAENMPVFLGGTKGGQDITDF--T 263

Qy      68 MLF 70
           | |
Db     264 MQF 266
```

RESULT 12
JC5646
interleukin-1 beta - horse
C;Species: Equus caballus (domestic horse)
C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 20-Jun-2000
C;Accession: JC5646
R;Kato, H.; Youn, H.Y.; Ohashi, T.; Watari, T.; Goitsuka, R.; Tsujimoto, H.; Hasegawa
Gene 177, 11-16, 1996
A;Title: Identification of an alternatively spliced transcript of equine interleukin-
A;Reference number: JC5646; MUID:97080493
A;Accession: JC5646
A;Molecule type: mRNA
A;Residues: 1-214 <KAT>
A;Cross-references: DDBJ:D42165; NID:g2463549; PIDN:BAA22528.1; PID:g2463550

C;Comment: This protein mediates a variety of physiological response to infections and i
synthesis by hepatocytes, and stimulation of chondrocytes and synovial cells to produce
C;Superfamily: interleukin-1

Query Match 21.8%; Score 81; DB 2; Length 214;
Best Local Similarity 31.6%; Pred. No. 0.029;
Matches 18; Conservative 9; Mismatches 30; Indels 0; Gaps 0;

```
Qy       8 YNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDF 64
           | : :  | |:|   :   |  |||  :| |:|: |     |: |    |  : |||
Db     151 YPKRKMEKRFVFNKMEIKGNVEFESAMYPNWYISTSQAEKSPVFLGNTRGGRDITDF 207
```

RESULT 13
A30584
interleukin-1 beta precursor - rabbit
N;Alternate names: hematopoietin-1; IL-1 beta; lymphocyte proliferation potentiating fac
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 25-May-1989 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999
C;Accession: A27714; A30584; JU0082; A32166
R;Mori, S.; Goto, F.; Goto, K.; Ohkawara, S.; Maeda, S.; Shimada, K.; Yoshinaga, M.
Biochem. Biophys. Res. Commun. 150, 1237-1243, 1988
A;Title: Cloning and sequence analysis of a cDNA for lymphocyte proliferation potentiati
A;Reference number: A27714; MUID:88134238
A;Accession: A27714
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-268 <MOR>
R;Cannon, J.G.; Clark, B.D.; Wingfield, P.; Schmeissner, U.; Losberger, C.; Dinarello, C
J. Immunol. 142, 2299-2306, 1989
A;Title: Rabbit IL-1. Cloning, expression, biologic properties, and transcription during
A;Reference number: A30584; MUID:89176242
A;Accession: A30584
A;Molecule type: mRNA
A;Residues: 1-268 <CAN>
A;Cross-references: GB:M26295; NID:g516632; PIDN:AAA31373.1; PID:g516633
R;Young, P.R.; Sylvester, D.
Protein Eng. 2, 545-551, 1989
A;Title: Cloning of rabbit interleukin-1 beta: differential evolution of IL-1 alpha and
A;Reference number: A94230; MUID:89315718
A;Accession: JU0082
A;Molecule type: mRNA
A;Residues: 1-268 <YOU>
C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavag
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;117-268/Product: interleukin-1 beta #status predicted <ILB>

Query Match 19.9%; Score 74; DB 1; Length 268;
Best Local Similarity 28.8%; Pred. No. 0.26;
Matches 17; Conservative 9; Mismatches 33; Indels 0; Gaps 0;

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Qy       8 YNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGL 66
           | : :  | |:|   :      |||  || |:|: |     |: |    |  :  || :
Db     205 YPKKKMEKRFVFNKIEIKDKLEFESAQFPNWYISTSQTEYMPVFLGNNSGGQDLIDFSM 263
```

RESULT 14
I55969
interleukin-1 beta precursor - mouse
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999
C;Accession: I55969; A24719; S13029
R;Gray, P.W.; Glaister, D.; Chen, E.; Goeddel, D.V.; Pennica, D.
J. Immunol. 137, 3644-3648, 1986
A;Title: Two interleukin 1 genes in the mouse: Cloning and expression of the cDNA for mu
A;Reference number: I55969; MUID:87058957
A;Accession: I55969
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-269 <RES>
A;Cross-references: GB:M15131; NID:g198293; PIDN:AAA39276.1; PID:g309398
R;Telford, J.L.; Macchia, G.; Massone, A.; Carinci, V.; Palla, E.; Melli, M.
Nucleic Acids Res. 14, 9955-9963, 1986
A;Title: The murine interleukin 1-beta gene: structure and evolution.
A;Reference number: A24719; MUID:87117546
A;Accession: A24719
A;Molecule type: mRNA
A;Residues: 1-269 <TEL>
A;Cross-references: GB:X04964; NID:g52666; PIDN:CAA28637.1; PID:g52667
R;Daumy, G.O.; Wilder, C.L.; Merenda, J.M.; McColl, A.S.; Geoghegan, K.F.; Otterness,
FEBS Lett. 278, 98-102, 1991
A;Title: Reduction of biological activity of murine recombinant interleukin-1beta by
A;Reference number: S13029; MUID:91130610
A;Accession: S13029
A;Status: preliminary
A;Molecule type: protein
A;Residues: 118-269 <DAU>
C;Comment: This protein lacks a conventional signal sequence for protein export. Clea
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin
C;Genetics:
A;Gene: IL-1-beta
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;118-269/Product: interleukin-1 beta #status experimental <IL1>

Query Match 17.7%; Score 65.5; DB 1; Length 269;
Best Local Similarity 29.8%; Pred. No. 2.9;
Matches 17; Conservative 9; Mismatches 30; Indels 1; Gaps 1;

```
Qy       8 YNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDF 64
           | : :  | |:|   :      |||  || |:|: |     |: |    |: : ||
Db     207 YPKKKMEKRFVFNKIEVKSKVEFESAEFPNWYISTSQAEHKPVFLGNNSGQ-DIIDF 262
```

RESULT 15
S56653
thioglucosidase (EC 3.2.3.1) 1 - Arabidopsis thaliana
N;Alternate names: myrosinase 1
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 22-Jun-1999
C;Accession: S56653
R;Xue, J.; Jorgensen, M.; Pihlgren, U.; Rask, L.
Plant Mol. Biol. 27, 911-922, 1995
A;Title: The myrosinase gene family in Arabidopsis thaliana: gene organization, expre
A;Reference number: S56653; MUID:95284348
A;Accession: S56653
A;Molecule type: DNA
A;Residues: 1-541 <XUE>
A;Cross-references: EMBL:X79194; NID:g871989; PIDN:CAA55786.1; PID:g871990
C;Genetics:
A;Gene: TGG1
A;Introns: 57/3; 78/1; 98/3; 124/1; 179/2; 264/3; 303/2; 377/1; 388/3; 422/1; 456/2
C;Superfamily: Agrobacterium beta-glucosidase
C;Keywords: glycosidase; hydrolase

Query Match 17.4%; Score 64.5; DB 2; Length 541;
Best Local Similarity 35.0%; Pred. No. 8.5;
Matches 14; Conservative 10; Mismatches 15; Indels 1; Gaps 1;

```
Qy      19 FYHSQSGRNSTFES-VAFPGWFIAVSSEGGCPLILTQELG 57
           | |||  :::|  : : | |||:   :||  | |: : :|
Db     283 FDHSQESKDATERAKIFFHGWFMGPLTEGKYPDIMREYVG 322
```

Search completed: June 20, 2002, 15:03:51
Job time: 161 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 20, 2002, 15:03:55 ; Search time 19.43 Seconds
(without alignments)
139.494 Million cell updates/sec

Title: US-09-763-498-6
Perfect score: 371
Sequence: 1 EKDIMDLYNQPEPVKSFLFY.....ILTQELGKANTTDFGLTMLF 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	107	28.8	177	1	IL1X_HORSE	O18999 equus cabal
2	107	28.8	177	1	IL1X_RABIT	P26890 oryctolagus
3	107	28.8	178	1	IL1X_RAT	P25086 rattus norv
4	105	28.3	178	1	IL1X_MOUSE	P25085 mus musculu
5	102	27.5	177	1	IL1X_PIG	Q29056 sus scrofa
6	101	27.2	177	1	IL1X_HUMAN	P18510 homo sapien
7	96	25.9	267	1	IL1B_PIG	P26889 sus scrofa
8	95	25.6	174	1	IL1X_BOVIN	O77482 bos taurus
9	89	24.0	266	1	IL1B_SHEEP	P21621 ovis aries
10	88	23.7	266	1	IL1B_CAPHI	P79162 capra hircu
11	87	23.5	266	1	IL1B_CEREL	P51745 cervus elap
12	86	23.2	267	1	IL1B_FELCA	P41687 felis silve
13	85	22.9	268	1	IL1B_MACFA	P79182 macaca fasc
14	85	22.9	269	1	IL1B_HUMAN	P01584 homo sapien
15	85	22.9	269	1	IL1B_MACMU	P48090 macaca mula
16	85	22.9	269	1	IL1B_MACNE	P51493 macaca neme
17	82	22.1	266	1	IL1B_BOVIN	P09428 bos taurus
18	81	21.8	268	1	IL1B_HORSE	Q28386 equus cabal
19	77.5	20.9	269	1	IL1B_TRIVU	Q9xs77 trichosurus
20	77	20.8	269	1	IL1B_CERTO	P46648 cercocebus
21	74	19.9	268	1	IL1B_RABIT	P14628 oryctolagus
22	71.5	19.3	266	1	IL1B_CAVPO	Q9wvg1 cavia porce
23	66.5	17.9	268	1	IL1B_RAT	Q63264 rattus norv
24	65.5	17.7	269	1	IL1B_MOUSE	P10749 mus musculu
25	65.5	17.7	270	1	IL1A_FELCA	O46613 felis silve
26	64.5	17.4	541	1	MYRO_ARATH	P37702 arabidopsis
27	62.5	16.8	268	1	IL1A_BOVIN	P08831 bos taurus
28	62.5	16.8	268	1	IL1A_CAPHI	P79161 capra hircu
29	62.5	16.8	268	1	IL1A_SHEEP	Q28579 ovis aries
30	62.5	16.8	270	1	IL1A_HORSE	Q28385 equus cabal
31	62.5	16.8	270	1	IL1A_PIG	P18430 sus scrofa
32	61.5	16.6	325	1	RIR2_MYCLE	Q9cbq2 mycobacteri
33	60.5	16.3	265	1	IL1A_CANFA	O46612 canis famil
34	60.5	16.3	872	1	MGR2_HUMAN	Q14416 homo sapien
35	60	16.2	444	1	KRAC_DICDI	P54644 dictyosteli
36	59.5	16.0	634	1	YGJI_CAEEL	Q9xub9 caenorhabdi
37	58.5	15.8	271	1	IL1A_HUMAN	P01583 homo sapien
38	58	15.6	267	1	IL1A_RABIT	P04822 oryctolagus
39	58	15.6	453	1	PSNH_ARATH	O64668 arabidopsis
40	57.5	15.5	271	1	IL1A_MACFA	P79340 macaca fasc
41	57.5	15.5	413	1	ARCA_CLOPE	Q46254 clostridium
42	57	15.4	271	1	IL1A_MACMU	P48089 macaca mula
43	57	15.4	605	1	VE1_HPV09	Q05111 human papil
44	56	15.1	419	1	VS48_TBRVC	P22048 tomato blac
45	56	15.1	459	1	CBIA_SALTY	P29946 salmonella

ALIGNMENTS

RESULT 1
IL1X_HORSE
ID IL1X_HORSE STANDARD; PRT; 177 AA.
AC O18999; O77745;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE (IRAP).
GN IL1RN OR IL1RA.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97366446; PubMed=9223227;
RA Kato H., Ohashi T., Matsushiro H., Watari T., Goitsuka R.,
RA Tsujimoto H., Hasegawa A.;
RT "Molecular cloning and functional expression of equine interleukin-1
RT receptor antagonist.";
RL Vet. Immunol. Immunopathol. 56:221-231(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98285942; PubMed=9622739;
RA Howard R.D., McIlwraith C.W., Trotter G.W., Nyborg J.K.;
RT "Cloning of equine interleukin-1 receptor antagonist and
RT determination of its full-length cDNA sequence.";
RL Am. J. Vet. Res. 59:712-716(1998).
CC -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC ---

CC ---
DR EMBL; D83714; BAA22529.1; -.
DR EMBL; U92482; AAC39257.1; -.
DR HSSP; P18510; 1ILR.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR PRINTS; PR00264; INTERLEUKIN1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 25 BY SIMILARITY.
FT CHAIN 26 177 INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT PROTEIN.
FT DISULFID 91 141 BY SIMILARITY.
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT   CONFLICT     19     19       F -> L (IN REF. 2).
SQ   SEQUENCE   177 AA;  20459 MW;  1ABC377F1F1CF80B CRC64;


  Query Match             28.8%;  Score 107;  DB 1;  Length 177;
  Best Local Similarity   41.5%;  Pred. No. 2.9e-06;
  Matches   22;  Conservative    7;  Mismatches   24;  Indels    0;  Gaps    0;

Qy       3 DIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQE 55
           :| ||    |  | | |  | ||  ::||| | ||||:  : |   |: || :
Db     109 NITDLSKNKEENKRFTFIRSNSGPTTSFESAACPGWFLCTAQEADRPVSLTNK 161


RESULT   2
IL1X_RABIT
ID   IL1X_RABIT     STANDARD;      PRT;   177 AA.
AC   P26890;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE   (IRAP).
GN   IL1RN OR IL1RA.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94165101; PubMed=7509813;
RA   Cominelli F., Bortolami M., Pizarro T.T., Monsacchi L., Ferretti M.,
RA   Brewer M.T., Eisenberg S.P., Ng R.K.;
RT   "Rabbit interleukin-1 receptor antagonist. Cloning, expression,
RT   functional characterization, and regulation during intestinal
RT   inflammation.";
RL   J. Biol. Chem. 269:6962-6971(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Hamada H., Mulligan R.C.;
RL   Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93052512; PubMed=1427977;
RA   Goto F., Goto K., Miyata T., Ohkawara S., Takao T., Mori S.,
RA   Furukawa S., Maeda T., Iwanaga S., Shimonishi Y., Yoshinaga M.;
RT   "Interleukin-1 receptor antagonist in inflammatory exudate cells of
RT   rabbits. Production, purification and determination of primary
RT   structure.";
RL   Immunology 77:235-244(1992).
CC   -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC       RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S68977; AAB30093.1; -.
DR   EMBL; M57526; AAA31374.1; -.
DR   EMBL; D21832; BAA04860.1; -.
DR   PIR; A54377; A54377.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Glycoprotein; Signal.
FT   SIGNAL       1     25       BY SIMILARITY.
FT   CHAIN       26    177       INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT                               PROTEIN.
FT   DISULFID     91    141       BY SIMILARITY.
FT   CARBOHYD    109    109       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   177 AA;  20214 MW;  F5BC087F097FFEAF CRC64;


  Query Match             28.8%;  Score 107;  DB 1;  Length 177;
  Best Local Similarity   41.0%;  Pred. No. 2.9e-06;
  Matches   25;  Conservative    6;  Mismatches   24;  Indels    6;  Gaps    1;

Qy       3 DIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTT 62
           :| ||    |  | | |  | ||  :|||| : ||||:  : |   |: ||      ||
Db     109 NITDLGKNKEQDKRFTFIRSNSGPTTTFESASCPGWFLCTALEADQPVSLT------NTP 162

Qy      63 D 63
           |
Db     163 D 163


RESULT   3
IL1X_RAT
ID   IL1X_RAT       STANDARD;      PRT;   178 AA.
AC   P25086;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE   (IRAP).
GN   IL1RN OR IL-1RA.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91271363; PubMed=1828896;
RA   Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
RA   Brandhuber B.J., Thompson R.C.;
RT   "Interleukin 1 receptor antagonist is a member of the interleukin 1
RT   gene family: evolution of a cytokine control mechanism.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
CC   -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC       RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M63101; AAA41434.1; -.
DR   PIR; C40956; C40956.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Glycoprotein; Signal.
FT   SIGNAL       1     26       BY SIMILARITY.
FT   CHAIN       27    178       INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT                               PROTEIN.
FT   DISULFID     92    142       BY SIMILARITY.
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   178 AA;  20282 MW;  F3A5754FB6C51B03 CRC64;
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  Query Match             28.8%;  Score 107;  DB 1;  Length 178;
  Best Local Similarity   41.5%;  Pred. No. 2.9e-06;
  Matches   22;  Conservative    9;  Mismatches   22;  Indels    0;  Gaps    0;

Qy       1 EKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILT 53
           | :| ||    |  | | |  |::|  ::|||:| ||||:  : |   |: ||
Db     108 EVNITDLNKNKEEDKRFTFIRSETGPTTSFESLACPGWFLCTTLEADHPVSLT 160


RESULT   4
IL1X_MOUSE
ID   IL1X_MOUSE     STANDARD;      PRT;   178 AA.
AC   P25085; O70207;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE   (IRAP).
GN   IL1RN OR IL-1RA.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=91250712; PubMed=1828262;
RA   Zahedi K., Seldin M.F., Rits M., Ezekowitz R.A., Whitehead A.S.;
RT   "Mouse IL-1 receptor antagonist protein. Molecular characterization,
RT   gene mapping, and expression of mRNA in vitro and in vivo.";
RL   J. Immunol. 146:4228-4233(1991).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=91316273; PubMed=1830498;
RA   Matsushime H., Roussel M.F., Matsushima K., Hishinuma A., Sherr C.J.;
RT   "Cloning and expression of murine interleukin-1 receptor antagonist
RT   in macrophages stimulated by colony-stimulating factor 1.";
RL   Blood 78:616-623(1991).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   STRAIN=SWISS;
RX   MEDLINE=94271931; PubMed=8003626;
RA   Zahedi K.A., Uhlar C.M., Rits M., Prada A.E., Whitehead A.S.;
RT   "The mouse interleukin 1 receptor antagonist protein: gene structure
RT   and regulation in vitro.";
RL   Cytokine 6:1-9(1994).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   STRAIN=FVBXDBA/1 LACJ;
RX   MEDLINE=98209757; PubMed=9550387;
RA   Gabay C., Porter B., Fantuzzi G., Arend W.P.;
RT   "Mouse IL-1 receptor antagonist isoforms: complementary DNA cloning
RT   and protein expression of intracellular isoform and tissue
RT   distribution of secreted and intracellular IL-1 receptor antagonist in
RT   vivo.";
RL   J. Immunol. 159:5905-5913(1997).
RN   [5]
RP   SEQUENCE OF 7-178 FROM N.A.
RX   MEDLINE=91271363; PubMed=1828896;
RA   Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
RA   Brandhuber B.J., Thompson R.C.;
RT   "Interleukin 1 receptor antagonist is a member of the interleukin 1
RT   gene family: evolution of a cytokine control mechanism.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
RN   [6]
RP   SEQUENCE OF 23-178 FROM N.A.
RX   MEDLINE=92037824; PubMed=1834470;
RA   Shuck M.E., Eessalu T.E., Tracey D.E., Bienkowski M.J.;
RT   "Cloning, heterologous expression and characterization of murine
RT   interleukin 1 receptor antagonist protein.";
RL   Eur. J. Immunol. 21:2775-2780(1991).
CC   -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC       RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC   -!- SUBCELLULAR LOCATION: SECRETED (ISOFORM 1) OR INTRACELLULAR
CC       (ISOFORM 2).
CC   -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC       produced by alternative splicing.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M74294; AAA39309.1; -.
DR   EMBL; M64404; AAA39277.1; -.
DR   EMBL; L32838; AAA20576.1; -.
DR   EMBL; AF001795; AAC15251.1; -.
DR   EMBL; M57525; AAA39278.1; -.
DR   EMBL; M63100; AAA39310.1; -.
DR   EMBL; S64082; AAB20265.1; -.
DR   PIR; B40956; B40956.
DR   PIR; A44610; A44610.
DR   HSSP; P18510; 1IRA.
DR   MGD; MGI:96547; Il1rn.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Glycoprotein; Signal; Alternative splicing.
FT   SIGNAL        1     26       BY SIMILARITY.
FT   CHAIN        27    178       INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT                                PROTEIN.
FT   DISULFID     92    142       BY SIMILARITY.
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC      1     21       MEICWGPYSHLISLLLILLFH -> MA (IN ISOFORM
FT                                2).
SQ   SEQUENCE   178 AA;  20274 MW;  84AA002A3119C024 CRC64;


  Query Match             28.3%;  Score 105;  DB 1;  Length 178;
  Best Local Similarity   41.5%;  Pred. No. 5.2e-06;
  Matches   22;  Conservative    7;  Mismatches   24;  Indels    0;  Gaps    0;

Qy       1 EKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILT 53
           | :| ||    |  | | |  |: |  ::||| | ||||:  : |   |: ||
Db     108 EVNITDLSKNKEEDKRFTFIRSEKGPTTSFESAACPGWFLCTTLEADRPVSLT 160


RESULT   5
IL1X_PIG
ID   IL1X_PIG       STANDARD;      PRT;   177 AA.
AC   Q29056;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE   (IRAP).
GN   IL1RN OR IRAP1.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CROSSBREED; TISSUE=Lung;
RA   Yin J., Murtaugh M.P.;
RT   "Characterization of IRAP in morphine treated pig.";
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC       RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
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CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L38849; AAA99424.1; -.
DR   HSSP; P18510; 1IRA.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Glycoprotein; Signal.
FT   SIGNAL        1     25       BY SIMILARITY.
FT   CHAIN        26    177       INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT                                PROTEIN.
FT   DISULFID     91    141       BY SIMILARITY.
FT   CARBOHYD    109    109       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   177 AA;  20093 MW;  2114DC6119A9D5F9 CRC64;


  Query Match             27.5%;  Score 102;  DB 1;  Length 177;
  Best Local Similarity   43.1%;  Pred. No. 1.2e-05;
  Matches   22;  Conservative    6;  Mismatches   23;  Indels    0;  Gaps    0;

Qy       3 DIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILT 53
           :| ||    |  | | |  | ||  ::||| | ||||:  : |   |: ||
Db     109 NITDLRKNSEQDKRFTFIRSDSGPTTSFESAACPGWFLCTALEADQPVGLT 159


RESULT   6
IL1X_HUMAN
ID   IL1X_HUMAN     STANDARD;      PRT;   177 AA.
AC   P18510; Q14628; Q9UPC0;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Interleukin-1 receptor antagonist protein precursor (IL-1RA) (ICIL-
DE   1RA) (IRAP) (IL-1RN).
GN   IL1RN OR IL1RA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=90220867; PubMed=2139180;
RA   Carter D.B., Deibel M.R. Jr., Dunn C.J., Tomich C.S.C., Laborde A.L.,
RA   Slightom J.L., Berger A.E., Bienkowski M.J., Sun F.F., McEwan R.N.,
RA   Harris P.K.W., Yem A.W., Waszak G.A., Chosay J.G., Sieu L.C.,
RA   Hardee M.M., Zurcher-Neely H.A., Reardon I.M., Heinrikson R.L.,
RA   Truesdell S.E., Shelly J.A., Eessalu T.E., Taylor B.M., Tracey D.E.;
RT   "Purification, cloning, expression and biological characterization of
RT   an interleukin-1 receptor antagonist protein.";
RL   Nature 344:633-638(1990).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=90136921; PubMed=2137201;
RA   Eisenberg S.P., Evans R.J., Arend W.P., Verderber E., Brewer M.T.,
RA   Hannum C.H., Thompson R.C.;
RT   "Primary structure and functional expression from complementary DNA
RT   of a human interleukin-1 receptor antagonist.";
RL   Nature 343:341-346(1990).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=91271363; PubMed=1828896;
RA   Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
RA   Brandhuber B.J., Thompson R.C.;
RT   "Interleukin 1 receptor antagonist is a member of the interleukin 1
RT   gene family: evolution of a cytokine control mechanism.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=92338323; PubMed=1385987;
RA   Lennard A., Gorman P., Carrier M., Griffiths S., Scotney H.,
RA   Sheer D., Solari R.;
RT   "Cloning and chromosome mapping of the human interleukin-1 receptor
RT   antagonist gene.";
RL   Cytokine 4:83-89(1992).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
RX   MEDLINE=97146044; PubMed=8992991;
RA   Jenkins J.K., Drong R.F., Shuck M.E., Bienkowski M.J., Slightom J.L.,
RA   Arend W.P., Smith M.F. Jr.;
RT   "Intracellular IL-1 receptor antagonist promoter: cell type-specific
RT   and inducible regulatory regions.";
RL   J. Immunol. 158:748-755(1997).
RN   [6]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RX   MEDLINE=91219436; PubMed=1827201;
RA   Haskill S., Martin G., van Le L., Morris J., Peace A., Bigler C.F.,
RA   Jaffe G.J., Hammerberg C., Sporn S.A., Fong S., Arend W.P., Ralph P.;
RT   "cDNA cloning of an intracellular form of the human interleukin 1
RT   receptor antagonist associated with epithelium.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:3681-3685(1991).
RN   [7]
RP   SEQUENCE FROM N.A. (ISOFORM 3).
RX   MEDLINE=95355865; PubMed=7629520;
RA   Muzio M., Polentarutti N., Sironi M., Poli G., De Gioia L.,
RA   Introna M., Mantovani A., Colotta F.;
RT   "Cloning and characterization of a new isoform of the interleukin 1
RT   receptor antagonist.";
RL   J. Exp. Med. 182:623-628(1995).
RN   [8]
RP   SEQUENCE OF 26-45.
RX   MEDLINE=90136920; PubMed=2137200;
RA   Hannum C.H., Wilcox C.J., Arend W.P., Joslin F.G., Dripps D.J.,
RA   Heimdal P.L., Armes L.G., Sommer A., Eisenberg S.P., Thompson R.C.;
RT   "Interleukin-1 receptor antagonist activity of a human interleukin-1
RT   inhibitor.";
RL   Nature 343:336-340(1990).
RN   [9]
RP   SEQUENCE OF 26-52.
RX   MEDLINE=90354444; PubMed=2143761;
RA   Bienkowski M.J., Eessalu T.E., Berger A.E., Truesdell S.E.,
RA   Shelly J.A., Laborde A.L., Zurcher-Neely H.A., Reardon I.M.,
RA   Heinrikson R.L., Chosay J.G., Tracey D.E.;
RT   "Purification and characterization of interleukin 1 receptor level
RT   antagonist proteins from THP-1 cells.";
RL   J. Biol. Chem. 265:14505-14511(1990).
RN   [10]
RP   SEQUENCE OF 35-177 FROM N.A. (ISOFORM 4).
RX   MEDLINE=98183404; PubMed=9514884;
RA   Weissbach L., Tran K., Colquhoun S.A., Champliaud M.F., Towle C.A.;
RT   "Detection of an interleukin-1 intracellular receptor antagonist mRNA
RT   variant.";
RL   Biochem. Biophys. Res. Commun. 244:91-95(1998).
RN   [11]
RP   STRUCTURE BY NMR.
RX   MEDLINE=92297633; PubMed=1534997;
RA   Stockman B.J., Scahill T.A., Roy M., Ulrich E.L., Strakalaitis N.A.,
RA   Brunner D.P., Yem A.W., Deibel M.R. Jr.;
RT   "Secondary structure and topology of interleukin-1 receptor
RT   antagonist protein determined by heteronuclear three-dimensional NMR
RT   spectroscopy.";
RL   Biochemistry 31:5237-5244(1992).
RN   [12]
RP   STRUCTURE BY NMR.
RX   MEDLINE=94320651; PubMed=8045306;
RA   Stockman B.J., Scahill T.A., Strakalaitis N.A., Brunner D.P.,
RA   Yem A.W., Deibel M.R. Jr.;
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RT   "Solution structure of human interleukin-1 receptor antagonist
RT   protein.";
RL   FEBS Lett. 349:79-83(1994).
RN   [13]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=94230368; PubMed=8175703;
RA   Vigers G.P.A., Caffes P., Evans R.J., Thompson R.C., Eisenberg S.P.,
RA   Brandhuber B.J.;
RT   "X-ray structure of interleukin-1 receptor antagonist at 2.0-A
RT   resolution.";
RL   J. Biol. Chem. 269:12874-12879(1994).
RN   [14]
RP   X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX   MEDLINE=95172072; PubMed=7867645;
RA   Schreuder H.A., Rondeau J.-M., Tardif C., Soffientini A., Sarubbi E.,
RA   Akeson A., Bowlin T.L., Yanofsky S., Barrett R.W.;
RT   "Refined crystal structure of the interleukin-1 receptor antagonist.
RT   Presence of a disulfide link and a cis-proline.";
RL   Eur. J. Biochem. 227:838-847(1995).
RN   [15]
RP   X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 32-177 IN COMPLEX WITH IL1R.
RX   MEDLINE=97215904; PubMed=9062194;
RA   Schreuder H., Tardif C., Trump-Kallmeyer S., Soffientini A.,
RA   Sarubbi E., Akeson A., Bowlin T., Yanofsky S., Barrett R.W.;
RT   "A new cytokine-receptor binding mode revealed by the crystal
RT   structure of the IL-1 receptor with an antagonist.";
RL   Nature 386:194-200(1997).
CC   -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC       RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC   -!- SUBCELLULAR LOCATION: SECRETED (ISOFORM 1) OR INTRACELLULAR
CC       (ISOFORMS 2, 3 AND 4).
CC   -!- ALTERNATIVE PRODUCTS: 4 isoforms; 1 (shown here), 2/icIL-1ra,
CC       3/icIL-1ra type II and 4; are produced by alternative splicing.
CC   -!- TISSUE SPECIFICITY: THE INTRACELLULAR FORM OF IL-1RA IS
CC       PREDOMINANTLY EXPRESSED IN EPITHELIAL CELLS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   -!- DATABASE: NAME=R&D Systems' cytokine source book: IL1RN;
CC       WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=205".
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M55646; AAA59138.1; -.
DR   EMBL; M63099; AAB41943.1; -.
DR   EMBL; X52015; CAA36262.1; -.
DR   EMBL; X53296; CAA37386.1; -.
DR   EMBL; X64532; CAA45832.1; -.
DR   EMBL; U65590; AAB92268.1; -.
DR   EMBL; U65590; AAB92270.1; -.
DR   EMBL; X84348; CAA59087.1; -.
DR   EMBL; U65590; AAB92269.1; -.
DR   EMBL; AF043143; AAC39672.1; -.
DR   PIR; A30368; A30368.
DR   PIR; A37822; A37822.
DR   PIR; S08160; S08160.
DR   PIR; S08159; S08159.
DR   PIR; A40956; A40956.
DR   PIR; A39386; A39386.
DR   PDB; 1ITN; 30-APR-94.
DR   PDB; 2IRT; 15-OCT-94.
DR   PDB; 1IRP; 27-FEB-95.
DR   PDB; 1ILR; 07-FEB-95.
DR   PDB; 1ILT; 01-APR-95.
DR   PDB; 1IRA; 17-JUN-98.
DR   Aarhus/Ghent-2DPAGE; 7104; IEF.
DR   Aarhus/Ghent-2DPAGE; 7105; IEF.
DR   MIM; 147679; -.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Glycoprotein; Signal; Alternative splicing; 3D-structure.
FT   SIGNAL       1     25
FT   CHAIN       26    177       INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT                               PROTEIN.
FT   DISULFID     91    141
FT   CARBOHYD    109    109       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC      1     21       MEICRGLRSHLITLLLFLFHS -> MAL (IN
FT                               ISOFORM 2).
FT   VARSPLIC      1     21       MEICRGLRSHLITLLLFLFHS -> MALADLYEEGGGGGGE
FT                               GEDNADSK (IN ISOFORM 3).
FT   VARSPLIC      1     34       MISSING (IN ISOFORM 4).
SQ   SEQUENCE   177 AA;  20055 MW;  D1690776A7394057 CRC64;


  Query Match             27.2%;  Score 101;  DB 1;  Length 177;
  Best Local Similarity   37.5%;  Pred. No. 1.6e-05;
  Matches   24;  Conservative    8;  Mismatches   26;  Indels    6;  Gaps    1;

Qy       3 DIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTT 62
           :| ||    :  | | |  | ||  ::||| | ||||:  : |   |: ||      |
Db     109 NITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWFLCTAMEADQPVSLT------NMP 162

Qy      63 DFGL 66
           | |:
Db     163 DEGV 166


RESULT   7
IL1B_PIG
ID   IL1B_PIG       STANDARD;      PRT;   267 AA.
AC   P26889;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Interleukin-1 beta precursor (IL-1 beta).
GN   IL1B.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93314975; PubMed=8325511;
RA   Huether M.J., Lin G., Smith D.M., Murtaugh M.P., Molitor T.W.;
RT   "Cloning, sequencing and regulation of an mRNA encoding porcine
RT   interleukin-1 beta.";
RL   Gene 129:285-289(1993).
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC   -!- SUBUNIT: MONOMER.
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   ------------------------------------------------------------------------
DR   EMBL; M86725; AAA02584.1; -.
DR   PIR; JN0724; JN0724.
DR   HSSP; P01584; 1HIB.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP        1    114       BY SIMILARITY.
FT   CHAIN       115    267       INTERLEUKIN-1 BETA.
SQ   SEQUENCE   267 AA;  30404 MW;  7F6B92B784D5086F CRC64;


  Query Match             25.9%;  Score 96;  DB 1;  Length 267;
  Best Local Similarity   30.6%;  Pred. No. 0.00011;
  Matches   19;  Conservative   13;  Mismatches   30;  Indels    0;  Gaps    0;

Qy       8 YNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLT 67
           | : :  | |:|| ::      |||  :| |:|: |     |: |    |: : ||| :
Db     204 YPKRDMEKRFVFYKTEIKNRVEFESALYPNWYISTSQAEQKPVFLGNSKGRQDITDFTME 263

Qy      68 ML 69
           :|
Db     264 VL 265


RESULT   8
IL1X_BOVIN
ID   IL1X_BOVIN     STANDARD;      PRT;   174 AA.
AC   O77482;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE   (IRAP).
GN   IL1RN.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98305607; PubMed=9643454;
RA   Kirisawa R., Fukuda T., Yamanaka H., Hagiwara K., Goto M., Obata Y.,
RA   Yoshino T., Iwai H.;
RT   "Enzymatic amplification and expression of bovine interleukin-1
RT   receptor antagonist cDNA.";
RL   Vet. Immunol. Immunopathol. 62:197-208(1998).
CC   -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC       RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; AB005148; BAA31854.1; -.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Glycoprotein; Signal.
FT   SIGNAL        1     23       BY SIMILARITY.
FT   CHAIN        24    174       INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT                                PROTEIN.
FT   DISULFID     89    139       BY SIMILARITY.
FT   CARBOHYD    107    107       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   174 AA;  19926 MW;  1E56E7F224FF851F CRC64;


  Query Match             25.6%;  Score 95;  DB 1;  Length 174;
  Best Local Similarity   41.2%;  Pred. No. 9.1e-05;
  Matches   21;  Conservative    6;  Mismatches   24;  Indels    0;  Gaps    0;

Qy       3 DIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILT 53
             :| ||    |  | | |    :|  ::||| | ||||:  | |   |: ||
Db     107 NITDLNQNREQDKRFAFIRFDNGPTTSFESAACPGWFLCTSLEADQPVGLT 157


RESULT   9
IL1B_SHEEP
ID   IL1B_SHEEP     STANDARD;      PRT;   266 AA.
AC   P21621;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Interleukin-1 beta precursor (IL-1 beta).
GN   IL1B.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92119335; PubMed=1840515;
RA   Seow H.F., Rothel J.S., David M.J., Wood P.R.;
RT   "Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.";
RL   DNA Seq. 1:423-426(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91088326; PubMed=2263490;
RA   Fiskerstrand C., Sargan D.;
RT   "Nucleotide sequence of ovine interleukin-1 beta.";
RL   Nucleic Acids Res. 18:7165-7165(1990).
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC   -!- SUBUNIT: MONOMER.
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ------------------------------------------------------------------------
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CC   ------------------------------------------------------------------------
DR   EMBL; X54796; CAA38566.1; -.
DR   EMBL; X56972; CAA40293.1; -.
DR   PIR; S13092; S13092.
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DR   PIR; S13810; S13810.
DR   PIR; S23010; S23010.
DR   HSSP; P01584; 5I1B.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP          1    113
FT   CHAIN         114    266       INTERLEUKIN-1 BETA.
FT   CONFLICT       14     14       Y -> C (IN REF. 2).
FT   CONFLICT       55     55       Q -> K (IN REF. 2).
FT   CONFLICT       64     64       V -> A (IN REF. 2).
FT   CONFLICT      145    145       P -> L (IN REF. 2).
SQ   SEQUENCE   266 AA;  30717 MW;  BDED07B58224AB78 CRC64;


  Query Match             24.0%;  Score 89;  DB 1;  Length 266;
  Best Local Similarity   31.7%;  Pred. No. 0.00085;
  Matches   20;  Conservative   12;  Mismatches   31;  Indels    0;  Gaps    0;

Qy       7 LYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGL 66
           :| :    | |:|| ::      |||| :| |:|: |     |: | :  |  : ||| :
Db     202 VYPKRNMEKRFVFYKTEIKNTVEFESVLYPNWYISTSQIEEKPVFLGRFRGGQDITDFRM 261

Qy      67 TML 69
             |
Db     262 ETL 264


RESULT  10
IL1B_CAPHI
ID   IL1B_CAPHI     STANDARD;      PRT;   266 AA.
AC   P79162;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Interleukin-1 beta precursor (IL-1 beta).
GN   IL1B.
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Capra.
OX   NCBI_TaxID=9925;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Takakura H., Hashimoto O., Mori Y., Tatsumi M.;
RT   "Molecular cloning and expression of caprine IL-1alpha and
RT   IL-1beta.";
RL   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS
CC       (BY SIMILARITY).
CC   -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D63351; BAA09675.1; -.
DR   HSSP; P01584; 1HIB.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP          1    113       BY SIMILARITY.
FT   CHAIN         114    266       INTERLEUKIN-1 BETA.
SQ   SEQUENCE   266 AA;  30769 MW;  59F7B39BD1D4DDA5 CRC64;


  Query Match             23.7%;  Score 88;  DB 1;  Length 266;
  Best Local Similarity   31.7%;  Pred. No. 0.0011;
  Matches   20;  Conservative   11;  Mismatches   32;  Indels    0;  Gaps    0;

Qy       7 LYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGL 66
           :| :    | |:|| ::      |||| :| |:|: |     |: |    |  : ||| :
Db     202 VYPKRNMEKRFVFYKTEIKNTVEFESVLYPNWYISTSQIEEKPVFLGHFRGGQDITDFRM 261

Qy      67 TML 69
             |
Db     262 ETL 264


RESULT  11
IL1B_CEREL
ID   IL1B_CEREL     STANDARD;      PRT;   266 AA.
AC   P51745;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Interleukin-1 beta precursor (IL-1 beta).
GN   IL1B.
OS   Cervus elaphus (Red deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Cervinae; Cervus.
OX   NCBI_TaxID=9860;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lockhart E.A.;
RL   Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION AND PROLIFERATION, AND FIBROBLAST GROWTH FACTOR
CC       ACTIVITY. IL-1S ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS
CC       (BY SIMILARITY).
CC   -!- SUBUNIT: MONOMER (By similarity).
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U20500; AAA62234.1; -.
DR   HSSP; P01584; 1HIB.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP        1    113       BY SIMILARITY.
FT   CHAIN       114    266       INTERLEUKIN-1 BETA.
SQ   SEQUENCE   266 AA;  30629 MW;  4F40B4E6F0D9F060 CRC64;


  Query Match             23.5%;  Score 87;  DB 1;  Length 266;
  Best Local Similarity   31.7%;  Pred. No. 0.0015;
  Matches   20;  Conservative   11;  Mismatches   32;  Indels    0;  Gaps    0;

Qy       7 LYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGL 66
           :| :    | |:|| ::      |||| :| |:|: |     |: |    |  : ||| :
Db     202 VYPKRNMEKRFVFYKTEIKDTVEFESVLYPNWYISTSHPEEKPVFLGHFRGGQDITDFRM 261

Qy      67 TML 69
             |
Db     262 ETL 264


RESULT  12
IL1B_FELCA
ID   IL1B_FELCA     STANDARD;      PRT;   267 AA.
AC   P41687;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Interleukin-1 beta precursor (IL-1 beta).
GN   IL1B.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow;
RA   Daniel S.L., Brenner C.A., Legendre A.M., Soloman A., Rouse B.T.;
RL   Submitted (XXX-1993) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC   -!- SUBUNIT: MONOMER.
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M92060; AAA30814.1; -.
DR   HSSP; P01584; 1HIB.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP        1    115       BY SIMILARITY.
FT   CHAIN       116    267       INTERLEUKIN-1 BETA.
SQ   SEQUENCE   267 AA;  30361 MW;  781F9971E32F6AE1 CRC64;


  Query Match             23.2%;  Score 86;  DB 1;  Length 267;
  Best Local Similarity   32.8%;  Pred. No. 0.002;
  Matches   19;  Conservative   10;  Mismatches   29;  Indels    0;  Gaps    0;

Qy       7 LYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDF 64
           :| : :  | |:|  ::   |  |||  || |:|: |     |: |    |  : |||
Db     204 VYPKKKMEKRFVFNKTEIKGNVEFESSQFPNWYISTSQAEEMPVFLGNTKGGQDITDF 261


RESULT  13
IL1B_MACFA
ID   IL1B_MACFA     STANDARD;      PRT;   268 AA.
AC   P79182;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Interleukin-1 beta precursor (IL-1 beta).
GN   IL1B.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Thymus;
RA   Totsuka K., Takakura H., Hashimoto O., Tatsumi M.;
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC   -!- SUBUNIT: MONOMER.
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; D63353; BAA09677.1; -.
DR   HSSP; P01584; 1HIB.
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```
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP        1    116       BY SIMILARITY.
FT   CHAIN       117    268       INTERLEUKIN-1 BETA.
SQ   SEQUENCE   268 AA;  30425 MW;  CFB7266E3E2C05B4 CRC64;


  Query Match             22.9%;  Score 85;  DB 1;  Length 268;
  Best Local Similarity   33.3%;  Pred. No. 0.0027;
  Matches   21;  Conservative    8;  Mismatches   32;  Indels    2;  Gaps    1;

Qy       8 YNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLT 67
           | : :  | |:|   :      |||  || |:|: |     |: |    |  : :|||  |
Db     206 YPKKKMEKRFVFNKIEINNKLEFESAQFPNWYISTSQAESMPVFLGGTRGGQDITDF--T 263

Qy      68 MLF 70
           | |
Db     264 MQF 266


RESULT  14
IL1B_HUMAN
ID   IL1B_HUMAN     STANDARD;      PRT;   269 AA.
AC   P01584; Q96HE5; Q9UCT6;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Interleukin-1 beta precursor (IL-1 beta) (Catabolin).
GN   IL1B.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85088517; PubMed=6083565;
RA   Auron P.E., Webb A.C., Rosenwasser L.J., Mucci S.F., Rich A.,
RA   Wolff S.M., Dinarello C.A.;
RT   "Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:7907-7911(1984).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85240547; PubMed=2989698;
RA   March C.J., Mosley B., Larsen A., Cerretti D.P., Braedt G., Price V.,
RA   Gillis S., Henney C.S., Kronheim S.R., Grabstein K., Conlon P.J.,
RA   Hopp T.P., Cosman D.;
RT   "Cloning, sequence and expression of two distinct human interleukin-1
RT   complementary DNAs.";
RL   Nature 315:641-647(1985).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87040762; PubMed=3490654;
RA   Clark B.D., Collins K.L., Gandy M.S., Webb A.C., Auron P.E.;
RT   "Genomic sequence for human prointerleukin 1 beta: possible evolution
RT   from a reverse transcribed prointerleukin 1 alpha gene.";
RL   Nucleic Acids Res. 14:7897-7914(1986).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87248099; PubMed=2954882;
RA   Bensi G., Raugei G., Palla E., Carinci V., Buonamassa D.T., Melli M.;
RT   "Human interleukin-1 beta gene.";
RL   Gene 52:95-101(1987).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90249285; PubMed=2635664;
RA   Kotenko S.V., Bulenkov M.T., Veiko V.P., Epishin S.M., Lomakin I.B.,
RA   Emel'Yanov A.V., Kozlov A.P., Konusova V.G., Kotov A.Y.,
RA   Kurbatova T.V., Reshetnikov V.L., Simbirtsev A.S., Ketlinskii S.A.,
RA   Vinetskii Y.P.;
RT   "Cloning of the cDNA coding for human prointerleukin-1 alpha and
RT   prointerleukin-1 beta.";
RL   Dokl. Akad. Nauk SSSR 309:1005-1008(1989).
RN   [6]
RP   SEQUENCE FROM N.A.
RA   Webb A.C., Dinarello C.A., Rosenwasser L.J., Mucci S.F., Rich A.,
RA   Wolff S.M., Auron P.E.;
RT   "Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.";
RL   Adv. Gene Technol. 22:339-340(1985).
RN   [7]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87156769; PubMed=3493774;
RA   Nishida T., Nishino N., Takano M., Kawai K., Bando K., Masui Y.,
RA   Nakai S., Hirai Y.;
RT   "cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell
RT   line.";
RL   Biochem. Biophys. Res. Commun. 143:345-352(1987).
RN   [8]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
RN   [9]
RP   SEQUENCE OF 117-128.
RX   MEDLINE=88184226; PubMed=3281727;
RA   Zsebo K.M., Wypych J., Yuschenkoff V.N., Lu H., Hunt P., Dukes P.P.,
RA   Langley K.E.;
RT   "Effects of hematopoietin-1 and interleukin 1 activities on early
RT   hematopoietic cells of the bone marrow.";
RL   Blood 71:962-968(1988).
RN   [10]
RP   SEQUENCE OF 114-135.
RC   TISSUE=Skin;
RX   MEDLINE=92013781; PubMed=1919436;
RA   Mizutani H., Schechter N., Lazarus G., Black R.A., Kupper T.S.;
RT   "Rapid and specific conversion of precursor interleukin 1 beta (IL-1
RT   beta) to an active IL-1 species by human mast cell chymase.";
RL   J. Exp. Med. 174:821-825(1991).
RN   [11]
RP   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX   MEDLINE=88211543; PubMed=3259176;
RA   Priestle J.P., Schar H.-P., Grutter M.G.;
RT   "Crystal structure of the cytokine interleukin-1 beta.";
RL   EMBO J. 7:339-343(1988).
RN   [12]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=90099325; PubMed=2602367;
RA   Priestle J.P., Schar H.-P., Grutter M.G.;
RT   "Crystallographic refinement of interleukin 1 beta at 2.0-A
RT   resolution.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:9667-9671(1989).
RN   [13]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=90064532; PubMed=2585509;
RA   Finzel B.C., Clancy L.L., Holland D.R., Muchmore S.W.,
RA   Watenpaugh K.D., Einspahr H.M.;
RT   "Crystal structure of recombinant human interleukin-1 beta at 2.0-A
RT   resolution.";
RL   J. Mol. Biol. 209:779-791(1989).
RN   [14]
RP   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF COMPLEX WITH RECEPTOR.
RX   MEDLINE=97215903; PubMed=9062193;
RA   Vigers G.P., Anderson L.J., Caffes P., Brandhuber B.J.;
RT   "Crystal structure of the type-I interleukin-1 receptor complexed
RT   with interleukin-1beta.";
RL   Nature 386:190-194(1997).
RN   [15]
RP   STRUCTURE BY NMR.
RX   MEDLINE=90321925; PubMed=2372550;
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RA   Driscoll P.C., Gronenborn A.M., Wingfield P.T., Clore G.M.;
RT   "Determination of the secondary structure and molecular topology of
RT   interleukin-1 beta by use of two- and three-dimensional heteronuclear
RT   15N-1H NMR spectroscopy.";
RL   Biochemistry 29:4668-4682(1990).
RN   [16]
RP   STRUCTURE BY NMR.
RX   MEDLINE=91159409; PubMed=2001363;
RA   Clore G.M., Wingfield P.T., Gronenborn A.M.;
RT   "High-resolution three-dimensional structure of interleukin 1 beta in
RT   solution by three- and four-dimensional nuclear magnetic resonance
RT   spectroscopy.";
RL   Biochemistry 30:2315-2323(1991).
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC   -!- SUBUNIT: MONOMER.
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
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CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
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CC   ---------------------------------------------------------------------
DR   EMBL; M15840; AAA74137.1; -.
DR   EMBL; X02532; CAA26372.1; -.
DR   EMBL; K02770; AAA36106.1; -.
DR   EMBL; X04500; CAA28185.1; -.
DR   EMBL; X56087; CAA39567.1; -.
DR   EMBL; M54933; AAA59136.1; -.
DR   EMBL; M15330; AAA59135.1; -.
DR   EMBL; BC008678; AAH08678.1; -.
DR   PIR; A01848; ICHU1B.
DR   PIR; A25542; A25542.
DR   PIR; A29019; A29019.
DR   PIR; B27616; B27616.
DR   PIR; S19626; S19626.
DR   PDB; 1I1B; 15-OCT-92.
DR   PDB; 2I1B; 15-JUL-93.
DR   PDB; 4I1B; 15-JAN-93.
DR   PDB; 5I1B; 15-OCT-94.
DR   PDB; 6I1B; 15-OCT-92.
DR   PDB; 7I1B; 15-OCT-92.
DR   PDB; 21BI; 15-APR-92.
DR   PDB; 31BI; 15-APR-92.
DR   PDB; 41BI; 15-JUL-92.
DR   PDB; 1HIB; 31-JAN-94.
DR   PDB; 1IOB; 17-AUG-96.
DR   PDB; 1ITB; 04-FEB-98.
DR   PDB; 9ILB; 06-JAN-99.
DR   MIM; 147720; -.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen;
KW   3D-structure.
FT   PROPEP        1    116
FT   CHAIN       117    269       INTERLEUKIN-1 BETA.
FT   CONFLICT      6      6       K -> E (IN REF. 2, 6 AND 8).
FT   CONFLICT     20     20       D -> H (IN REF. 7).
FT   CONFLICT    111    111       E -> Q (IN REF. 7).
FT   CONFLICT    177    177       G -> A (IN REF. 7).
FT   CONFLICT    214    214       R -> P (IN REF. 7).
FT   STRAND      121    128
FT   TURN        129    130
FT   STRAND      132    138

  Query Match           22.9%;  Score 85;  DB 1;  Length 269;
  Best Local Similarity  33.3%;  Pred. No. 0.0027;
  Matches   21;  Conservative    8;  Mismatches   32;  Indels    2;  Gaps    1;

Qy       8 YNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLT 67
           | : :  | |:|   :      |||  || |:|: |     |: |    |  : |||  |
Db     206 YPKKKMEKRFVFNKIEINNKLEFESAQFPNWYISTSQAENMPVFLGGTKGGQDITDF--T 263

Qy      68 MLF 70
            | |
Db     264 MQF 266


RESULT  15
IL1B_MACMU
ID   IL1B_MACMU     STANDARD;      PRT;   269 AA.
AC   P48090;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Interleukin-1 beta precursor (IL-1 beta).
GN   IL1B.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and
RT   nonhuman primates.";
RL   J. Immunol. 155:3946-3954(1995).
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC   -!- SUBUNIT: MONOMER.'
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U19845; AAA86709.1; -.
DR   HSSP; P01584; 1HIB.
DR   InterPro; IPR002348; IL1_HBGF.
```

```
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP        1    116       BY SIMILARITY.
FT   CHAIN       117    269       INTERLEUKIN-1 BETA.
SQ   SEQUENCE   269 AA;  30481 MW;  A7CD59EBAC120EC7 CRC64;


  Query Match             22.9%;  Score 85;  DB 1;  Length 269;
  Best Local Similarity   33.3%;  Pred. No. 0.0027;
  Matches   21;  Conservative    8;  Mismatches   32;  Indels    2;  Gaps    1;

Qy       8 YNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLT 67
           | : :  | |:|   :      |||  || |:|: |     |: |    |  : |||  |
Db     206 YPKKKMEKRFVFNKIEINNKLEFESAQFPNWYISTSQAENMPVFLGGTRGGQDITDF--T 263

Qy      68 MLF 70
           | |
Db     264 MQF 266


Search completed: June 20, 2002, 15:11:19
Job time: 444 sec
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 20, 2002, 15:03:09 ; Search time 61.16 Seconds
(without alignments)
197.999 Million cell updates/sec

Title: US-09-763-498-6
Perfect score: 371
Sequence: 1 EKDIMDLYNQPEPVKSFLFY.....ILTQELGKANTTDFGLTMLF 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	371	100.0	158	4	Q9UHA7	Q9uha7 homo sapien
2	238	64.2	160	11	Q9JLA2	Q9jla2 mus musculu
3	208.5	56.2	169	4	Q9NZH8	Q9nzh8 homo sapien
4	184	49.6	157	4	Q9UHA5	Q9uha5 homo sapien
5	158	42.6	183	11	Q9D6Z6	Q9d6z6 mus musculu
6	127	34.2	155	11	Q9QYY1	Q9qyy1 mus musculu
7	127	34.2	156	11	Q9JIG2	Q9jig2 mus musculu
8	124	33.4	155	4	Q9UBH0	Q9ubh0 homo sapien
9	107	28.8	72	6	O77771	O77771 equus cabal
10	101	27.2	159	4	Q96GD6	Q96gd6 homo sapien
11	101	27.2	177	6	Q9GMZ4	Q9gmz4 tursiops tr
12	98	26.4	176	6	Q9BEH0	Q9beh0 canis famil
13	97	26.1	144	4	Q9BYX1	Q9byx1 homo sapien
14	97	26.1	152	4	Q969H5	Q969h5 homo sapien
15	96.5	26.0	283	13	Q9PVZ5	Q9pvz5 xenopus lae
16	96	25.9	267	6	Q29082	Q29082 sus scrofa
17	93.5	25.2	267	13	O73909	O73909 gallus gall
18	91	24.5	276	13	O57398	O57398 cyprinus ca
19	91	24.5	276	13	Q9PW18	Q9pw18 cyprinus ca
20	89	24.0	272	13	Q9DDF3	Q9ddf3 cyprinus ca
21	88	23.7	176	6	Q9GKK2	Q9gkk2 canis famil
22	87	23.5	272	13	Q9DDF2	Q9ddf2 cyprinus ca
23	86.5	23.3	178	4	Q9HBF2	Q9hbf2 homo sapien
24	86.5	23.3	192	4	Q9UHA6	Q9uha6 homo sapien
25	86.5	23.3	218	4	Q9NZH6	Q9nzh6 homo sapien
26	86.5	23.3	218	4	Q9HBF3	Q9hbf3 homo sapien
27	85	22.9	153	4	O43645	O43645 homo sapien
28	85	22.9	269	4	Q96HE5	Q96he5 homo sapien
29	83.5	22.5	261	13	Q90W84	Q90w84 dicentrarch
30	81	21.8	266	6	Q9TTK1	Q9ttk1 tursiops tr
31	79.5	21.4	253	13	Q90W32	Q90w32 sparus aura
32	73.5	19.8	260	13	Q9YGD3	Q9ygd3 oncorhynchu
33	68.5	18.5	64	13	Q98SG5	Q98sg5 scophthalmu
34	66.5	17.9	267	11	Q91ZL5	Q91zl5 sigmodon hi
35	66.5	17.9	957	4	Q9UKN0	Q9ukn0 homo sapien
36	65.5	17.7	599	11	Q91WP7	Q91wp7 mus musculu
37	64.5	17.4	541	10	Q940N8	Q940n8 arabidopsis
38	64.5	17.4	541	10	Q93Z31	Q93z31 arabidopsis
39	64	17.3	357	2	Q93SK6	Q93sk6 myxococcus
40	63	17.0	364	16	P73423	P73423 synechocyst
41	62.5	16.8	148	15	Q90M28	Q90m28 human immun
42	62.5	16.8	254	13	Q9PT12	Q9pt12 oncorhynchu
43	62.5	16.8	533	5	O17592	O17592 caenorhabdi
44	62.5	16.8	1003	15	O93086	O93086 human immun
45	62	16.7	939	16	Q9KQC8	Q9kqc8 vibrio chol

ALIGNMENTS

RESULT 1
Q9UHA7
ID Q9UHA7 PRELIMINARY; PRT; 158 AA.
AC Q9UHA7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE FIL1 EPSILON.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092888; PubMed=10625660;
RA Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
RA Sims J.E.;
RT "Four New Members Expand the IL-1 Superfamily.";
RL J. Biol. Chem. 275:1169-1175(2000).
DR EMBL; AF201831; AAF25211.1; -.
DR HSSP; P18510; 1ILR.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 158 AA; 17684 MW; 469AC84306B0E280 CRC64;

Query Match 100.0%; Score 371; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 2e-39;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 EKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKAN 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     89 EKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKAN 148

Qy     61 TTDFGLTMLF 70
          ||||||||||
Db    149 TTDFGLTMLF 158
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RESULT   2
Q9JLA2
ID   Q9JLA2      PRELIMINARY;      PRT;   160 AA.
AC   Q9JLA2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN-1 HOMOLOG 1 (INTERLEUKIN-1 EPSILON) (INTERLEUKIN 1
DE   SUPERFAMILY 1, EPSILON).
GN   IL1F6 OR FIL1 OR IL1E.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20209405; PubMed=10744718;
RA   Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA   Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA   Young P.R.;
RT   "Identification and initial characterization of four novel members of
RT   the interleukin-1 family.";
RL   J. Biol. Chem. 275:10308-10314(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Debets R., Timans J., Zurawski S., Bazan J.F., Kastelein R.A.;
RT   "Novel IL-1 family member IL-1e responds through the orphan IL-1R-
RT   related protein 2; response is antagonized by IL-1d.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AF200493; AAF69249.1; -.
DR   EMBL; AF206697; AAG35671.1; -.
DR   EMBL; AK004061; BAB23147.1; -.
DR   HSSP; P01584; 1HIB.
DR   MGD; MGI:1859324; Il1f6.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
SQ   SEQUENCE   160 AA;  18015 MW;  AA0434D68FF62F4A CRC64;


  Query Match             64.2%;  Score 238;  DB 11;  Length 160;
  Best Local Similarity   63.8%;  Pred. No. 1.8e-22;
  Matches   44;  Conservative   11;  Mismatches   14;  Indels    0;  Gaps    0;

Qy       1 EKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKAN 60
           | :||::||: ||||: |||| :||  ||||| ||||||||| |:| ||||||||||:

Db      91 EGNIMEMYNKKEPVKASLFYHKKSGTTSTFESAAFPGWFIAVCSKGSCPLILTQELGEIF 150

Qy      61 TTDFGLTML 69
             ||| : ::
Db     151 ITDFEMIVV 159


RESULT   3
Q9NZH8
ID   Q9NZH8      PRELIMINARY;      PRT;   169 AA.
AC   Q9NZH8;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN-1 HOMOLOG 1 (INTERLEUKIN-1 EPSILON).
GN   IL1E.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20209405; PubMed=10744718;
RA   Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA   Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA   Young P.R.;
RT   "Identification and initial characterization of four novel members of
RT   the interleukin-1 family.";
RL   J. Biol. Chem. 275:10308-10314(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=AIRWAY EPITHELIAL CELLS INDUCED WITH TNF ALPHA, AND IFN;
RA   Debets R., Timans J., Zurawski S., Bazan J.F., Kastelein R.A.;
RT   "Novel IL-1 family member IL-1e responds through the orphan IL-1R-
RT   related protein 2; response is antagonized by IL-1d.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF200492; AAF69248.1; -.
DR   EMBL; AF206696; AAG35670.1; -.
DR   HSSP; P18510; 1ITN.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
SQ   SEQUENCE   169 AA;  18721 MW;  F00A9243706F4154 CRC64;


  Query Match             56.2%;  Score 208.5;  DB 4;  Length 169;
  Best Local Similarity   63.2%;  Pred. No. 1.1e-18;
  Matches   43;  Conservative    8;  Mismatches   16;  Indels    1;  Gaps    1;

Qy       1 EKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKAN 60
           |: ||||| |||||| |||| :::|| || |||||| |||| ||:   |:||| ||||:
Db     101 EQKIMDLYGQPEPVKPFLFYRAKTGRTSTLESVAFPDWFIA-SSKRDQPIILTSELGKSY 159

Qy      61 TTDFGLTM 68
             | | | :
Db     160 NTAFELNI 167


RESULT   4
Q9UHA5
ID   Q9UHA5      PRELIMINARY;      PRT;   157 AA.
AC   Q9UHA5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   FIL1 ETA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
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RX   MEDLINE=20092888; PubMed=10625660;
RA   Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
RA   Sims J.E.;
RT   "Four New Members Expand the IL-1 Superfamily.";
RL   J. Biol. Chem. 275:1169-1175(2000).
DR   EMBL; AF201833; AAF25213.1; -.
DR   HSSP; P10749; 2MIB.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
SQ   SEQUENCE   157 AA;  17702 MW;  7A54F3D7557A3EE3 CRC64;


  Query Match             49.6%;  Score 184;  DB 4;  Length 157;
  Best Local Similarity   51.5%;  Pred. No. 1.4e-15;
  Matches   34;  Conservative   13;  Mismatches   19;  Indels    0;  Gaps    0;

Qy       1 EKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKAN 60
           ||:||||| : :  | |||:|:: |   | |:||::|||||| |:  | |: ||:| |  |
Db      88 EKNIMDLYVEKKAQKPFLFFHNKEGSTSVFQSVSYPGWFIATSTTSGQPIFLTKERGITN 147

Qy      61 TTDFGL 66
             |:| |
Db     148 NTNFYL 153


RESULT   5
Q9D6Z6
ID   Q9D6Z6      PRELIMINARY;      PRT;   183 AA.
AC   Q9D6Z6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   2310043N20RIK PROTEIN.
GN   2310043N20RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=TONGUE;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK009787; BAB26505.1; -.
DR   HSSP; P01584; 1HIB.
DR   MGD; MGI:1916927; 2310043N20Rik.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
SQ   SEQUENCE   183 AA;  20878 MW;  A3ACE339FB96F02F CRC64;


  Query Match             42.6%;  Score 158;  DB 11;  Length 183;
  Best Local Similarity   50.0%;  Pred. No. 3.4e-12;
  Matches   32;  Conservative    9;  Mismatches   23;  Indels    0;  Gaps    0;

Qy       1 EKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKAN 60
           | |||:|| : :  |:|||||   |  | |:|| :|||||| ||     :||| : ||
Db     114 EVDIMNLYKERKAQKAFLFYHGIEGSTSVFQSVLYPGWFIATSSIERQTIILTHQRGKLV 173

Qy      61 TTDF 64
             |:|
Db     174 NTNF 177


RESULT   6
Q9QYY1
ID   Q9QYY1      PRELIMINARY;      PRT;   155 AA.
AC   Q9QYY1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   IL-1L1 PROTEIN (INTERLEUKIN-1 HOMOLOG 3).
GN   IL1F5 OR IL1HY1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Barton J.L., Nicklin M.J.H.;
RT   "IL-1L1: A Novel Member of the Interleukin-1 Gene Family is Expressed
RT   in Trophoblasts and Macrophages.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20209405; PubMed=10744718;
RA   Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA   Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA   Young P.R.;
RT   "Identification and initial characterization of four novel members of
RT   the interleukin-1 family.";
RL   J. Biol. Chem. 275:10308-10314(2000).
DR   EMBL; AJ250429; CAB59831.1; -.
DR   EMBL; AF200495; AAF69251.1; -.
DR   HSSP; P18510; 1ILR.
DR   MGD; MGI:1859325; Il1f5.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
SQ   SEQUENCE   155 AA;  17004 MW;  A4B1770F2E12533A CRC64;


  Query Match             34.2%;  Score 127;  DB 11;  Length 155;
  Best Local Similarity   43.9%;  Pred. No. 2.5e-08;
  Matches   29;  Conservative    7;  Mismatches   26;  Indels    4;  Gaps    1;

Qy       3 DIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQ----ELGK 58
             :||:||   :  ||| ||    |  |:||| |:||||:  | |   |: |||
Db      84 NIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTSPEADQPVRLTQIPEDPAWD 143

Qy      59 ANTTDF 64
             |  |||
Db     144 APITDF 149


RESULT   7
Q9JIG2
ID   Q9JIG2      PRELIMINARY;      PRT;   156 AA.
AC   Q9JIG2;
```

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DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN-1 DELTA (INTERLEUKIN 1 RECEPTOR ANTAGONIST HOMOLOG
DE   1).
GN   IL1F5 OR IL1HY1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Debets R., Timans J.C., Zurawski S., Sana T.R., Bazan F.,
RA   Kastelein R.A.;
RT   "Novel IL-1 ligands IL-1d and IL-1e use IL-1R related protein 2.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=TONGUE, AND STOMACH;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AF230378; AAF91275.1; -.
DR   EMBL; AK009741; BAB26471.1; -.
DR   EMBL; AK008977; BAB26002.1; -.
DR   HSSP; P18510; 1ILR.
DR   MGD; MGI:1859325; Il1f5.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
SQ   SEQUENCE   156 AA;  17136 MW;  A4D1EE2F93CF77A7 CRC64;


  Query Match             34.2%;  Score 127;  DB 11;  Length 156;
  Best Local Similarity   43.9%;  Pred. No. 2.5e-08;
  Matches   29;  Conservative    7;  Mismatches   26;  Indels    4;  Gaps    1;

Qy       3 DIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQ----ELGK 58
           :||:||   :  ||| ||    |  |:||| |:|||||:  | |   |: |||
Db      85 NIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTSPEADQPVRLTQIPEDPAWD 144

Qy      59 ANTTDF 64
           |  |||
Db     145 APITDF 150


RESULT   8
Q9UBH0
ID   Q9UBH0      PRELIMINARY;      PRT;   155 AA.
AC   Q9UBH0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   FIL1 DELTA (INTERLEUKIN-1 LIKE PROTEIN 1) (INTERLEUKIN-1 RECEPTOR
DE   ANTAGONIST HOMOLOG 1) (INTERLEUKIN-1 DELTA).
GN   IL1HY1 OR IL1L1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20092888; PubMed=10625660;
RA   Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
RA   Sims J.E.;
RT   "Four New Members Expand the IL-1 Superfamily.";
RL   J. Biol. Chem. 275:1169-1175(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99443727; PubMed=10512743;
RA   Mulero J.J., Pace A.M., Nelken S.T., Loeb D.B., Correa T.R.,
RA   Drmanac R., Ford J.E.;
RT   "IL1HY1: A Novel Interleukin-1 Receptor Antagonist Gene.";
RL   Biochem. Biophys. Res. Commun. 263:702-706(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RA   Barton J.L., di Giovine F.S., Symons J.A., Nicklin M.J.H.;
RT   "A tissue specific interleukin-1 receptor antagonist homolog from the
RT   IL1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18ra activities.";
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Barton J.L., Herbst R., Bosisio D., Nicklin M.J.H.;
RT   "A tissue specific interleukin-1 receptor antagonist homolog from the
RT   IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18ra activities.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20322477; PubMed=10866108;
RA   Mulero J.J., Nelken S.T., Ford J.E.;
RT   "Organization of the Human Interleukin-1 Receptor Antagonist Gene
RT   IL1HY1.";
RL   Immunogenetics 51:425-428(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RA   Debets R., Timans J.C., Zurawski S., Sana T.R., Bazan F.,
RA   Kastelein R.A.;
RT   "Novel IL-1 ligands IL-1d and IL-1e use IL-1R related protein 2.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF201830; AAF25210.1; -.
DR   EMBL; AF186094; AAF02757.1; -.
DR   EMBL; AJ242737; CAB59822.1; -.
DR   EMBL; AJ242738; CAB59823.1; -.
DR   EMBL; AJ271338; CAB67704.1; -.
DR   EMBL; AF216693; AAF76981.1; -.
DR   EMBL; AF230377; AAF91274.1; -.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
KW   Receptor.
SQ   SEQUENCE   155 AA;  16962 MW;  B96DB5EFA2612E25 CRC64;


  Query Match             33.4%;  Score 124;  DB 4;  Length 155;
  Best Local Similarity   45.5%;  Pred. No. 6e-08;
  Matches   30;  Conservative    7;  Mismatches   25;  Indels    4;  Gaps    2;

Qy       3 DIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQ--ELG--K 58
           :||:||   :  ||| ||    |  |:||| |:||||:    |   |: |||  | |
Db      84 NIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQPVRLTQLPENGGWN 143

Qy      59 ANTTDF 64
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          |  |||
Db    144 APITDF 149


RESULT   9
O77771
ID   O77771      PRELIMINARY;      PRT;    72 AA.
AC   O77771;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN-1 RECEPTOR ANTAGONIST SECRETORY FORM (FRAGMENT).
GN   IL-1RA.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BREED THOROUGHBRED;
RA   Dhar A.K., Thompson M.S., Paradis M.R., Alcivar-Warren A.;
RT   "Molecular Characterization of Equine Interleukin 1 Receptor
RT   Antagonist (IL-1ra) Gene.";
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF072476; AAC62237.1; -.
DR   HSSP; P18510; 1IRA.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Receptor.
FT   NON_TER       1      1
SQ   SEQUENCE   72 AA;  8215 MW;  290CC9B9D4C413D9 CRC64;


  Query Match             28.8%;  Score 107;  DB 6;  Length 72;
  Best Local Similarity   41.5%;  Pred. No. 3.6e-06;
  Matches   22;  Conservative    7;  Mismatches   24;  Indels    0;  Gaps    0;

Qy       3 DIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQE 55
           :| ||    |  | | |  | ||  ::||| | ||||:  : |   |: || :
Db       4 NITDLSKNKEENKRFTFIRSNSGPTTSFESAACPGWFLCTAQEADRPVSLTNK 56


RESULT  10
Q96GD6
ID   Q96GD6      PRELIMINARY;      PRT;   159 AA.
AC   Q96GD6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN 1 RECEPTOR ANTAGONIST.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PANCREATIC ADENOCARCINOMA;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC009745; AAH09745.1; -.
KW   Receptor.
SQ   SEQUENCE   159 AA;  17888 MW;  C1D66CDF0D2F7B44 CRC64;


  Query Match             27.2%;  Score 101;  DB 4;  Length 159;
  Best Local Similarity   37.5%;  Pred. No. 5.3e-05;
  Matches   24;  Conservative    8;  Mismatches   26;  Indels    6;  Gaps    1;

Qy       3 DIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTT 62
           :| ||    :  | | |  | ||  ::||| | ||||:  : |   |: ||      |

Db      91 NITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWFLCTAMEADQPVSLT------NMP 144

Qy      63 DFGL 66
           | |:
Db     145 DEGV 148


RESULT  11
Q9GMZ4
ID   Q9GMZ4      PRELIMINARY;      PRT;   177 AA.
AC   Q9GMZ4;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN-1 RECEPTOR ANTAGONIST.
GN   IL-1RA.
OS   Tursiops truncatus (Atlantic bottle-nosed dolphin).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC   Tursiops.
OX   NCBI_TaxID=9739;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21109087; PubMed=11182153;
RA   Inoue Y., Itou T., Jimbo T., Syouji Y., Ueda K., Sakai T.;
RT   "Molecular cloning and functional expression of bottle-nosed dolphin
RT   (Tursiops truncatus) interleukin-1 receptor antagonist.";
RL   Vet. Immunol. Immunopathol. 78:131-141(2001).
DR   EMBL; AB038268; BAB11806.1; -.
DR   HSSP; P18510; 1IRA.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Receptor.
SQ   SEQUENCE   177 AA;  19923 MW;  6FD19A06C09B131B CRC64;


  Query Match             27.2%;  Score 101;  DB 6;  Length 177;
  Best Local Similarity   43.1%;  Pred. No. 5.9e-05;
  Matches   22;  Conservative    7;  Mismatches   22;  Indels    0;  Gaps    0;

Qy       3 DIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILT 53
           :| ||  :  |  | | |  | ||  ::||| | ||||:  : |   |: ||
Db     109 NITDLNSSKEEDKRFAFIRSDSGPTTSFESAACPGWFLCTALETDQPVGLT 159


RESULT  12
Q9BEH0
ID   Q9BEH0      PRELIMINARY;      PRT;   176 AA.
AC   Q9BEH0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN-1 RECEPTOR ANTAGONIST.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Shin I.-S., Youn H.-Y.;
RT   "Molecular cloning of canine interleukin-1 receptor antagonist (IL-
RT   1ra).";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY026462; AAK01472.1; -.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
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```
KW   Receptor.
SQ   SEQUENCE   176 AA;  19922 MW;  8486CA54A240212B CRC64;


  Query Match             26.4%;  Score 98;  DB 6;  Length 176;
  Best Local Similarity   41.2%;  Pred. No. 0.00014;
  Matches   21;  Conservative    7;  Mismatches   23;  Indels    0;  Gaps    0;

Qy      3 DIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILT 53
          :| ||    :  | | |  | ||  ::||| | ||||:  : |   |: ||
Db    109 NITDLSKNKDQDKRFTFILSDSGPTTSFESAACPGWFLCTALEADRPVSLT 159


RESULT  13
Q9BYX1
ID   Q9BYX1      PRELIMINARY;      PRT;   144 AA.
AC   Q9BYX1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN-1 RECEPTOR ANTAGONIST FKSG75.
GN   FKSG75.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wang Y.-g, Li T., Gong L.;
RT   "Identification and characterization of FKSG75, a novel member of the
RT   interleukin-1 family.";
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY026753; AAK01948.1; -.
DR   HSSP; P18510; 1IRP.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
KW   Receptor.
SQ   SEQUENCE   144 AA;  15811 MW;  8733B16D6F118BB9 CRC64;


  Query Match             26.1%;  Score 97;  DB 4;  Length 144;
  Best Local Similarity   35.5%;  Pred. No. 0.00015;
  Matches   22;  Conservative   10;  Mismatches   30;  Indels    0;  Gaps    0;

Qy      3 DIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTT 62
          :| :||   |    | |: | ||     |: |:||||:   :|   |: ||:|   :  |
Db     77 NIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTKESEPSART 136

Qy     63 DF 64
           |
Db    137 KF 138


RESULT  14
Q969H5
ID   Q969H5      PRELIMINARY;      PRT;   152 AA.
AC   Q969H5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN-1 HY2.
GN   IL1HY2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21282953; PubMed=11278614;
RA   Lin H., Ho A.S., Haley-Vicente D., Zhang J., Bernal-Fussell J.,
RA   Pace A.M., Hansen D., Schweighofer K., Mize N.K., Ford J.E.;
RT   "Cloning and characterization of IL1HY2, a novel interleukin-1 family
RT   member.";
RL   J. Biol. Chem. 276:20597-20602(2001).
DR   EMBL; AF334756; AAK68049.1; -.
DR   EMBL; AF334755; AAK68048.1; -.
SQ   SEQUENCE   152 AA;  16975 MW;  DF9735100FC711B2 CRC64;


  Query Match             26.1%;  Score 97;  DB 4;  Length 152;
  Best Local Similarity   35.5%;  Pred. No. 0.00016;
  Matches   22;  Conservative   10;  Mismatches   30;  Indels    0;  Gaps    0;

Qy      3 DIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTT 62
          :| :||   |    | |: | ||     |: |:||||:   :|   |: ||:|   :  |
Db     85 NIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTKESEPSART 144

Qy     63 DF 64
           |
Db    145 KF 146


RESULT  15
Q9PVZ5
ID   Q9PVZ5      PRELIMINARY;      PRT;   283 AA.
AC   Q9PVZ5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN-1-BETA.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BLOOD;
RX   MEDLINE=20260991; PubMed=10803846;
RA   Zou J., Bird S., Minter R., Horton J., Cunningham C., Secombes C.J.;
RT   "Molecular cloning of the gene for interleukin-1 beta from Xenopus
RT   laevis and analysis of expression in vivo and in vitro.";
RL   Immunogenetics 51:332-338(2000).
DR   EMBL; AJ010497; CAB53499.1; -.
DR   HSSP; P01584; 1HIB.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
SQ   SEQUENCE   283 AA;  31729 MW;  0FD19B1006722722 CRC64;


  Query Match             26.0%;  Score 96.5;  DB 13;  Length 283;
  Best Local Similarity   34.8%;  Pred. No. 0.00038;
  Matches   24;  Conservative   10;  Mismatches   26;  Indels    9;  Gaps    2;

Qy      2 KDIMDLYNQPEPVKSFLFYHSQSGRNST----FESVAFPGWFIAVSSEGGCPLILTQELG 57
          ||:     : | :  |:|  |+| | | |    |||||||||:|: |      : :  :
Db    216 KDV-----KGEDLNRFIFMKSQDGLNETSTNSFESVAFPGWYISTSQRENELVQMVHQKN 270

Qy     58 KANTTDFGL 66
          :    || |
Db    271 QEAIKDFNL 279


Search completed: June 20, 2002, 15:10:54
Job time: 465 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: June 21, 2002, 11:09:00 ; Search time 2828.95 Seconds
(without alignments)
2275.773 Million cell updates/sec

Title: US-09-763-498-7
Perfect score: 477
Sequence: 1 atggaaaaagcattgaaaat.....ggttaactatgctgttttaa 477

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	238.6	50.0	883	11	AK004061	AK004061 Mus muscu
	2	129.2	27.1	479	9	AA030324	AA030324 mi08c10.r
c	3	124.4	26.1	612	10	BM386666	BM386666 UI-R-CN1-
c	4	122	25.6	539	9	AW368430	AW368430 CM3-HT019
	5	122	25.6	555	9	AW361172	AW361172 RC1-CT025
c	6	122	25.6	557	9	AW368437	AW368437 CM3-HT019
c	7	122	25.6	559	9	AW578451	AW578451 RC1-CT025
c	8	121	25.4	555	10	BE695960	BE695960 RC1-CT025
c	9	120.4	25.2	436	9	AW361164	AW361164 RC1-CT025
	10	120.4	25.2	536	9	AW853610	AW853610 RC1-CT025
	11	120	25.2	1219	11	AK009787	AK009787 Mus muscu
	12	113.2	23.7	870	10	BF244205	BF244205 601863146
c	13	111	23.3	434	9	AW753217	AW753217 RC1-CT025
	14	97.4	20.4	560	9	AW361245	AW361245 RC1-CT025
	15	74.8	15.7	1020	10	BG245180	BG245180 602357579
	16	72	15.1	997	9	AL554778	AL554778 AL554778
	17	71.8	15.1	594	10	BI961215	BI961215 MONO1_7_E
	18	71.6	15.0	626	9	BB612586	BB612586 BB612586
	19	71.4	15.0	435	10	W78043	W78043 zd72d01.r1
	20	70.8	14.8	635	9	AW262191	AW262191 xq62f01.x
	21	70.8	14.8	889	9	AL540334	AL540334 AL540334
	22	70.8	14.8	910	9	AL549965	AL549965 AL549965
	23	70.8	14.8	938	10	BE563703	BE563703 601335323
	24	70.8	14.8	955	10	BM009048	BM009048 603618892
	25	69.2	14.5	640	10	BG288796	BG288796 602388126
	26	69.2	14.5	864	10	BI489807	BI489807 603031536
c	27	67.6	14.2	371	10	BI020838	BI020838 CM4-MT021
	28	67.6	14.2	549	10	BE706905	BE706905 QV0-HT036
	29	65.6	13.8	508	9	AW464284	AW464284 BP230015A
	30	65	13.6	531	9	AW951593	AW951593 EST363663
	31	62.6	13.1	393	9	AV011778	AV011778 AV011778
	32	62	13.0	832	10	BI517352	BI517352 603041588
	33	61.4	12.9	900	11	AY026753	AY026753 Homo sapi
c	34	61.2	12.8	350	10	BI020732	BI020732 CM4-MT021
	35	61.2	12.8	1051	11	AK009741	AK009741 Mus muscu
	36	61.2	12.8	1199	11	AK008977	AK008977 Mus muscu
	37	60.8	12.7	726	10	BI089828	BI089828 602855071
	38	60.8	12.7	858	10	BI090567	BI090567 602855674
	39	60.8	12.7	932	9	AL545100	AL545100 AL545100
	40	60.4	12.7	726	10	BI766516	BI766516 603052319
	41	56.8	11.9	824	10	BI762103	BI762103 603049281
	42	56.2	11.8	690	10	BI912302	BI912302 603069864
	43	56	11.7	281	10	R50241	R50241 yj58a03.r1
	44	55.8	11.7	260	10	R46871	R46871 yj54f05.r1
	45	54.4	11.4	2843	11	AK014576	AK014576 Mus muscu

ALIGNMENTS

RESULT 1
AK004061
LOCUS AK004061 883 bp mRNA linear HTC 19-JAN-2002
DEFINITION Mus musculus 18 days embryo whole body cDNA, RIKEN full-length enriched library, clone:1110033G16:interleukin 1 family, member 6 (epsilon), full insert sequence.
ACCESSION AK004061
VERSION AK004061.1 GI:12835089
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (strain:C57BL/6J) 18 days embryo cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:1110033G16.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2 (sites)
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3 (sites)
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913
PUBMED 11076861
REFERENCE 4 (sites)
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5 (bases 1 to 883)
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0. Second strand cDNA was prepared with the primer adapter of sequence[5' GAGAGAGAGAAGGATCCAAGAGCTCAATTAATTTAATTAAACCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.

FEATURES Location/Qualifiers
source 1. .883
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="MGD:MGI:1900693"
/db_xref="taxon:10090"
/clone="1110033G16"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="18 days embryo"
gene 162. .644
/gene="Il1f6"
CDS 162. .644
/gene="Il1f6"
/note="data source:MGD, source key:MGI:1859324, evidence:ISS
interleukin 1 family, member 6 (epsilon)
putative"
/codon_start=1
/protein_id="BAB23147.1"
/db_xref="GI:12835090"
/translation="MNKEKELRAASPSLRHVQDLSSRVWILQNNILTAVPRKEQTVPV TITLLPCQYLDTLETNRGDPTYMGVQRPMSCLFCTKDGEQPVLQLGEGNIMEMYNKKE PVKASLFYHKKSGTTSTFESAAFPGWFIAVCSKGSCPLILTQELGEIFITDFEMIVVH "
polyA_signal 860. .865
/note="putative"
polyA_site 883
/note="putative"

BASE COUNT 255 a 193 c 200 g 235 t
ORIGIN

Query Match 50.0%; Score 238.6; DB 11; Length 883;
Best Local Similarity 68.8%; Pred. No. 1.4e-60;
Matches 328; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

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Qy      1 atggaaaaagcattgaaaattgacacacctcagcaggggagcattcaggatatcaatcat 60
          | ||| |||| | | | |   |  |||||  ||   |    ||||||||| | | |  |
Db    168 AAGGAGAAAGAACTAAGAGCAGCATCACCTTCGCTTAGACATGTTCAGGATCTTAGTAGT 227

Qy     61 cgggtgtgggttcttcaggaccagacgctcatagcagtcccgaggaaggaccgtatgtct 120
          || |||||| | || ||| || | |  |||| |||||||| ||||| || |  |    |
Db    228 CGTGTGTGGATCCTGCAGAACAATATCCTCACTGCAGTCCCAAGGAAAGAGCAAACAGTT 287

Qy    121 ccagtcactattgccttaatctcatgccgacatgtggagacccttgagaaagacagaggg 180
          |||||||||||| ||||  || |||||| | || |||| || |||||||   |||| |||
Db    288 CCAGTCACTATTACCTTGCTCCCATGCCAATATCTGGACACTCTTGAGACGAACAGGGGG 347

Qy    181 aaccccatctacctgggcctgaatggactcaatctctgcctgatgtgtgctaaagtcggg 240
          | ||||  ||| ||||  || |  | |  |    |||||||  | ||  | || |  |||
Db    348 GATCCCACGTACATGGGAGTGCAAAGGCCGATGAGCTGCCTGTTCTGCACAAAGGATGGG 407

Qy    241 gaccagcccacactgcagctgaaggaaaaggatataatggatttgtacaaccaacccgag 300
          || |||||    || |||||   ||||  | | ||||||||  ||||||||  ||   ||
Db    408 GAGCAGCCTGTGCTACAGCTTGGGGAAGGGAACATAATGGAAATGTACAACAAAAAGGAA 467

Qy    301 cctgtgaagtcctttctcttctaccacagccagagtggcaggaactccaccttcgagtct 360
          ||||| ||  ||| |||||||| ||||   |||||||  |  | ||| || || |||||||
Db    468 CCTGTAAAAGCCTCTCTCTTCTATCACAAGAAGAGTGGTACAACCTCTACATTTGAGTCT 527

Qy    361 gtggctttccctggctggttcatcgctgtcagctctgaaggaggctgtcctctcatcctt 420
          |  || |||||||| |||||||||||||| ||||| ||||  |||| || |||||  ||
Db    528 GCAGCCTTCCCTGGTTGGTTCATCGCTGTCTGCTCTAAAGGGAGCTGCCCACTCATTCTG 587

Qy    421 acccaagaactggggaaagccaacactactgactttgggttaactatgctgttttaa 477
          |||||||||||||||  ||  |  ||  |||||||| | | | | | || |   ||||
Db    588 ACCCAAGAACTGGGGGAAATCTTCATCACTGACTTCGAGATGATTGTGGTACATTAA 644
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RESULT 2
AA030324
LOCUS AA030324 479 bp mRNA linear EST 21-JAN-1997
DEFINITION mi08c10.r1 Soares mouse placenta 4NbMP13.5 14.5 Mus musculus cDNA clone IMAGE:459858 5', mRNA sequence.
ACCESSION AA030324
VERSION AA030324.1 GI:1497479
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 479)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N.; Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:276746
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 467.

```
FEATURES             Location/Qualifiers
     source          1. .479
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                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:459858"
                     /clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
                     /sex="unknown"
                     /tissue_type="placenta"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
                     with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Not I - oligo(dT) primer
                     [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGGAAATTTTTTTTTTTTTTTTTTTTT
                     T 3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      148 a    108 c    102 g    121 t
ORIGIN
```

```
  Query Match           27.1%;  Score 129.2;  DB 9;  Length 479;
  Best Local Similarity  73.9%;  Pred. No. 6.7e-28;
  Matches  164;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy     256 cagctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtccttt 315
           ||| |  |||||  | | ||||||||  ||||||||  ||   || |||||  ||  ||| |
Db     195 CAGTTCCAGGAAGGGAACATAATGGAAATGTACAACAAAAAGGAACCTGTAAAAGCCTCT 254

Qy     316 ctcttctaccacagccagagtggcaggaactccaccttcgagtctgtggctttccctggc 375
           |||||||| ||||   |||||||  |  | |||  ||  ||  ||||||||  ||  ||||||||
Db     255 CTCTTCTATCACAAGAAGAGTGGTACAACCTCTACATTTGAGTCTGCAGCCTTCCCTGGT 314

Qy     376 tggttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaagaactgggg 435
           ||||||||||||||| |||||  ||||  ||||  ||  |||||  ||  ||||||||||||||
Db     315 TGGTTCATCGCTGTCTGCTCTAAAGGGAGCTGCCCACTCATTCTGACCCAAGAACTGGGG 374

Qy     436 aaagccaacactactgactttgggttaactatgctgttttaa 477
             ||  |  ||  |||||||| | | | | | ||  |   ||||
Db     375 GAAATCTTCATCACTGACTTCGAGATGATTGTGGTACATTAA 416
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```
RESULT   3
BM386666/c
LOCUS       BM386666                612 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  UI-R-CN1-cjg-1-09-0-UI.s1 UI-R-CN1 Rattus norvegicus cDNA clone
            UI-R-CN1-cjg-1-09-0-UI 3', mRNA sequence.
ACCESSION   BM386666
VERSION     BM386666.1  GI:18186719
KEYWORDS    EST.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 612)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to identify it as a clone from the
            normalized fundus library cDNA Library Preparation: M.B. Soares Lab
            Clone distribution: clones will be available through Research
            Genetics (www.resgen.com)
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .612
                     /organism="Rattus norvegicus"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-CN1-cjg-1-09-0-UI"
                     /clone_lib="UI-R-CN1"
                     /dev_stage="adult"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CN1
                     library is a subtracted library derived from the following
                     pool of seven normalized rat libraries: normalized rat
                     seminal vesicles, normalized rat penis, normalized rat
                     bladder, normalized rat cervix, normalized rat brown
                     adipose, normalized rat fundus, and normalized rat
                     salivary gland.  It was constructed according to the
                     procedure described by Bonaldo, Lennon & Soares (Genome
                     Research Genome 6:  791-806, 1996).  For construction of
                     the CN1 library, plasmid DNA from the pool of normalized
                     libraries was electroporated into competent bacteria for
                     the production of single-stranded circular DNA.  This was
                     then used as a tracer in a subtractive hybridization with
                     a driver (PCR amplified inserts from a plamid DNA template
                     preparation) comprising: a) a pool of about 34,000 clones
                     from the Rat Unigene Set corresponding to plates R-5-AA-NN
                     excluding plates R-5-MM and MN.  This pool represented 40%
                     of the final driver population.  b) a pool of about 29,000
                     clones from subtracted libraries CA0 and CA1 corresponding
                     to plates R-CA0-AWV through R-CA0-AXS, R-CA0-AZX through
                     R-CA0-BAZ, R-CA0-BFE through R-CA0-BHY, R-CA0-BJS,
                     R-CA0-BKE, R-CA0-BKG-H, R-CA0-BKJ-K, R-CA0-BKP through
                     R-CA0-BKS, R-CA0-BKU-V, R-CA0-BLY through R-CA0-BMA,
                     R-CA0-BMC through R-CA0-BME, R-CA0-BNS, R-CA0-BOB through
                     R-CA0-BOJ, R-CA0-BPA through R-CA0-BPG, R-CA1-BBA through
                     R-CA1-BDA, R-CA1-BHZ through R-CA1-BJF, R-CA1-BJR,
                     R-CA1-BJT through R-CA1-BKB, R-CA1-BKD, R-CA1-BKF,
                     R-CA1-BKI, R-CA1-BKT, R-CA1-BLF, R-CA1-BLH through
                     R-CA1-BLN, R-CA1-BLS, R-CA1-BLU-V, R-CA1-BNR, and
                     R-CA1-BLE.  The resulting pool represented 20% of the
                     final driver population.  c) a pool of about 15,000 clones
                     from non-normalized libraries CS0s, CT0s, CU0s, CW0s, CX0s
                     and normalized libaries CS0, CT0, CU0, CW0, and CX0
                     corresponding to plates R-CS0s-CBD through R-CS0s-CBO,
                     R-CT0s-CAM through R-CT0s-CAX, R-CU0s-CBP through
                     R-CU0s-CCA, R-CW0s-CCB through R-CW0s-CCM, R-CX0s-CCN
                     through R-CX0s-CCX, R-CS0-BSD, R-CS0-BTD through R-CS0-BTV
                     , R-CS0-BVM, R-CT0-BTW through R-CT0-BUP, R-CT0-BVN,
                     R-CU0-BUQ through R-CU0-BVL, R-CW0-BVV through R-CW0-BWP,
                     R-CW0-BXN through R-CW0-BXO, R-CX0-BWQ through R-CX0-BXM.
                     The resulting pool represented 5% of the final driver
                     population.  d) a pool of about 5,000 clones (1,000 from
                     non-normalized eye library CV0 and 4,000 from normalized
                     eye library CV1) corresponding to plates R-CV0-BRH through
                     R-CV0-BRR, R-CV1-BRS through R-CV1-BSC, R-CV1-BSE through
                     R-CV1-BTC, and R-CV1-BVO through R-CV1-BVU. This pool
                     represented about 5% of the final driver population.  e) A
                     pool of about 10,000 clones from subtracted library BS2,
                     BV0 and BV0p (7-9.5 kb cDNA library fraction from rat
                     whole embryo), and BX0 (0.5-7kb cDNA library fraction from
                     rat whole embryo) corresponding to plates R-BS2-BDB
                     through R-BS2-BFB, R-BV0-ANK through R-BV0-ANR, R-BV0p-AOI
                     through R-BV0p-AOX, and R-BX0-AQY through R-BX0-ASH.  The
                     resulting pool represented 5% of the final driver
```

population. f) a pool of about 7,000 clones from the seven non-normalized libraries that make up the tracer including CY0, CZ0, DA0, DB0, DC0, DD0, and DE0 corresponding to plates R-CY0-BXP through R-CY0-BXZ, R-CZ0-BYA through R-CZ0-BYI, R-CZ0-BZB-C, R-DA0-BYJ through R-DA0-BYP, R-DA0-BZD through R-DA0-BZH, R-DB0-BYQ through R-DB0-BZA, R-DC0-BZI through R-DC0-BZQ, R-DC0-CAY through R-DC0-CBA, R-DD0-BZR through R-DD0-CAA, R-DD0-CBB-C, and R-DE0-CAB through R-DE0-CAL. The resulting pool represented about 10% of the final driver population., g) a pool of about 2,000 clones from the pool of normalized libraries, CN0, that makes up the tracer. The corresponding plates are R-CN0-BKW through R-CN0-BLD, R-CN0-BLG, R-CN0-BLP through R-CN0-BLR, R-CN0-BLT, R-CN0-BLW-X, R-CN0-BMB, and R-CN0-BMF through R-CN0-BML. This pool represented 5% of the final driver population. h) a pool of the 28 most abundant clones in the CN0 pool corresponding to the following addresses: bkw-a-09-0-UI, bkw-b-09-0-UI, bkw-b-11-0-UI, bkx-b-10-0-UI, bkx-d-01-0-UI , bkx-d-06-0-UI, bkx-g-08-0-UI, bkx-h-12-0-UI, bky-a-05-0-UI, bkz-a-06-0-UI, bkz-a-11-0-UI, bkz-c-06-0-UI , bkz-c-09-0-UI, bkz-d-10-0-UI, bla-a-01-0-UI, bla-a-02-0-UI, bla-f-04-0-UI, bla-g-07-0-UI, bla-g-12-0-UI , blb-a-12-0-UI, blb-f-02-0-UI, blc-a-11-0-UI, blc-e-95-0-UI, bld-1-08-0-UI, bld-f-02-0-UI, blq-h-04-0-UI , blr-a-05-0-UI, blt-f-08-0-UI. This pool represented 5% of the final driver population. i) One abundant CN0 clone (corresponding to the address bkz-a-11-0-UI) was digested with Not I and Eco RI and the resulting insert was gel purified. This purified insert was added directly to the driver so that it represented 5% of the final driver population.
TAG_LIB=UI-R-CN1
TAG_TISSUE=fundus
TAG_SEQ=TTCGG"

BASE COUNT 160 a 130 c 124 g 198 t
ORIGIN

Query Match 26.1%; Score 124.4; DB 10; Length 612;
Best Local Similarity 58.3%; Pred. No. 2.1e-26;
Matches 218; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

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Qy      89 tcatagcagtcccgaggaaggaccgtatgtctccagtcactattgccttaatctcatgcc 148
           | | ||| || ||    |   || |  |     | |||| | ||  ||| ||  ||||
Db     579 TGACAGCGGTTCCTGCTAGCAACAGCGTCAAATCTGTCATTCTTAGCTTGATAGCATGTA 520

Qy     149 gacatgtggagacccttgagaaagacagagggaaccccatctacctgggcctgaatggac 208
           || |  ||||   ||  ||  || | |  || || |   | |.||||||  | || ||
Db     519 GAGACATGGAATTCCAAGATGAAAAGAAGGGTAATCTAGTTTTCCTGGGAATCAAAGGCA 460

Qy     209 tcaatctctgcctgatgtgtgctaaagtcggggaccagcccacactgcagctgaaggaaa 268
             | |||||||||  | ||||||  |  ||| || | | || ||  |||||||  |||||
Db     459 GAAGTCTCTGCCTCTTCTGTGCTGAGATCGAGGGCAAACCGACTTTGCAGCTTAAGGATG 400

Qy     269 aggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctaccaca 328
             || || ||||||||||||||  |     |  |  |||  ||||||||||||||||
Db     399 TAGACATCATGGATTTGTACAATGAGAAAAAAGCACAGAAAGCCTTTCTCTTCTACCATG 340

Qy     329 gccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatcgctg 388
           ||      ||    |  ||   |||  |||| ||    |  |||||||||| || ||
Db     339 GCATAGAGGGATCTACTTCTGTCTTTCAGTCAGTCTTGTATCCTGGCTGGTTTATAGCCA 280

Qy     389 tcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaacacta 448
           |   ||   || | |     |  |||| |||||  || ||   |||  |||| || |  |
Db     279 CCTCTTCCACAGCAAGACAAACAATCATTCTTACACAGGAGAGGGGTGAAGCTAATAACA 220

Qy     449 ctgactttgggtta 462
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Db     219 CTAACTTCTACTTA 206
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RESULT 4

AW368430/c
LOCUS AW368430 539 bp mRNA linear EST 04-FEB-2000
DEFINITION CM3-HT0192-071099-022-e12 HT0192 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW368430
VERSION AW368430.1 GI:6873080
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 539)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM3&t2=CM3-HT0192-071099-022-e12&t3=1999-10-07&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 21
High quality sequence stop: 539.

FEATURES Location/Qualifiers
source 1. .539
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0192"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 145 a 131 c 123 g 140 t
ORIGIN

Query Match 25.6%; Score 122; DB 9; Length 539;
Best Local Similarity 71.9%; Pred. No. 1e-25;
Matches 174; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

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Qy     226 tgtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggatataatggatttg 285
           ||||  || || || ||||||||| |||||| || ||  || | || |||||| ||
Db     536 TGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCTG 477

Qy     286 tacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcaggaac 345
           ||   |||||||||||| |||||  |||| || |||||||    | ||| ||| |||| |
Db     476 TATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACC 417

Qy     346 tccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaaggaggc 405
           |||||| | |||||||||| ||||| | |||||||||   || |  ||| |  ||| |
Db     416 TCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT---TGCCTCCTCCAAGAGAGAC 360

Qy     406 tgtcctctcatccttacccaagaactggggaaagccaacactactgactttgggttaact 465
             ||  |||| || ||   |||||| |||||  |  |||  |||| |||||  |||| |
Db     359 CAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGAATTAAAT 300

Qy     466 at 467
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Db     299 AT 298
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RESULT 5
AW361172

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LOCUS       AW361172                 555 bp    mRNA    linear   EST 04-FEB-2000
DEFINITION  RC1-CT0251-141099-012-h04 CT0251 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW361172
VERSION     AW361172.1  GI:6865822
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 555)
  AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
  TITLE     The FAPESP/LICR Human Cancer Genome Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC1&t2=RC1-CT0251-
            141099-012-h04&t3=1999-10-14&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 555.
FEATURES             Location/Qualifiers
     source          1. .555
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="CT0251"
                     /dev_stage="Adult"
                     /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT      148 a    129 c    130 g    147 t      1 others
ORIGIN
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  Query Match             25.6%;  Score 122;  DB 9;  Length 555;
  Best Local Similarity   71.9%;  Pred. No. 1e-25;
  Matches  174;  Conservative    0;  Mismatches   65;  Indels    3;  Gaps    1;

Qy     226 tgtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggatataatggatttg 285
           ||||  || || || || |||||||||| ||||||| || ||  || | || ||||||| ||
Db       4 TGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCTG 63

Qy     286 tacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcaggaac 345
           ||   |||||||||||| |||||  |||| || |||||||    | ||| ||| |||| |
Db      64 TATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACC 123

Qy     346 tccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaaggaggc 405
           |||||| | |||||||||| ||||| | |||||||||   || |  |||  |  ||| |
Db     124 TCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT---TGCCTCCTCCAAGAGAGAC 180

Qy     406 tgtcctctcatccttacccaagaactggggaaagccaacactactgactttgggttaact 465
             ||  |||| || ||   |||||| |||||  |  |||  |||| |||||  |||| |
Db     181 CAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGAATTAAAT 240

Qy     466 at 467
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Db     241 AT 242
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RESULT   6
AW368437/c
LOCUS       AW368437                 557 bp    mRNA    linear   EST 04-FEB-2000
DEFINITION  CM3-HT0192-071099-022-h06 HT0192 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW368437
VERSION     AW368437.1  GI:6873087
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 557)
  AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
  TITLE     The FAPESP/LICR Human Cancer Genome Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM3&t2=CM3-HT0192-
            071099-022-h06&t3=1999-10-07&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 43
            High quality sequence stop: 557.
FEATURES             Location/Qualifiers
     source          1. .557
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="HT0192"
                     /dev_stage="Adult"
                     /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT      149 a    130 c    130 g    147 t      1 others
ORIGIN
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  Query Match             25.6%;  Score 122;  DB 9;  Length 557;
  Best Local Similarity   71.9%;  Pred. No. 1e-25;
  Matches  174;  Conservative    0;  Mismatches   65;  Indels    3;  Gaps    1;

Qy     226 tgtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggatataatggatttg 285
           ||||  || || || || |||||||||| ||||||| || ||  || | || ||||||| ||
Db     554 TGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCTG 495

Qy     286 tacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcaggaac 345
           ||   |||||||||||| |||||  |||| || |||||||    | ||| ||| |||| |
Db     494 TATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACC 435

Qy     346 tccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaaggaggc 405
           |||||| | |||||||||| ||||| | |||||||||   || |  |||  |  ||| |
Db     434 TCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT---TGCCTCCTCCAAGAGAGAC 378

Qy     406 tgtcctctcatccttacccaagaactggggaaagccaacactactgactttgggttaact 465
             ||  |||| || ||   |||||| |||||  |  |||  |||| |||||  |||| |
Db     377 CAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGAATTAAAT 318

Qy     466 at 467
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Db     317 AT 316
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RESULT   7
AW578451/c
LOCUS       AW578451                 559 bp    mRNA    linear   EST 16-MAR-2000
DEFINITION  RC1-CT0252-030100-023-b06 CT0252 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW578451
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VERSION     AW578451.1  GI:7253500
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 559)
  AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
  TITLE     The FAPESP/LICR Human Cancer Genome Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC1&t2=RC1-CT0252-
            030100-023-b06&t3=2000-01-03&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 37
            High quality sequence stop: 559.
FEATURES             Location/Qualifiers
     source          1. .559
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="CT0252"
                     /dev_stage="Adult"
                     /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT      148 a    130 c    132 g    149 t
ORIGIN


  Query Match             25.6%;  Score 122;  DB 9;  Length 559;
  Best Local Similarity   71.9%;  Pred. No. 1.1e-25;
  Matches  174;  Conservative    0;  Mismatches   65;  Indels    3;  Gaps    1;

Qy     226 tgtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggatataatggatttg 285
           ||||  || || || || |||||||| ||||||| || ||  || | || ||||||
Db     556 TGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCTG 497

Qy     286 tacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcaggaac 345
           ||   |||||||||||| |||||  |||| || |||||||    | ||| ||| |||| |
Db     496 TATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACC 437

Qy     346 tccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaaggaggc 405
           |||||| | |||||||||| ||||| | |||||||||   || |  |||  |  ||| |
Db     436 TCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT---TGCCTCCTCCAAGAGAGAC 380

Qy     406 tgtcctctcatccttacccaagaactggggaaagccaacactactgactttgggttaact 465
             ||  |||| || ||   |||||| |||||  |  |||  |||| |||||  |||| |
Db     379 CAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGACTTAAAT 320

Qy     466 at 467
           ||
Db     319 AT 318


RESULT   8
BE695960/c
LOCUS       BE695960                555 bp    mRNA    linear   EST 11-SEP-2000
DEFINITION  RC1-CT0252-150600-028-h05 CT0252 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE695960
VERSION     BE695960.1  GI:10083120
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 555)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=RC1-CT0252-150
            600-028-h05&t3=2000-06-15&t4=1)
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            High quality sequence start: 9
            High quality sequence stop: 555.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone_lib="CT0252"
                     /dev_stage="Adult"
                     /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT      147 a    131 c    129 g    148 t
ORIGIN


  Query Match             25.4%;  Score 121;  DB 10;  Length 555;
  Best Local Similarity   71.8%;  Pred. No. 2.1e-25;
  Matches  173;  Conservative    0;  Mismatches   65;  Indels    3;  Gaps    1;

Qy     227 gtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggatataatggatttgt 286
           |||  || || || || ||||||||| ||||||| || ||  || | || |||||| |||
Db     555 GTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCTGT 496

Qy     287 acaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcaggaact 346
           |   |||||||||||| |||||  |||| || |||||||    | ||| ||| |||| ||
Db     495 ATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACCT 436

Qy     347 ccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaaggaggct 406
           ||||| | |||||||||| ||||| | |||||||||   || |  |||  |  ||| |
Db     435 CCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT---TGCCTCCTCCAAGAGAGACC 379

Qy     407 gtcctctcatccttacccaagaactggggaaagccaacactactgactttgggttaacta 466
             ||  |||| || ||   |||||| ||||| |  |||  |||| ||||| |||| ||
Db     378 AGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGAATTAAATA 319

Qy     467 t 467
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Db     318 T 318
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RESULT   9
AW361164/c
LOCUS       AW361164                436 bp    mRNA    linear   EST 04-FEB-2000
DEFINITION  RC1-CT0251-141099-012-c02 CT0251 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW361164
VERSION     AW361164.1  GI:6865814
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 436)
  AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
  TITLE     The FAPESP/LICR Human Cancer Genome Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC1&t2=RC1-CT0251-
            141099-012-c02&t3=1999-10-14&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 35
            High quality sequence stop: 436.
FEATURES             Location/Qualifiers
     source          1. .436
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                     /db_xref="taxon:9606"
                     /clone_lib="CT0251"
                     /dev_stage="Adult"
                     /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT      123 a     96 c    103 g    114 t
ORIGIN


  Query Match             25.2%;  Score 120.4;  DB 9;  Length 436;
  Best Local Similarity   71.5%;  Pred. No. 2.8e-25;
  Matches  173;  Conservative    0;  Mismatches   66;  Indels    3;  Gaps    1;

Qy     226 tgtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggatataatggatttg 285
           ||||  || || || || |||||||||| ||||||| || ||  || | || |||||| ||
Db     433 TGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCTG 374

Qy     286 tacaaccaacccgagcctgtgaagtccttttctcttctaccacagccagagtggcaggaac 345
           ||   |||||||||||| |||||  |||| || |||||||    | ||| ||| |||| |
Db     373 TATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACC 314

Qy     346 tccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaaggaggc 405
           |||||| | |||||||||||| ||||| | |||||||||   || |  |||  |  ||| |
Db     313 TCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT---TGCCTCCTCCAAGAGAGAC 257

Qy     406 tgtcctctcatccttacccaagaactggggaaagccaacactactgactttgggttaact 465
             ||  |||| || ||   |||||| |||||  |  |||  |||| |||||   ||| |
Db     256 CAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGCAGTAAAT 197

Qy     466 at 467
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Db     196 AT 195


RESULT  10
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AW853610
LOCUS       AW853610                536 bp    mRNA    linear   EST 19-MAY-2000
DEFINITION  RC1-CT0252-170200-025-c06 CT0252 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW853610
VERSION     AW853610.1  GI:7949212
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 536)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=RC1-CT0252-170
            200-025-c06&t3=2000-02-17&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 15
            High quality sequence stop: 535.
FEATURES             Location/Qualifiers
     source          1. .536
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="CT0252"
                     /dev_stage="Adult"
                     /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT      140 a    123 c    129 g    144 t
ORIGIN


  Query Match             25.2%;  Score 120.4;  DB 9;  Length 536;
  Best Local Similarity   71.5%;  Pred. No. 3.1e-25;
  Matches  173;  Conservative    0;  Mismatches   66;  Indels    3;  Gaps    1;

Qy     226 tgtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggatataatggatttg 285
           |||| || || || || |||||||| ||||||| || ||  || | || |||||| ||
Db       4 TGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCTG 63

Qy     286 tacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcaggaac 345
           ||   |||||||||||| |||||  |||| || |||||||    | ||| ||| |||| |
Db      64 TATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACC 123

Qy     346 tccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaaggaggc 405
           |||||| | |||||||||||| ||||| | |||||||||   || |  | |  |  ||| |
Db     124 TCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT---TGCCTCCACCAAGAGAGAC 180

Qy     406 tgtcctctcatccttacccaagaactggggaaagccaacactactgactttgggttaact 465
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Db     181 CAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGACTTAAAT 240
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Qy     466 at 467
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Db     241 AT 242


RESULT  11
AK009787
LOCUS       AK009787                1219 bp    mRNA    linear   HTC 19-JAN-2002
DEFINITION  Mus musculus adult male tongue cDNA, RIKEN full-length enriched
            library, clone:2310043N20:homolog to FIL1 ETA, full insert
            sequence.
ACCESSION   AK009787
VERSION     AK009787.1  GI:12844799
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA,
            clone_lib:RIKEN full-length enriched mouse cDNA library
            clone:2310043N20.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (sites)
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2  (sites)
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3  (sites)
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4  (sites)
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5  (bases 1 to 1219)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
            Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
            Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
            Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
            Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
            Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,
            Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
            Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. cDNA went
            through one round of normalization to Rot = 5.0 and subtraction to
            Rot = 25.0. Second strand cDNA was prepared with the primer adapter
            of sequence [5'
            GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved
            with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
            Host: SOLR.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="MGD:MGI:1901829"
                     /db_xref="taxon:10090"
                     /clone="2310043N20"
                     /sex="male"
                     /tissue_type="tongue"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="adult"
     CDS             78. .629
                     /note="data source:SPTR, source key:Q9UHA5, evidence:ISS
                     homolog to FIL1 ETA
                     putative"
                     /codon_start=1
                     /protein_id="BAB26505.1"
                     /db_xref="GI:12844800"
                     /translation="MMAFPPQSCVHVLPPKSIQMWEPNHNTMHGSSQSPRNYRVHDSQ
                     QMVWVLTGNTLTAVPASNNVKPVILSLIACRDTEFQDVKKGNLVFLGIKNRNLCFCCV
                     EMEGKPTLQLKEVDIMNLYKERKAQKAFLFYHGIEGSTSVFQSVLYPGWFIATSSIER
                     QTIILTHQRGKLVNTNFYIESEK"
     polyA_signal    1199. .1204
                     /note="putative"
     polyA_site      1219
                     /note="putative"
BASE COUNT      380 a    272 c    217 g    350 t
ORIGIN


  Query Match           25.2%;  Score 120;  DB 11;  Length 1219;
  Best Local Similarity   55.5%;  Pred. No. 6.2e-25;
  Matches  231;  Conservative    0;  Mismatches  185;  Indels    0;  Gaps    0;

Qy      40 agcattcaggatatcaatcatcgggtgtgggttcttcaggaccagacgctcatagcagtc 99
           ||  |||| ||     | ||   ||| ||||| ||    |   | ||  | | ||||||
Db     192 AGGGTTCATGACTCACAACAGATGGTATGGGTCCTGACTGGAAATACTTTAACAGCAGTT 251

Qy     100 ccgaggaaggaccgtatgtctccagtcactattgccttaatctcatgccgacatgtggag 159
           ||    |   ||  | |    || |||| | ||  ||| ||  |||| || |   |||
Db     252 CCTGCTAGCAACAATGTCAAGCCTGTCATTCTTAGCTTGATAGCATGTAGAGACACGGAA 311

Qy     160 acccttgagaaagacagagggaaccccatctacctgggcctgaatggactcaatctctgc 219
             ||  ||   | | | ||| || |   | | ||||||  | ||       |||||||||
Db     312 TTCCAAGATGTAAAGAAAGGTAATCTAGTTTTCCTGGGAATCAAGAACAGAAATCTCTGC 371

Qy     220 ctgatgtgtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggatataatg 279
             |   |||| | |  | | || | | || ||  |||||||  ||||||   || || |||
Db     372 TTCTGCTGTGTTGAGATGGAGGGCAAACCAACTTTGCAGCTTAAGGAAGTAGACATCATG 431

Qy     280 gatttgtacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggc 339
           ||||||||||  |     |  |    ||  ||||||| ||||| ||  ||      |||
Db     432 AATTTGTACAAAGAGAGAAAAGCACAAAAAGCCTTTCTGTTCTATCATGGCATAGAGGGC 491

Qy     340 aggaactccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaa 399
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Db    492 TCCACTTCTGTCTTTCAGTCAGTCCTCTATCCTGGCTGGTTTATAGCCACCTCTTCCATA 551

Qy    400 ggaggctgtcctctcatccttacccaagaactggggaaagccaacactactgactt 455
Db    552 GAAAGACAGACAATCATCCTCACACATCAGCGGGGTAAATTGGTTAACACTAACTT 607
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RESULT 12
BF244205
LOCUS BF244205 870 bp mRNA linear EST 14-NOV-2000
DEFINITION 601863146F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4080899 5', mRNA sequence.
ACCESSION BF244205
VERSION BF244205.1 GI:11158135
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 870)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM941 row: k column: 12
High quality sequence stop: 582.

FEATURES Location/Qualifiers
source 1. .870
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4080899"
/clone_lib="NIH_MGC_57"
/tissue_type="glioblastoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

BASE COUNT 256 a 216 c 171 g 227 t
ORIGIN

Query Match 23.7%; Score 113.2; DB 10; Length 870;
Best Local Similarity 58.2%; Pred. No. 5.7e-23;
Matches 199; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

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Qy    136 ttaatctcatgccgacatgtggagacccttgagaaagacagagggaaccccatctacctg 195
Db      5 TTAATAGCCTGTAGAGACACAGAATTCAGTGACAAGGAAAAGGGTAATATGGTTTACCTG 64

Qy    196 ggcctgaatggactcaatctctgcctgatgtgtgctaaagtcggggaccagcccacactg 255
Db     65 GGAATCAAGGGAAAAGATCTCTGTCTCTTCTGTGCAGAAATTCAGGGCAAGCCTACTTTG 124

Qy    256 cagctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtccttt 315
Db    125 CAGCTTAAGGAAAAAAATATCATGGACCTGTATGTGGAGAAGAAAGCACAGAAGCCCTTT 184

Qy    316 ctcttctaccacagccagagtggcaggaactccaccttcgagtctgtggctttccctggc 375
Db    185 CTCTTTTTCCACAATAAAGAAGGCTCCACTTCTGTCTTTCAGTCAGTCTCTTACCCTGGC 244

Qy    376 tggttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaagaactgggg 435
Db    245 TGGTTCATAGCCACCTCCACCACATCAGGACAGCCCATCTTTCTCACCAAGGAGAGAGGC 304

Qy    436 aaagccaacactactgactttgggttaactatgctgttttaa 477
Db    305 ATAACTAATAACACTAACTTCTACTTAGATTCTGTGGAATAA 346
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RESULT 13
AW753217/c
LOCUS AW753217 434 bp mRNA linear EST 28-APR-2000
DEFINITION RC1-CT0251-081099-011-a04 CT0251 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW753217
VERSION AW753217.1 GI:7668149
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 434)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC1&t2=RC1-CT0251-081099-011-a04&t3=1999-10-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 42
High quality sequence stop: 67.

FEATURES Location/Qualifiers
source 1. .434
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0251"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 125 a 94 c 101 g 114 t
ORIGIN

Query Match 23.3%; Score 111; DB 9; Length 434;
Best Local Similarity 71.6%; Pred. No. 1.8e-22;
Matches 174; Conservative 0; Mismatches 65; Indels 4; Gaps 2;

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Qy    226 tgtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggata-taatggattt 284
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Db    431 TGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATTCATGGATCT 372

Qy    285 gtacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcaggaa 344
          |||   |||||||||||| |||||  |||| || |||||||    | ||| ||| ||||
Db    371 GTATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGAC 312

Qy    345 ctccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaaggagg 404
          ||||||| | |||||||||||| ||||| | |||||||||   || |  |||  |  |||
Db    311 CTCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT---TGCCTCCTCCAAGAGAGA 255

Qy    405 ctgtcctctcatccttacccaagaactggggaaagccaacactactgactttgggttaac 464
          |   ||  |||| || ||   |||||| |||||  |  |||  |||| |||||  ||||
Db    254 CCAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGAATTAAA 195

Qy    465 tat 467
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Db    194 TAT 192
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RESULT 14
AW361245
LOCUS AW361245 560 bp mRNA linear EST 04-FEB-2000
DEFINITION RC1-CT0252-181299-022-e08 CT0252 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW361245
VERSION AW361245.1 GI:6865895
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 560)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC1&t2=RC1-CT0252-181299-022-e08&t3=1999-12-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 13
High quality sequence stop: 551.
FEATURES Location/Qualifiers
source 1. .560
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0252"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 143 a 131 c 141 g 145 t
ORIGIN

Query Match 20.4%; Score 97.4; DB 9; Length 560;
Best Local Similarity 65.4%; Pred. No. 2.5e-18;
Matches 159; Conservative 0; Mismatches 81; Indels 3; Gaps 1;

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Qy    225 gtgtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggatataatggattt 284
          || ||  | |    ||  | |   |    ||||||| |  ||  ||   || |||||| |
```

```
Db     21 GTATGTGAGAAGGTGGAGCAAAGGCCATATGCAGCTCAGAGAGCAGACGATCATGGATCT 80

Qy    285 gtacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcaggaa 344
          |||   |  | |||||||| |||||  |||| ||  ||||||    | ||| ||| ||||
Db     81 GTATGGCACAACCGAGCCCGTGAAACCCTTCCTTGTCTACCGGGCCAAGACTGGTAGGAC 140

Qy    345 ctccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaaggagg 404
          ||||||| | |||||||||||| ||||| | ||||||||||||   |  |||  |  |||
Db    141 CTCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCATCGC---CTCCTCCAAGAGAGA 197

Qy    405 ctgtcctctcatccttacccaagaactggggaaagccaacactactgactttgggttaac 464
          |   ||  |||| || ||   |||||| |||||  |  |||  |||| |||||  ||||
Db    198 CCAGCCCATCATTCTGACTTCAGAACTCGGGAAGTCATACAACACTGCCTTTGAATTAAA 257

Qy    465 tat 467
          |||
Db    258 TAT 260
```

RESULT 15
BG245180
LOCUS BG245180 1020 bp mRNA linear EST 13-FEB-2001
DEFINITION 602357579F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4486098 5', mRNA sequence.
ACCESSION BG245180
VERSION BG245180.1 GI:12754995
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1020)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10328 row: n column: 19
High quality sequence start: 4
High quality sequence stop: 653.
FEATURES Location/Qualifiers
source 1. .1020
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4486098"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT 282 a 269 c 268 g 201 t
ORIGIN

Query Match 15.7%; Score 74.8; DB 10; Length 1020;
Best Local Similarity 55.9%; Pred. No. 2e-11;
Matches 142; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

```
Qy    188 tctacctgggcctgaatggactcaatctctgcctgatgtgtgctaaagtcggggaccagc 247
          | | | ||||| |  | ||   ||| || ||||||   ||||| ||    || ||  |
Db    288 TGTTCTTGGGCATCCACGGGGGCAAGCTGTGCCTGTCTTGTGCCAAGTCTGGAGATGATA 347
```

```
Qy     248 ccacactgcagctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtga 307
           ||  || |||||| |||||    | || |  ||| ||  |||  |    ||    |  |
Db     348 TCAAGCTCCAGCTGGAGGAAGTTAACATCACTGATCTGAGCAAGAACAAAGAAGAAGACA 407

Qy     308 agtcctttctcttctaccacagccagagtggcaggaactccaccttcgagtctgtggctt 367
           ||  ||||  ||||  || |    |||  |||   | | ||| ||| ||||| |  || |
Db     408 AGCGCTTTACCTTCATCCGCTCTGAGAAAGGCCCCACCACCAGCTTTGAGTCAGCTGCCT 467

Qy     368 tccctggctggttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaag 427
             || || |||||| ||      |     || |  | | ||||| | | ||| ||| |
Db     468 GTCCAGGATGGTTCCTCTGCACAACACTAGAGGCTGACCGTCCTGTGAGCCTCACCAACA 527

Qy     428 aactggggaaagcc 441
           || ||   |  ||
Db     528 CACCGGAAGAGCCC 541


Search completed: June 21, 2002, 11:09:01
Job time: 17649 sec
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 20, 2002, 15:03:07 ; Search time 73.84 Seconds
(without alignments)
237.671 Million cell updates/sec

Title: US-09-763-498-8
Perfect score: 830
Sequence: 1 MEKALKIDTPQQGSIQDINH.....ILTQELGKANTTDFGLTMLF 158

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*
1: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:*
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11: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT:*
12: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
13: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:*
14: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*
15: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1994.DAT:*
16: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
17: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT:*
18: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1997.DAT:*
19: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	830	100.0	158	21	AAY70217	Human Interleukin-
2	826	99.5	158	21	AAY70218	Human Interleukin-
3	802	96.6	273	22	AAE03417	Human interleukin-
4	646	77.8	130	22	AAB85001	Human interleukin-
5	466.5	56.2	169	19	AAW63136	Interleukin-1 rece
6	466.5	56.2	169	20	AAY24043	A human SPOIL-I pr
7	466.5	56.2	169	20	AAY24395	Human interleukin-
8	466.5	56.2	169	22	AAE06656	Human interleukin-
9	466.5	56.2	169	22	AAB83008	Human IL-1ra prote
10	466.5	56.2	173	22	AAU16937	Human novel secret
11	466.5	56.2	208	20	AAY24044	A human SPOIL-II p
12	463	55.8	157	22	AAE06662	Mouse interleukin-
13	463	55.8	160	19	AAW86286	Rodent interleukin
14	463	55.8	160	20	AAY24049	Amino acid sequenc
15	459.5	55.4	172	22	AAU17010	Human novel secret
16	459.5	55.4	172	22	AAE09702	Human gene 13 enco
17	390	47.0	170	22	AAB85000	Human interleukin-
18	385	46.4	157	22	AAE04299	Human Interleukin-
19	385	46.4	157	22	AAB50444	Human IL-1 eta. H
20	371	44.7	70	21	AAY70216	Partial human Inte
21	367.5	44.3	134	21	AAB18924	A novel polypeptid
22	367.5	44.3	134	21	AAY96935	Human IL-1 recepto
23	244.5	29.5	98	20	AAY24040	Amino acid sequenc
24	239	28.8	72	19	AAW86285	Rodent interleukin
25	213	25.7	218	21	AAY71084	Human zil1a4-E200D
26	210	25.3	176	22	AAB48081	Human extracellula
27	209	25.2	163	21	AAY97069	Human IL-1 recepto
28	209	25.2	167	21	AAY96932	Human IL-1 recepto
29	209	25.2	192	21	AAY95297	Human interleukin-
30	209	25.2	193	21	AAY96934	Processed human IL
31	209	25.2	193	22	AAB87596	Human PRO3435. Ho
32	209	25.2	197	21	AAY95300	Human interleukin-
33	209	25.2	198	22	AAB85138	Interleukin-1 homo
34	209	25.2	203	21	AAY96933	Human IL-1R1a fuse
35	209	25.2	207	21	AAY96938	Human IL-1 recepto
36	209	25.2	218	21	AAB28266	Human interleukin-
37	209	25.2	218	21	AAY96940	Human IL-1 recepto
38	209	25.2	218	21	AAY70927	Human zil1a4 prote
39	209	25.2	218	21	AAY95299	Human interleukin-
40	209	25.2	218	21	AAY91885	Primate interleuki
41	209	25.2	218	22	AAG68116	Human interleukin
42	209	25.2	218	22	AAB85136	Interleukin-1 homo
43	209	25.2	218	22	AAB47186	IL-1 related polyp
44	207	24.9	218	21	AAY70933	Human zil1a4-E200K
45	204	24.6	218	21	AAY91884	Primate interleuki

ALIGNMENTS

RESULT 1
AAY70217
ID AAY70217 standard; Protein; 158 AA.
XX
AC AAY70217;
XX
DT 06-JUN-2000 (first entry)
XX
DE Human Interleukin-1 epsilon protein.
XX
KW Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;
KW gene mapping; immune system; treatment; inflammatory disease;
KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
KW psoriasis; human.
XX
OS Homo sapiens.
XX
PN WO200011174-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US18771.
XX
PR 21-AUG-1998; 98US-0097413.
PR 31-AUG-1998; 98US-0098595.
PR 11-SEP-1998; 98US-0099974.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Sims JE, Smith DE;
XX
DR WPI; 2000-237653/20.
DR N-PSDB; AAZ51247.

XX
PT Nucleotide sequences encoding human interleukin -1 epsilon, useful to
PT treat inflammatory and immune system-related diseases such as
PT rheumatoid arthritis and inflammatory bowel disease -
XX
PS Claim 1b; Fig 2; 76pp; English.
XX
CC The present sequence is that of human Interleukin-1 (IL-1) epsilon
CC protein. IL-1 epsilon gene is mapped to chromosome 2q and is mainly
CC expressed in spleen, lymph node, thymus, tonsil and leucocyte
CC tissues. IL-1 epsilon is a cytokine, with antiinflammatory,
CC immunosuppressant, antirheumatic, antiarthritic and antipsoriatic
CC activity. It can be used in the treatment of inflammatory or autoimmune
CC diseases such as rheumatoid arthritis, inflammatory bowel disease and
CC psoriasis. The DNA sequence can be used in chromosome identification,
CC gene mapping and study of immune system.
XX
SQ Sequence 158 AA;

Query Match 100.0%; Score 830; DB 21; Length 158;
Best Local Similarity 100.0%; Pred. No. 1e-80;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MEKALKIDTPQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 mekalkidtpqqgsiqdinhrvwvlqdqtliavprkdrmspvtialiscrhvetlekdrg 60

Qy     61 NPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFES 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 npiylglnglnlclmcakvgdqptlqlkekdimdlynqpepvksflfyhsqsgrnstfes 120

Qy    121 VAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTMLF 158
          |||||||||||||||||||||||||||||||||||||||
Db    121 vafpgwfiavsseggcpliltqelgkanttdfgltmlf 158
```

RESULT 2
AAY70218
ID AAY70218 standard; Protein; 158 AA.
XX
AC AAY70218;
XX
DT 06-JUN-2000 (first entry)
XX
DE Human Interleukin-1 epsilon polymorphic variant.
XX
KW Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;
KW gene mapping; immune system; treatment; inflammatory disease;
KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
KW psoriasis; polymorphic variant; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 12
FT /note= "Wild type Gln replaced with Arg"
XX
PN WO200011174-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US18771.
XX
PR 21-AUG-1998; 98US-0097413.
PR 31-AUG-1998; 98US-0098595.
PR 11-SEP-1998; 98US-0099974.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Sims JE, Smith DE;
XX
DR WPI; 2000-237653/20.
DR N-PSDB; AAZ51248.
XX
PT Nucleotide sequences encoding human interleukin -1 epsilon, useful to
PT treat inflammatory and immune system-related diseases such as
PT rheumatoid arthritis and inflammatory bowel disease -
XX
PS Claim 1b; Fig 2; 76pp; English.
XX
CC The present protein sequence is that of human Interleukin-1 (IL-1)
CC epsilon polymorphic variant. IL-1 epsilon gene is mapped to chromosome 2q
CC and is mainly expressed in spleen, lymph node, thymus, tonsil and
CC leucocyte tissues. IL-1 epsilon is a cytokine, with antiinflammatory,
CC immunosuppressant, antirheumatic, antiarthritic and antipsoriatic
CC activity. It can be used in the treatment of inflammatory or autoimmune
CC diseases such as rheumatoid arthritis, inflammatory bowel disease and
CC psoriasis. The DNA sequence can be used in chromosome identification,
CC gene mapping and study of immune system.
XX
SQ Sequence 158 AA;

Query Match 99.5%; Score 826; DB 21; Length 158;
Best Local Similarity 99.4%; Pred. No. 2.7e-80;
Matches 157; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEKALKIDTPQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRG 60
          ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 mekalkidtpqrgsiqdinhrvwvlqdqtliavprkdrmspvtialiscrhvetlekdrg 60

Qy     61 NPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFES 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 npiylglnglnlclmcakvgdqptlqlkekdimdlynqpepvksflfyhsqsgrnstfes 120

Qy    121 VAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTMLF 158
          |||||||||||||||||||||||||||||||||||||||
Db    121 vafpgwfiavsseggcpliltqelgkanttdfgltmlf 158
```

RESULT 3
AAE03417
ID AAE03417 standard; Protein; 273 AA.
XX
AC AAE03417;
XX
DT 03-AUG-2001 (first entry)
XX
DE Human interleukin-1 receptor antagonist-like (IL-1ra-L).
XX
KW Human; interleukin-1 receptor antagonist-like protein; IL-1ra-L; therapy;
KW rheumatoid arthritis; psoriatic arthritis; inflammatory arthritis; lupus;
KW joint disease; autoimmune disease; multiple sclerosis; diabetes; obesity;
KW transplant rejection; graft versus host disease; strain; sprain; leprosy;
KW cartilage damage; hepatitis; human immunodeficiency virus; HIV; anorexia;
KW clostridium-associated diarrhoea; pulmonary tuberculosis; septic shock;
KW myopathy; Alzheimer's disease; Parkinson's disease; memory disorder;
KW acute respiratory disease syndrome; cystic fibrosis; asthma; psoriasis;
KW eczema; glomerulonephritis; osteoporosis; Paget's disease; lymphoma;
KW hypercalcaemia; haemorrhage; ischaemia; atherosclerosis; leukaemia;
KW infertility; endometriosis; retinal neuropathy; acute pancreatitis;
KW Kawasaki's disease; cancer.
XX
OS Homo sapiens.
XX
PN WO200141792-A1.
XX
PD 14-JUN-2001.
XX
PF 04-DEC-2000; 2000WO-US32891.
XX
PR 10-DEC-1999; 99US-0170105.
PR 28-NOV-2000; 2000US-0724859.
XX

PA (AMGE-) AMGEN INC.
XX
PI Calzone FJ, Luethy R, Boedigheimer MJ, Zhu J, Chung Y, Jing S;
XX
DR WPI; 2001-381495/40.
DR N-PSDB; AAD06911.
XX
PT Novel Interleukin-1 Receptor Antagonist-Like nucleic acid molecule, the
PT polypeptide encoded by the nucleic acid is useful diagnosis, treatment,
PT and prevention of diseases such as arthritis, diabetes, transplant
PT rejection -
XX
PS Claim 13; Fig 1A; 127pp; English.
XX
CC The present sequence is human interleukin-1 receptor antagonist-like
CC (IL-1ra-L) protein. IL-1ra-L is useful for treating, preventing or
CC ameliorating IL-1ra-L polypeptide-related disease, condition or disorder
CC which include rheumatoid arthritis, psoriatic arthritis, inflammatory
CC arthritis, osteoarthritis, autoimmune disease, multiple sclerosis,
CC lupus, diabetes, transplant rejection, inflammatory joint disease, graft
CC versus host disease and inflammatory conditions resulting from strain,
CC sprain, cartilage damage, trauma, orthopaedic surgery, hepatitis, human
CC immunodeficiency virus (HIV) infection, clostridium-associated
CC diarrhoea, leprosy, pulmonary tuberculosis, septic shock, obesity,
CC anorexia, myopathies, Alzheimer's disease, Parkinson's disease, memory
CC disorders, acute respiratory disease syndrome, cystic fibrosis, asthma,
CC psoriasis, eczema, acute and chronic glomerulonephritis, osteoporosis,
CC Paget's disease, hypercalcaemia, haemorrhage, ischaemia, atherosclerosis,
CC lymphomas, lung and breast cancer, leukaemias, infertility,
CC endometriosis, retinal degeneration, retinal neuropathy, acute
CC pancreatitis and Kawasaki's disease.
XX
SQ Sequence 273 AA;

Query Match 96.6%; Score 802; DB 22; Length 273;
Best Local Similarity 98.7%; Pred. No. 2e-77;
Matches 152; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy       5 LKIDTPQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIY 64
           |||||||:|||||||||||||||||||||||||||||||||||||||||||||||:|||
Db     120 lkidtpqrgsiqdinhrvwvlqdqtliavprkdrmspvtialiscrhvetlekdrgdpiy 179

Qy      65 LGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFP 124
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     180 lglnglnlclmcakvgdqptlqlkekdimdlynqpepvksflfyhsqsgrnstfesvafp 239

Qy     125 GWFIAVSSEGGCPLILTQELGKANTTDFGLTMLF 158
           ||||||||||||||||||||||||||||||||
Db     240 gwfiavsseggcpliltqelgkanttdfgltmlf 273
```

RESULT 4
AAB85001
ID AAB85001 standard; Protein; 130 AA.
XX
AC AAB85001;
XX
DT 06-AUG-2001 (first entry)
XX
DE Human interleukin-1 receptor antagonist (NOVINTRA C) polypeptide.
XX
KW NOVX; transmembrane protein; NOVTRAN; neuromedin peptide; NOVNEUR;
KW gonadotropin-like protein; NOVGON; interleukin-1; NOVINTRA; human;
KW cytostatic; neuroprotective; reproductive; antiinflammatory; cancer;
KW antibacterial; cerebroprotective; antidiabetic; antiarthritic;
KW antiasthmatic; antiallergic.
XX
OS Homo sapiens.
XX
PN WO200140291-A2.
XX
PD 07-JUN-2001.
XX
PF 06-DEC-2000; 2000WO-US33029.
XX
PR 06-DEC-1999; 99US-0169056.
PR 09-DEC-1999; 99US-0169866.
PR 09-DEC-1999; 99US-0169886.
PR 10-DEC-1999; 99US-0170252.
PR 12-JAN-2000; 2000US-0175740.
PR 05-DEC-2000; 2000US-0170252.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Burgess CE, Prayaga SK, Shimkets RA, Rastelli L, Zerhusen BD;
PI Mezes PS;
XX
DR WPI; 2001-374790/39.
DR N-PSDB; AAF83870.
XX
PT Novel isolated human transmembrane, neuromedin peptide
PT gonadotropin-like protein and interleukin-1 receptor antagonist
PT proteins, useful for treating cancer, immune response disorder,
PT metabolic function disorders -
XX
PS Claim 53; Fig 15B; 138pp; English.
XX
CC The invention provides novel polypeptides (NOVX) selected from human
CC transmembrane protein (NOVTRAN), neuromedin peptide (NOVNEUR),
CC gonadotropin-like protein (NOVGON) and two interleukin-1 receptor
CC antagonist proteins (NOVINTRA A and B). The invention also provides
CC methods in which a NOVX polypeptide, polynucleotide and antibody are
CC used in the detection, prevention and treatment of a broad range of
CC pathological states. NOVTRAN can be used to treat is a cell signaling
CC disorder such as cancer, immune response disorder, hematopoietic
CC disorder, neurodegenerative disorder. NOVNEUR can be used to treat
CC endocrine disorder, muscle disorder, neurologic disorder, cancers of
CC central nervous system, breast, colon, ovary, kidney, prostate and
CC thyroid. NOVGON can be used to treat reproductive development disorder,
CC metabolic function disorder and melanoma. NOVINTRA A and B can be used
CC to treat bone metabolism or structure disorder, inflammatory response
CC disorder, immune regulation disorder, septic shock, stroke, diabetes,
CC arthritis and cancer. The present sequence represents the NOVINTRA C
CC polypeptide.
XX
SQ Sequence 130 AA;

Query Match 77.8%; Score 646; DB 22; Length 130;
Best Local Similarity 95.5%; Pred. No. 3.6e-61;
Matches 126; Conservative 1; Mismatches 1; Indels 4; Gaps 2;

```
Qy      17 DINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNGLNLCLMC 76
           |||||||||||||||||||  : ||||||||||||||||||||||||||||||||||||
Db       1 dinhrvwvlqdqtliavprk--vfpvtialiscrhvetlekdrgnpiylglnglnlclmc 58

Qy      77 AKVGDQPTLQLK--EKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEG 134
           ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db      59 akvgdqptlqlklqekdimdlynqpepvksflfyhsqsgrnstfesvafpgwfiavsseg 118

Qy     135 GCPLILTQELGK 146
           ||||||||||||
Db     119 gcpliltqelgk 130
```

RESULT 5
AAW63136
ID AAW63136 standard; Protein; 169 AA.
XX
AC AAW63136;
XX
DT 14-OCT-1998 (first entry)
XX
DE Interleukin-1 receptor antagonist beta (IL-1ra-beta).
XX

KW Interleukin-1 receptor antagonist beta; IL-1ra-beta; IL-1 alpha;
KW IL-1 beta; inflammatory response; treatment; inflammation; septicaemia;
KW cancer; anaemia; arthritis; inflammatory bowel disease;
KW graft vs. host rejection; autoimmunity; stroke; cardiac ischaemia;
KW acute respiratory disease syndrome; psoriasis; restenosis;
KW traumatic brain injury; acquired immune deficiency syndrome;
KW cachexia.
XX
OS Homo sapiens.
XX
PN EP855404-A1.
XX
PD 29-JUL-1998.
XX
PF 27-JAN-1998; 98EP-0300572.
XX
PR 28-JAN-1997; 97US-0790032.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Young PR;
XX
DR WPI; 1998-389778/34.
DR N-PSDB; AAV42659.
XX
PT New nucleic acid encoding human interleukin-1 receptor antagonist
PT beta polypeptides - and related expression systems, transformed
PT cells, proteins, antibodies, agonists and antagonists, useful for
PT treatment, prevention and diagnosis of inflammation, septicaemia,
PT cancer etc
XX
PS Claim 13; Fig 2; 20pp; English.
XX
CC The present sequence represents human Interleukin-1 receptor antagonist
CC beta (IL-ra-beta). IL-1 alpha and IL-1 beta play key roles in
CC inflammatory responses, and are produced as zymogens which are cleaved
CC upon secretion to yield mature carboxyl terminal 17 kD fragments.
CC IL-1ra-beta polypeptides and polynucleotides are useful in treatment of
CC chronic and acute inflammation, septicaemia, cancer, anaemia, arthritis,
CC inflammatory bowel disease, graft vs. host rejection, autoimmunity,
CC stroke, cardiac ischaemia, acute respiratory disease syndrome (ARDS),
CC psoriasis, restenosis, traumatic brain injury, acquired immune
CC deficiency syndrome (AIDS) and cachexia. These conditions (or
CC susceptibility to them) may be diagnosed by detecting mutations in the
CC IL-1ra-beta coding sequence analysing a sample for presence or amount
CC of IL-1ra-beta.
XX
SQ Sequence 169 AA;

```
  Query Match             56.2%;  Score 466.5;  DB 19;  Length 169;
  Best Local Similarity   59.9%;  Pred. No. 7.4e-42;
  Matches   88;  Conservative   24;  Mismatches   34;  Indels    1;  Gaps    1;

Qy      10 PQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNG 69
           |  |:| |:| :|| || | |:|||| | ::|||:|:|:|:: | ||: ||:|||||:
Db      22 pitgtindlnqqvwtlqgqnlvavprsdsvtpvtvavitckypealeqgrgdpiylgiqn 81

Qy      70 LNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIA 129
             :|| | |||:||||||||: ||||| |||||| |||| :::|| || |||||| ||||
Db      82 pemclycekvgeqptlqlkeqkimdlygqpepvkpflfyraktgrtstlesvafpdwfia 141

Qy     130 VSSEGGCPLILTQELGKANTTDFGLTM 156
            ||:   |:||| ||||:  | | | :
Db     142 -sskrdqpiiltselgksyntafelni 167
```

RESULT 6
AAY24043
ID AAY24043 standard; Protein; 169 AA.
XX
AC AAY24043;
XX

DT 30-SEP-1999 (first entry)
XX
DE A human SPOIL-I protein (also known as hTANGO 080-I).
XX
KW SPOIL-I; interleukin-1 receptor antagonist; IL-1ra; modulating agent;
KW bone metabolism disorder; proinflammatory disorder; immune disorder;
KW inflammatory disease; septic shock; stroke; diabetes; arthritis;
KW intercolitis; pneumonitis; epithelial cell; skin disease;
KW proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;
KW epithelial cancer; squamous cell carcinoma; bone resorption disorder;
KW osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;
KW osteogenesis imperfecta; fibrous displasia; hypophosphatasia;
KW bone sarcoma; myeloma bone disorder; osteolytic bone lesion;
KW hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;
KW bone fracture; hTANGO 80-I.
XX
OS Homo sapiens.
XX
PN WO9937662-A1.
XX
PD 29-JUL-1999.
XX
PF 26-JAN-1999; 99WO-US01575.
XX
PR 27-JAN-1998; 98US-0013810.
XX
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI Busfield SJ;
XX
DR WPI; 1999-458675/38.
DR N-PSDB; AAX86458.
XX
PT New isolated SPOIL proteins, used to develop products for treating,
PT e.g. inflammatory and immune disorders
XX
PS Example 1; Fig 4A-B; 126pp; English.
XX
CC The present sequence represents a SPOIL-I protein. SPOIL proteins have
CC homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.
CC The SPOIL proteins are used as modulating agents in regulating a variety
CC of cellular processes. The products can be used for treating disorders
CC characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone
CC metabolism disorder, a proinflammatory disorder or an immune disorder.
CC They can be used for treating e.g. inflammatory diseases and disorders
CC e.g. inflammation, septic shock, stroke, diabetes, arthritis,
CC intercolitis and pneumonitis, epithelial cell and/or skin diseases and
CC disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma
CC and Kaposi's sarcoma and other epithelial cancers including squamous cell
CC carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and
CC bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's
CC disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,
CC fibrous displasia, hypophosphatasia, bone sarcoma, myeloma bone disorder
CC (e.g. osteolytic bone lesions) and hypercalcemia. SPOIL molecules and
CC SPOIL modulators are useful for regulation of bone mass (e.g. increase in
CC bone mass and/or inhibit bone loss), management of bone fragility (e.g.
CC decrease bone fragility); and prevention and/or treatment of bone pain,
CC bone deformities and/or bone fractures. The products can also be used for
CC detection, diagnosis and screening assays.
XX
SQ Sequence 169 AA;

```
  Query Match             56.2%;  Score 466.5;  DB 20;  Length 169;
  Best Local Similarity   59.9%;  Pred. No. 7.4e-42;
  Matches   88;  Conservative   24;  Mismatches   34;  Indels    1;  Gaps    1;

Qy      10 PQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNG 69
           |  |:| |:| :|| || | |:|||| | ::|||:|:|:|:: | ||: ||:|||||:
Db      22 pitgtindlnqqvwtlqgqnlvavprsdsvtpvtvavitckypealeqgrgdpiylgiqn 81

Qy      70 LNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIA 129
             :|| | |||:||||||||: ||||| |||||| |||| :::|| || |||||| ||||
```

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Db      82 pemclycekvgeqptlqlkeqkimdlygqpepvkpflfyraktgrtstlesvafpdwfia 141

Qy     130 VSSEGGCPLILTQELGKANTTDFGLTM 156
           ||:   |:||| |||||:  | | | :
Db     142 -sskrdqpiiltselgksyntafelni 167


RESULT   7
AAY24395
ID   AAY24395 standard; Protein; 169 AA.
XX
AC   AAY24395;
XX
DT   20-SEP-1999  (first entry)
XX
DE   Human interleukin-1 receptor antagonist beta.
XX
KW   Human; interleukin-1 receptor antagonist beta; IL-1RA beta; septicemia;
KW   chronic inflammation; acute inflammation; arthritis; autoimmunity;
KW   inflammatory bowel disease; graft vs. host disease; stroke; psoriasis;
KW   cardiac ischaemia; acute respiratory disease syndrome; ARDS; restenosis;
KW   traumatic brain injury; AIDS; cachexia; allergy; parasite infection;
KW   allergic rhinitis; allergic asthma; atopic dermatitis; gene therapy;
KW   allergic inflammatory disease; delayed hypersensitivity; vaccine.
XX
OS   Homo sapiens.
XX
PN   WO9936541-A1.
XX
PD   22-JUL-1999.
XX
PF   14-JAN-1999;   99WO-US00847.
XX
PR   29-APR-1998;   98US-0069619.
PR   14-JAN-1998;   98US-0007464.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Marshall L,  Young PR;
XX
DR   WPI; 1999-430615/36.
DR   N-PSDB; AAX90135.
XX
PT   New interleukin-1 receptor antagonist beta, useful for treating
PT   inflammation and autoimmune diseases
XX
PS   Claim 15; Fig 1; 34pp; English.
XX
CC   The present sequence represents human interleukin-1 receptor antagonist
CC   beta (IL-1RA beta). IL-1RA beta polypeptides and polynucleotides are
CC   useful for diagnosing diseases (or susceptibility to diseases) related
CC   to the expression or activity of IL-1RA beta, by determining mutations
CC   in the IL-1RA beta nucleic acid sequences and/or analysing for the
CC   presence or amount of IL-1RA beta polypeptide. IL-1RA beta polypeptides
CC   are also useful for screening for compounds which affect activity of the
CC   protein. These can be used in treatment to inhibit (antagonist) or
CC   enhance (agonist) IL-1RA beta activity, in addition to direct
CC   administration of IL-1RA beta polypeptides to treat conditions, or
CC   direct administration of antisense sequences to prevent expression.
CC   IL-1RA beta polypeptides (administered directly, in a vector i.e. gene
CC   therapy, and as a vaccine) and antibodies induce an immune response to
CC   immunise and prevent disease. Diseases diagnosed, prevented or treated
CC   include chronic and acute inflammation, septicemia, arthritis,
CC   inflammatory bowel disease, graft vs. host disease, autoimmunity,
CC   stroke, cardiac ischaemia, acute respiratory disease syndrome (ARDS),
CC   psoriasis, restenosis, traumatic brain injury, AIDS, cachexia, allergy,
CC   parasite infection, allergic rhinitis, allergic asthma, atopic
CC   dermatitis, allergic inflammatory diseases and delayed hypersensitivity.
XX
SQ   Sequence   169 AA;

  Query Match          56.2%;  Score 466.5;  DB 20;  Length 169;
  Best Local Similarity   59.9%;  Pred. No. 7.4e-42;
  Matches   88;  Conservative   24;  Mismatches   34;  Indels    1;  Gaps    1;

Qy      10 PQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNG 69
           |  |:| |:| :|| || | |:|||| | ::|||:|:|:|:: | ||: ||:|||||:
Db      22 pitgtindlnqqvwtlqgqnlvavprsdsvtpvtvavitckypealeqgrgdpiylgiqn 81

Qy      70 LNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIA 129
             :|| | |||:|||||||||: ||||| |||||| |||| :::|| || |||||| ||||
Db      82 pemclycekvgeqptlqlkeqkimdlygqpepvkpflfyraktgrtstlesvafpdwfia 141

Qy     130 VSSEGGCPLILTQELGKANTTDFGLTM 156
           ||:   |:||| |||||:  | | | :
Db     142 -sskrdqpiiltselgksyntafelni 167


RESULT   8
AAE06656
ID   AAE06656 standard; Protein; 169 AA.
XX
AC   AAE06656;
XX
DT   16-OCT-2001  (first entry)
XX
DE   Human interleukin-1epsilon (IL-1epsilon) protein.
XX
KW   Human; interleukin-1epsilon; IL-1epsilon; virucide; hepatotropic; fever;
KW   immunological disorder; tumour; inflammatory disorder; hypoglycaemia;
KW   autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;
KW   psoriasis; viral infection; allergy; cytokine; HIV; drug screening.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Binding-site    17..20
FT                   /note= "IL-1 receptor beta subunit binding region"
FT   Binding-site    23
FT                   /note= "IL-1 receptor beta subunit binding region"
FT   Region          23..27
FT                   /note= "Beta sheet region"
FT   Binding-site    28
FT                   /note= "IL-1 receptor alpha subunit binding region"
FT   Binding-site    30..32
FT                   /note= "IL-1 receptor alpha subunit binding region"
FT   Region          34..36
FT                   /note= "Beta sheet region"
FT   Binding-site    36..38
FT                   /note= "IL-1 receptor alpha subunit binding region"
FT   Region          42..45
FT                   /note= "Beta sheet region"
FT   Binding-site    43
FT                   /note= "IL-1 receptor alpha subunit binding region"
FT   Binding-site    45..50
FT                   /note= "IL-1 receptor alpha subunit binding region"
FT   Binding-site    52
FT                   /note= "IL-1 receptor alpha subunit binding region"
FT   Region          56..61
FT                   /note= "Beta sheet region"
FT   Binding-site    61
FT                   /note= "IL-1 receptor beta subunit binding region"
FT   Binding-site    63
FT                   /note= "IL-1 receptor beta subunit binding region"
FT   Binding-site    68
FT                   /note= "IL-1 receptor beta subunit binding region"
FT   Binding-site    70..71
FT                   /note= "IL-1 receptor beta subunit binding region"
FT   Binding-site    73
FT                   /note= "IL-1 receptor beta subunit binding region"
FT   Binding-site    73..97
FT                   /note= "IL-1 receptor alpha subunit binding region"
FT   Region          74..79
FT                   /note= "Beta sheet region"
FT   Region          84..89
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FT                   /note= "Beta sheet region"
FT   Region          96..101
FT                   /note= "Beta sheet region"
FT   Binding-site    110..112
FT                   /note= "IL-1 receptor beta subunit binding region"
FT   Region          117..122
FT                   /note= "Beta sheet region"
FT   Binding-site    121
FT                   /note= "IL-1 receptor beta subunit binding region"
FT   Binding-site    123..124
FT                   /note= "IL-1 receptor beta subunit binding region"
FT   Binding-site    126..127
FT                   /note= "IL-1 receptor beta subunit binding region"
FT   Region          129..132
FT                   /note= "Beta sheet region"
FT   Region          138..142
FT                   /note= "Beta sheet region"
FT   Binding-site    144..145
FT                   /note= "IL-1 receptor alpha subunit binding region"
FT   Binding-site    147..148
FT                   /note= "IL-1 receptor alpha subunit binding region"
FT   Region          148..152
FT                   /note= "Beta sheet region"
FT   Region          159..167
FT                   /note= "Beta sheet region"
FT   Binding-site    164
FT                   /note= "IL-1 receptor alpha subunit binding region"
FT   Binding-site    166
FT                   /note= "IL-1 receptor alpha subunit binding region"
FT   Binding-site    167
FT                   /note= "IL-1 receptor beta subunit binding region"
FT   Binding-site    169
FT                   /note= "IL-1 receptor beta subunit binding region"
XX
PN   WO200157219-A2.
XX
PD   09-AUG-2001.
XX
PF   01-FEB-2001; 2001WO-US03285.
XX
PR   02-FEB-2000; 2000US-0179638.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Debets JEMA,  Timans JC,  Bazan JF,  Kastelein RA;
XX
DR   WPI; 2001-488886/53.
DR   N-PSDB; AAD12296.
XX
PT   Novel isolated or recombinant antigenic interleukin-1 delta or epsilon
PT   polypeptide useful for treating conditions exhibiting abnormal
PT   expression of interleukin such as immunological disorders, tumor and
PT   allergy  -
XX
PS   Claim 18; Fig 1; 103pp; English.
XX
CC   The invention relates to recombinant antigenic interleukin-1 like
CC   molecules and their corresponding nucleic acid sequences, designated
CC   as interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon).
CC   IL-1delta and IL-1epsilon are useful for treating conditions exhibiting
CC   abnormal expression of the interleukin such as immunological disorders,
CC   tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis,
CC   allergy, autoimmune diseases and infectious diseases (e.g., pulmonary
CC   tuberculosis, leprosy, fulminant hepatitis, and viral infections such as
CC   HIV). The invention also relates to methods of using the composition
CC   containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic
CC   utilities. IL-1delta is used as an immunogen for the production of
CC   antisera or antibodies specific, e.g., capable of distinguishing between
CC   IL-1 family members and an IL-1delta, for the interleukin or its
CC   fragment. The purified interleukin is used as a reagent to detect any
CC   antibodies generated in response to the presence of elevated levels of
CC   expression, or immunological disorders which lead to antibody production
CC   to the endogenous cytokine. The invention also contemplates the use of
CC   competitive drug screening assays. The present sequence is human
CC   interleukin-1epsilon (IL-1epsilon) protein.
XX
SQ   Sequence   169 AA;


  Query Match             56.2%;  Score 466.5;  DB 22;  Length 169;
  Best Local Similarity   59.9%;  Pred. No. 7.4e-42;
  Matches   88;  Conservative   24;  Mismatches   34;  Indels    1;  Gaps    1;

Qy      10 PQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNG 69
           |  |:| |:| :|| || | |:|||| | ::|||:|:|:|:: | ||: ||:|||||:
Db      22 pitgtindlnqqvwtlqgqnlvavprsdsvtpvtvavitckypealeqqrgdpiylgiqn 81

Qy      70 LNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIA 129
             :|| | |||:||||||||: |||||  |||||| |||| :::|| || |||||| ||||
Db      82 pemclycekvgeqptlqlkeqkimdlygqpepvkpflfyraktgrtstlesvafpdwfia 141

Qy     130 VSSEGGCPLILTQELGKANTTDFGLTM 156
             ||:   |:||| ||||:  | | | :
Db     142 -sskrdqpiiltselgksyntafelni 167


RESULT   9
AAB83008
ID   AAB83008 standard; protein; 169 AA.
XX
AC   AAB83008;
XX
DT   21-JUN-2001  (first entry)
XX
DE   Human IL-1ra protein.
XX
KW   Human; IL-1ra; interleukin-1 receptor antagonist; antibacterial;
KW   immunosuppressive; antiinflammatory; antiarthritic; nephrotropic;
KW   hepatotropic; virucide; cardiant; vasotropic; antidiabetic; cancer;
KW   neuroprotective; osteopathic; cytostatic; immunomodulator; nootropic;
KW   cerebroprotective; antidepressant; antiarteriosclerotic; infection;
KW   immune disease; autoimmune disease; bone disease; neuronal disease;
KW   cardiovascular disease.
XX
OS   Homo sapiens.
XX
PN   WO200119390-A1.
XX
PD   22-MAR-2001.
XX
PF   28-AUG-2000; 2000WO-IB01192.
XX
PR   14-SEP-1999;   99US-0154010.
XX
PA   (PFIZ ) PFIZER PROD INC.
XX
PI   Littman BH,  Woodworth TLG,  Dombroski MA;
XX
DR   WPI; 2001-327986/34.
XX
PT   Synergistic treatment of interleukin (IL)-mediated diseases, useful for
PT   e.g. septic shock, comprises adjunctively administering IL-1 receptor
PT   antagonist polypeptide and non-steroidal IL-1 processing and release
PT   inhibiting agent -
XX
PS   Disclosure; Page 91; 112pp; English.
XX
CC   The present sequence is a human interleukin-1 receptor antagonist
CC   (IL-1ra). The present sequence or its variant may be administered
CC   in combination with a non-steroidal IL-1 processing and release
CC   inhibiting agent for the treatment or prevention of IL-mediated disease
CC   states. The composition is useful for treating inappropriate host
CC   responses to infectious diseases where active infection exists at any
CC   body site, e.g. septic shock, disseminated intravascular coagulation,
CC   and/or adult respiratory distress syndrome; acute or chronic
CC   inflammation due to antigen, antibody and/or complement deposition;
```

CC inflammatory conditions including arthritis, cholangitis, colitis,
CC encephalitis, endocarditis, glomerulonephritis, hepatitis, myocarditis,
CC pancreatitis, pericarditis, and reperfusion injury vasculitis. It is
CC also useful for treating immune-based diseases including conditions
CC involving T cells and/or macrophages e.g. acute and delayed
CC hypersensitivity, graft rejection, graft-versus-host disease;
CC autoimmune diseases including Type 1 diabetes mellitus and multiple
CC sclerosis. The composition may be used for treating bone and cartilage
CC resorption as well as diseases resulting in excess deposition of
CC extracellular matrix. Such diseases include osteoporosis, periodontal
CC diseases, interstitial pulmonary fibrosis, cirrhosis, systemic sclerosis
CC and keloid formation. It is also useful for treating tumours which
CC produce IL-1 as an autocrine growth factor and for preventing the
CC cachexia associated with certain tumours. It may be used for
CC treating neuronal diseases with an inflammatory component e.g.
CC Alzheimer's disease, stroke, depression and percussion injury and for
CC cardiovascular diseases in which recruitment of monocytes into the
CC subendothelial space plays a role, e.g. the development of
CC atherosclerotic plaques.
XX
SQ Sequence 169 AA;

Query Match 56.2%; Score 466.5; DB 22; Length 169;
Best Local Similarity 59.9%; Pred. No. 7.4e-42;
Matches 88; Conservative 24; Mismatches 34; Indels 1; Gaps 1;

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Qy      10 PQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNG 69
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Db      22 pitgtindlnqqvwtlqgqnlvavprsdsvtpvtvavitckypealeqgrgdpiylgiqn 81

Qy      70 LNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIA 129
             :|| | |||:||||||||: ||||| |||||| |||| :::|| || |||||| ||||
Db      82 pemclycekvgeqptlqlkeqkimdlygqpepvkpflfyraktgrtstlesvafpdwfia 141

Qy     130 VSSEGGCPLILTQELGKANTTDFGLTM 156
             ||:   |:||| |||||:  | | | :
Db     142 -sskrdqpiiltselgksyntafelni 167
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RESULT 10
AAU16937
ID AAU16937 standard; Protein; 173 AA.
XX
AC AAU16937;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human novel secreted protein, SEQ ID 178.
XX
KW Human; immunosuppressive; antiarthritic; antirheumatic;
KW cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;
KW neuroprotective; antibacterial; virucide; fungicide; opthalmalogical;
KW vulnerary; secreted protein; rheumatoid arthritis;
KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;
KW corneal infection; wound healing; epithelial cell proliferation;
KW skin ageing; food additive; preservative; antiproliferative.
XX
OS Homo sapiens.
XX
PN WO200155441-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01320.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.

PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-476222/51.
DR N-PSDB; AAS26842.
XX
PT Novel polypeptides and polynucleotides useful as diagnostic reagents to
PT diagnose diseases or disorders associated with aberrant expression or
PT activity of polypeptides, for treating blood clotting disorder,
PT haemophilia -
XX
PS Claim 11; SEQ ID No 178; 601pp; English.
XX

CC The invention relates to isolated nucleic acid molecules and their
CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They
CC are also used in diagnosing a pathological condition or susceptibility
CC to a pathological condition. Antibodies to the proteins can also
CC be used in alleviating symptoms associated with the disorders and in
CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked
CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated
CC include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi
CC and ocular disorders e.g. corneal infection, and many other
CC disorders listed in the specification. The polypeptides can also
CC be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present

Query Match 56.2%; Score 466.5; DB 22; Length 173;
Best Local Similarity 59.9%; Pred. No. 7.6e-42;
Matches 88; Conservative 24; Mismatches 34; Indels 1; Gaps 1;

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Qy      10 PQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNG 69
           |  |:| |:| :|| || | |:|||| | ::|||:|:|:|:: | ||: ||:|||||:
Db      26 pitgtindlnqqvwtlqgqnlvavprsdsvtpvtvavitckypealeqggrgdpiylgiqn 85

Qy      70 LNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIA 129
             :|| | |||:|||||||: ||||| |||||| |||| :::|| || |||||| ||||
Db      86 pemclycekvgeqptlqlkeqkimdlygqpepvkpflfyraktgrtstlesvafpdwfia 145

Qy     130 VSSEGGCPLILTQELGKANTTDFGLTM 156
             ||:   |:||| |||||:  | | | :
Db     146 -sskrdqpiiltselgksyntafelni 171
```

RESULT 11
AAY24044
ID AAY24044 standard; Protein; 208 AA.
XX
AC AAY24044;
XX
DT 30-SEP-1999 (first entry)
XX
DE A human SPOIL-II protein (also known as hTANGO 080-II).
XX
KW SPOIL-II; interleukin-1 receptor antagonist; IL-1ra; modulating agent;
KW bone metabolism disorder; proinflammatory disorder; immune disorder;
KW inflammatory disease; septic shock; stroke; diabetes; arthritis;
KW intercolitis; pneumonitis; epithelial cell; skin disease;
KW proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;
KW epithelial cancer; squamous cell carcinoma; bone resorption disorder;
KW osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;
KW osteogenesis imperfecta; fibrous displasia; hypophosphatasia;
KW bone sarcoma; myeloma bone disorder; osteolytic bone lesion;
KW hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;
KW bone fracture; hTANGO 80-I.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 98..724
FT /*tag= a
FT /product= SPOIL-II
XX
PN WO9937662-A1.
XX
PD 29-JUL-1999.

XX
PF 26-JAN-1999; 99WO-US01575.
XX
PR 27-JAN-1998; 98US-0013810.
XX
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI Busfield SJ;
XX
DR WPI; 1999-458675/38.
DR N-PSDB; AAX86459.
XX
PT New isolated SPOIL proteins, used to develop products for treating,
PT e.g. inflammatory and immune disorders
XX
PS Claim 8; Fig 5; 126pp; English.
XX
CC The present sequence represents a SPOIL-II protein. SPOIL proteins have
CC homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.
CC The SPOIL proteins are used as modulating agents in regulating a variety
CC of cellular processes. The products can be used for treating disorders
CC characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone
CC metabolism disorder, a proinflammatory disorder or an immune disorder.
CC They can be used for treating e.g. inflammatory diseases and disorders
CC e.g. inflammation, septic shock, stroke, diabetes, arthritis,
CC intercolitis and pneumonitis, epithelial cell and/or skin diseases and
CC disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma
CC and Kaposi's sarcoma and other epithelial cancers including squamous cell
CC carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and
CC bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's
CC disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,
CC fibrous displasia, hypophosphatasia, bone sarcoma, myeloma bone disorder
CC (e.g. osteolytic bone lesions) and hypercalcemia. SPOIL molecules and
CC SPOIL modulators are useful for regulation of bone mass (e.g. increase in
CC bone mass and/or inhibit bone loss), management of bone fragility (e.g.
CC decrease bone fragility); and prevention and/or treatment of bone pain,
CC bone deformities and/or bone fractures. The products can also be used for
CC detection, diagnosis and screening assays.
XX
SQ Sequence 208 AA;

Query Match 56.2%; Score 466.5; DB 20; Length 208;
Best Local Similarity 59.9%; Pred. No. 9.7e-42;
Matches 88; Conservative 24; Mismatches 34; Indels 1; Gaps 1;

```
Qy      10 PQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNG 69
           |  |:| |:| :|| || | |:|||| | ::|||:|:|:|:: | ||: ||:|||||:
Db      61 pitgtindlnqqvwtlqgqnlvavprsdsvtpvtvavitckypealeqgrgdpiylgiqn 120

Qy      70 LNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIA 129
             :|| | |||:||||||||: ||||| |||||| |||| :::|| || |||||| ||||
Db     121 pemclycekvgeqptlqlkeqkimdlygqpepvkpflfyraktgrtstlesvafpdwfia 180

Qy     130 VSSEGGCPLILTQELGKANTTDFGLTM 156
           ||:   |:||| ||||:  | | | :
Db     181 -sskrdqpiiltselgksyntafelni 206
```

RESULT 12
AAE06662
ID AAE06662 standard; Protein; 157 AA.
XX
AC AAE06662;
XX
DT 16-OCT-2001 (first entry)
XX
DE Mouse interleukin-1epsilon (IL-1epsilon) protein.
XX
KW Mouse; interleukin-1epsilon; IL-1epsilon; virucide; hepatotropic; fever;
KW immunological disorder; tumour; inflammatory disorder; hypoglycaemia;
KW autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;
KW psoriasis; viral infection; allergy; cytokine; HIV; drug screening.
XX
OS Mus sp.
XX
PN WO200157219-A2.
XX
PD 09-AUG-2001.
XX
PF 01-FEB-2001; 2001WO-US03285.
XX
PR 02-FEB-2000; 2000US-0179638.
XX
PA (SCHE) SCHERING CORP.
XX
PI Debets JEMA, Timans JC, Bazan JF, Kastelein RA;
XX
DR WPI; 2001-488886/53.
XX
PT Novel isolated or recombinant antigenic interleukin-1 delta or epsilon
PT polypeptide useful for treating conditions exhibiting abnormal
PT expression of interleukin such as immunological disorders, tumor and
PT allergy -
XX
PS Disclosure; Fig 1; 103pp; English.
XX
CC The invention relates to recombinant antigenic interleukin-1 like
CC molecules and their corresponding nucleic acid sequences, designated
CC as interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon).
CC IL-1delta and IL-1epsilon are useful for treating conditions exhibiting
CC abnormal expression of the interleukin such as immunological disorders,
CC tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis,
CC allergy, autoimmune diseases and infectious diseases (e.g., pulmonary
CC tuberculosis, leprosy, fulminant hepatitis, and viral infections such as
CC HIV). The invention also relates to methods of using the composition
CC containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic
CC utilities. IL-1delta is used as an immunogen for the production of
CC antisera or antibodies specific, e.g., capable of distinguishing between
CC IL-1 family members and an IL-1delta, for the interleukin or its
CC fragment. The purified interleukin is used as a reagent to detect any
CC antibodies generated in response to the presence of elevated levels of
CC expression, or immunological disorders which lead to antibody production
CC to the endogenous cytokine. The invention also contemplates the use of
CC competitive drug screening assays. The present sequence is mouse
CC interleukin-1epsilon (IL-1epsilon) protein related to the invention.
XX
SQ Sequence 157 AA;

Query Match 55.8%; Score 463; DB 22; Length 157;
Best Local Similarity 54.5%; Pred. No. 1.6e-41;
Matches 85; Conservative 30; Mismatches 41; Indels 0; Gaps 0;

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Qy       2 EKALKIDTPQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGN 61
           || |:  :|    :||:: |||:||:  | |||||::  |||| |: |::::||| :||:
Db       1 ekelraaspslrhvqdlssrvwilqnniltavprkeqtvpvtitllpcqyldtletnrgd 60

Qy      62 PIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESV 121
           | |:|:     || | | |:|| ||| | :||::||: |||| |||| :||  ||||
Db      61 ptymgvqrpmsclfctkdgeqpvlqlgegnimemynkkepvkaslfyhkksgttstfesa 120

Qy     122 AFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
           ||||||||| |:| |||||||||:   ||| : ::
Db     121 afpgwfiavcskgscpliltqelgeifitdfemivv 156
```

RESULT 13
AAW86286
ID AAW86286 standard; Protein; 160 AA.
XX
AC AAW86286;
XX
DT 19-FEB-1999 (first entry)
XX
DE Rodent interleukin (IL)-1 epsilon polypeptide.

XX
KW Interleukin; IL-1 delta; polyclonal antibody; IL-1 epsilon; cytokine;
KW inflammatory response; immune system; diagnosis; agonist; antagonist;
KW chemokine.
XX
OS Mus sp.
XX
PN WO9847921-A1.
XX
PD 29-OCT-1998.
XX
PF 17-APR-1998; 98WO-US06879.
XX
PR 06-AUG-1997; 97US-0055111.
PR 21-APR-1997; 97US-0837627.
XX
PA (SCHE) SCHERING CORP.
XX
PI Bażan JF, Hedrick JA, Kastelein RA, Sana TR;
XX
DR WPI; 1998-609976/51.
DR N-PSDB; AAV71960.
XX
PT Mammalian interleukin 1-delta and 1-epsilon - useful for, e.g.
PT regulating the immune system and inflammatory responses
XX
PS Claim 1; Pages 92-93; 113pp; English.
XX
CC This represents a rodent interleukin (IL)-1 epsilon polypeptide. The
CC invention relates to a recombinant polypeptide that specifically binds
CC polyclonal antibodies (Abs) generated against a 12 consecutive amino acid
CC segment of IL-1 delta or IL-1 epsilon. Agonists or antagonists of these
CC IL polypeptides are used to regulate a cell involved in an inflammatory
CC response. The IL-1 delta or IL-1 epsilon polypeptides and peptides are
CC used to produce Abs and antigen-Ab complexes. The polypeptides, Abs and
CC the corresponding nucleic acids regulate development and/or the immune
CC system, and can be used to diagnose and treat conditions associated with
CC abnormal expression of IL. Agonists or antagonists of IL-1 delta or IL-1
CC epsilon polypeptides are used with agonists or antagonists of IL-1 alpha,
CC IL-1RA, IL-1 beta, IL-1 gamma, IL-2 and/or IL-12. The IL-1 delta or IL-1
CC epsilon polypeptides may be used as a soluble polypeptide or as a fusion
CC protein with another cytokine or chemokine.
XX
SQ Sequence 160 AA;

```
  Query Match             55.8%;  Score 463;  DB 19;  Length 160;
  Best Local Similarity   54.5%;  Pred. No. 1.6e-41;
  Matches   85;  Conservative   30;  Mismatches   41;  Indels    0;  Gaps    0;

Qy       2 EKALKIDTPQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGN 61
           || |:  :|    :||:: |||:||:  | |||||:: |||| |: |::::||| :||:
Db       4 ekelraaspslrhvqdlssrvwilqnniltavprkeqtvpvtitllpcqyldtletnrgd 63

Qy      62 PIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESV 121
           | |:|:     || | | |:|| ||| | :||::||: |||| |||| :||  |||||
Db      64 ptymgvqrpmsclfctkdgeqpvlqlgegnimemynkkepvkaslfyhkksgttstfesa 123

Qy     122 AFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
           ||||||||| |:| |||||||||:   ||| : ::
Db     124 afpgwfiavcskgscpliltqelgeifitdfemivv 159
```

RESULT 14
AAY24049
ID AAY24049 standard; Protein; 160 AA.
XX
AC AAY24049;
XX
DT 30-SEP-1999 (first entry)
XX
DE Amino acid sequence of a murine SPOIL-II protein.
XX
KW SPOIL-II; interleukin-1 receptor antagonist; IL-1ra; modulating agent;
KW bone metabolism disorder; proinflammatory disorder; immune disorder;
KW inflammatory disease; septic shock; stroke; diabetes; arthritis;
KW intercolitis; pneumonitis; epithelial cell; skin disease;
KW proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;
KW epithelial cancer; squamous cell carcinoma; bone resorption disorder;
KW osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;
KW osteogenesis imperfecta; fibrous displasia; hypophosphatasia;
KW bone sarcoma; myeloma bone disorder; osteolytic bone lesion;
KW hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;
KW bone fracture.
XX
OS Mus sp.
XX
PN WO9937662-A1.
XX
PD 29-JUL-1999.
XX
PF 26-JAN-1999; 99WO-US01575.
XX
PR 27-JAN-1998; 98US-0013810.
XX
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI Busfield SJ;
XX
DR WPI; 1999-458675/38.
DR N-PSDB; AAX86460.
XX
PT New isolated SPOIL proteins, used to develop products for treating,
PT e.g. inflammatory and immune disorders
XX
PS Claim 8; Fig 6; 126pp; English.
XX
CC The present sequence represents a SPOIL-II protein. SPOIL proteins have
CC homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.
CC The SPOIL proteins are used as modulating agents in regulating a variety
CC of cellular processes. The products can be used for treating disorders
CC characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone
CC metabolism disorder, a proinflammatory disorder or an immune disorder.
CC They can be used for treating e.g. inflammatory diseases and disorders
CC e.g. inflammation, septic shock, stroke, diabetes, arthritis,
CC intercolitis and pneumonitis, epithelial cell and/or skin diseases and
CC disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma
CC and Kaposi's sarcoma and other epithelial cancers including squamous cell
CC carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and
CC bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's
CC disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,
CC fibrous displasia, hypophosphatasia, bone sarcoma, myeloma bone disorder
CC (e.g. osteolytic bone lesions) and hypercalcemia. SPOIL molecules and
CC SPOIL modulators are useful for regulation of bone mass (e.g. increase in
CC bone mass and/or inhibit bone loss), management of bone fragility (e.g.
CC decrease bone fragility); and prevention and/or treatment of bone pain,
CC bone deformities and/or bone fractures. The products can also be used for
CC detection, diagnosis and screening assays.
XX
SQ Sequence 160 AA;

```
  Query Match             55.8%;  Score 463;  DB 20;  Length 160;
  Best Local Similarity   54.5%;  Pred. No. 1.6e-41;
  Matches   85;  Conservative   30;  Mismatches   41;  Indels    0;  Gaps    0;

Qy       2 EKALKIDTPQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGN 61
           || |:  :|    :||:: |||:||:  | |||||:: |||| |: |::::||| :||:
Db       4 ekelraaspslrhvqdlssrvwilqnniltavprkeqtvpvtitllpcqyldtletnrgd 63

Qy      62 PIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESV 121
           | |:|:     || | | |:|| ||| | :||::||: |||| |||| :||  |||||
Db      64 ptymgvqrpmsclfctkdgeqpvlqlgegnimemynkkepvkaslfyhkksgttstfesa 123

Qy     122 AFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
           ||||||||| |:| |||||||||:   ||| : ::
Db     124 afpgwfiavcskgscpliltqelgeifitdfemivv 159
```

Db 124 afpgwfiavcskgscpliltqelgeifitdfemivv 159

RESULT 15
AAU17010
ID AAU17010 standard; Protein; 172 AA.
XX
AC AAU17010;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human novel secreted protein, SEQ ID 251.
XX
KW Human; immunosuppressive; antiarthritic; antirheumatic;
KW cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;
KW neuroprotective; antibacterial; virucide; fungicide; opthalmalogical;
KW vulnerary; secreted protein; rheumatoid arthritis;
KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;
KW corneal infection; wound healing; epithelial cell proliferation;
KW skin ageing; food additive; preservative; antiproliferative.
XX
OS Homo sapiens.
XX
PN WO200155441-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01320.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.

PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-476222/51.
DR N-PSDB; AAS26915.
XX
PT Novel polypeptides and polynucleotides useful as diagnostic reagents to
PT diagnose diseases or disorders associated with aberrant expression or
PT activity of polypeptides, for treating blood clotting disorder,
PT haemophilia -
XX
PS Claim 11; SEQ ID No 251; 601pp; English.
XX
CC The invention relates to isolated nucleic acid molecules and their
CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They
CC are also used in diagnosing a pathological condition or susceptibility
CC to a pathological condition. Antibodies to the proteins can also
CC be used in alleviating symptoms associated with the disorders and in
CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked
CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated
CC include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi
CC and ocular disorders e.g. corneal infection, and many other
CC disorders listed in the specification. The polypeptides can also
CC be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present

Query Match 55.4%; Score 459.5; DB 22; Length 172;
Best Local Similarity 59.2%; Pred. No. 4.2e-41;
Matches 87; Conservative 24; Mismatches 35; Indels 1; Gaps 1;

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Qy      10 PQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNG 69
           |  |:| |:| :|| || | |:|||| | ::|||:|:|:|:: | ||: ||:|||||:
Db      26 pitgtindlnqqvwtlqgqnlvavprsdsvtpvtvavitckypealeqgrgdpiylgign 85

Qy      70 LNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIA 129
             :|| | |||:||||||||: ||||| |||||| |||| :::|| || |||||| ||||
Db      86 pemclycekvgeqptlqlkeqkimdlygqpepvkpflfyraktgrtstlesvafpdwfia 145

Qy     130 VSSEGGCPLILTQELGKANTTDFGLTM 156
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||: |:||| || |: | | | :
Db 146 -sskrdqpiiltselxksyntafelni 171

Search completed: June 20, 2002, 15:03:08
Job time: 119 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 20, 2002, 15:03:51 ; Search time 36.86 Seconds
(without alignments)
411.886 Million cell updates/sec

Title: US-09-763-498-8
Perfect score: 830
Sequence: 1 MEKALKIDTPQQGSIQDINH.....ILTQELGKANTTDFGLTMLF 158

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	195.5	23.6	178	2	A44610	interleukin-1 rece
2	190.5	23.0	178	2	C40956	interleukin-1 rece
3	185.5	22.3	155	2	JC7104	interleukin-1 rece
4	183.5	22.1	177	2	A30368	interleukin-1 rece
5	183.5	22.1	180	2	A39386	interleukin-1 rece
6	173.5	20.9	266	1	S23010	interleukin-1 beta
7	170.5	20.5	177	2	A54377	interleukin-1 rece
8	170	20.5	266	1	ICBO1B	interleukin-1 beta
9	160	19.3	267	2	S38373	interleukin-1 beta
10	155	18.7	267	1	JN0724	interleukin-1 beta
11	143.5	17.3	269	1	ICHU1B	interleukin-1 beta
12	141.5	17.0	268	1	A30584	interleukin-1 beta
13	138.5	16.7	214	2	JC5646	interleukin-1 beta
14	121	14.6	269	1	I55969	interleukin-1 beta
15	81	9.8	256	2	F86463	hypothetical prote
16	79	9.5	501	2	AG0939	glycerol kinase [i
17	77	9.3	268	1	ICBO1A	interleukin-1 alph
18	77	9.3	268	1	A61246	interleukin-1 alph
19	77	9.3	502	1	KIECGL	glycerol kinase (E
20	77	9.3	502	2	C91235	glycerol kinase [i
21	77	9.3	509	2	C86082	glycerol kinase [i
22	75.5	9.1	270	1	S10532	interleukin-1 alph
23	75	9.0	15281	2	S41309	cyclosporin synthe
24	74.5	9.0	1077	2	T01474	hypothetical prote
25	74	8.9	407	2	T22554	hypothetical prote
26	73.5	8.9	1320	2	H64090	phosphoribosylform
27	73	8.8	403	2	AC2271	precorrin-6y-depen
28	73	8.8	837	2	T48407	hypothetical prote
29	72.5	8.7	325	2	E87125	ribonucleotide red
30	72.5	8.7	421	2	A47713	chitin deacetylase
31	72	8.7	1132	2	T43483	translation initia
32	71.5	8.6	325	2	S48698	3-dehydroquinate d
33	71.5	8.6	460	2	AG2262	hypothetical prote
34	71	8.6	1426	2	T30817	homeotic protein C
35	70.5	8.5	270	2	I46620	interleukin-1 alph
36	70.5	8.5	556	2	A44441	B-cell antigen CD1
37	70.5	8.5	944	2	G86720	translation initia
38	70.5	8.5	1093	2	T51503	valine--tRNA ligas
39	70	8.4	447	2	H97146	siderophore/Surfac
40	70	8.4	516	2	H84424	probable MAP kinas
41	69.5	8.4	268	1	B24073	interleukin-1 alph
42	69.5	8.4	454	2	G70476	conserved hypothet
43	69	8.3	327	1	OWPSY	ornithine carbamoy
44	69	8.3	333	2	B86567	proteinase [import
45	69	8.3	333	2	G72058	proteinase IV, pro

ALIGNMENTS

RESULT 1
A44610
interleukin-1 receptor antagonist precursor - mouse
N;Alternate names: IL-1Ra
C;Species: Mus musculus (house mouse)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 16-Jul-1999
C;Accession: A44610; B40956; A49031; I56106; I52970
R;Matsushime, H.; Roussel, M.F.; Matsushima, K.; Hishinuma, A.; Sherr, C.J.
Blood 78, 616-623, 1991
A;Title: Cloning and expression of murine interleukin-1 receptor antagonist in macrop
A;Reference number: A44610; MUID:91316273
A;Accession: A44610
A;Molecule type: mRNA
A;Residues: 1-178 <MAT>
A;Cross-references: GB:M64404; NID:g198296; PIDN:AAA39277.1; PID:g198297
R;Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thomps
Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A;Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene fami
A;Reference number: A40956; MUID:91271363
A;Accession: B40956
A;Molecule type: DNA
A;Residues: 7-178 <EIS>
A;Cross-references: GB:M63100; NID:g198389; PIDN:AAA39310.1; PID:g198390
R;Shuck, M.E.; Eessalu, T.E.; Tracey, D.E.; Bienkowski, M.J.
Eur. J. Immunol. 21, 2775-2780, 1991
A;Title: Cloning, heterologous expression and characterization of murine interleukin
A;Reference number: A49031; MUID:92037824
A;Accession: A49031
A;Molecule type: mRNA
A;Residues: 23-178 <SHU>
A;Cross-references: GB:S64082; NID:g238584; PIDN:AAB20265.1; PID:g238585
A;Experimental source: peritoneal macrophages, ICR strain
A;Note: sequence extracted from NCBI backbone (NCBIN:64082, NCBIP:64085)
R;Zahedi, K.; Seldin, M.F.; Rits, M.; Ezekowitz, R.B.; Whitehead, A.S.
J. Immunol. 146, 4228-4233, 1991
A;Title: Mouse IL-1 receptor antagonist protein: Molecular characterization, gene map
A;Reference number: I56106; MUID:91250712
A;Accession: I56106
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-178 <RES>
A;Cross-references: GB:M74294; NID:g198387; PIDN:AAA39309.1; PID:g198388
R;Zahedi, K.A.; Uhlar, C.M.; Rits, M.; Prada, A.E.; Whitehead, A.S.
Cytokine 6, 1-9, 1994
A;Title: The mouse interleukin 1 receptor antagonist protein: gene structure and regu
A;Reference number: I52970; MUID:94271931
A;Accession: I52970
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-178 <RE2>
A;Cross-references: GB:L32838; NID:g487864; PIDN:AAA20576.1; PID:g528978
C;Genetics:

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A;Gene: IL-1rn
A;Introns: 40/2; 70/1; 107/3
C;Superfamily: interleukin-1
C;Keywords: cytokine receptor
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-178/Product: interleukin-1 receptor antagonist #status predicted <MA2>


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  Best Local Similarity  35.1%;  Pred. No. 4.9e-12;
  Matches   47;  Conservative   21;  Mismatches   45;  Indels   21;  Gaps    2;

Qy      15 IQDINHRVWVLQDQTLIA-------VPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGL 67
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Db      41 IWDTNQKTFYLRNNQLIAGYLQGPNIKLEEKIDMVPIDLHS-------------VFLGI 86

Qy      68 NGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWF 127
           :|  ||| ||| ||   |||:| :| ||    |  | | |  |: |  ::||| | ||||
Db      87 HGGKLCLSCAKSGDDIKLQLEEVNITDLSKNKEEDKRFTFIRSEKGPTTSFESAACPGWF 146

Qy     128 IAVSSEGGCPLILT 141
           :  : |   |: ||
Db     147 LCTTLEADRPVSLT 160


RESULT   2
C40956
interleukin-1 receptor antagonist precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 16-Jul-1999
C;Accession: C40956
R;Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson,
Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A;Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family:
A;Reference number: A40956; MUID:91271363
A;Accession: C40956
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-178 <EIS>
A;Cross-references: GB:M63101; NID:g204928; PIDN:AAA41434.1; PID:g204929
C;Superfamily: interleukin-1
C;Keywords: cytokine receptor


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  Best Local Similarity  35.1%;  Pred. No. 1.5e-11;
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Db      41 IWDTNQKTFYLRNNQLIAGYLQGPNTKLEEKIDMVPIDFRNV----------FLGIHGG 89

Qy      71 NLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAV 130
            ||| | | ||   |||:| :| ||    |  | | |  |::|  ::|||:| ||||:
Db      90 KLCLSCVKSGDDTKLQLEEVNITDLNKNKEEDKRFTFIRSETGPTTSFESLACPGWFLCT 149

Qy     131 SSEGGCPLILT 141
           : |   |: ||
Db     150 TLEADHPVSLT 160


RESULT   3
JC7104
interleukin-1 receptor antagonist - human
C;Species: Homo sapiens (man)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C;Accession: JC7104
R;Mulero, J.J.; Pace, A.M.; Nelken, S.T.; Loeb, D.B.; Correa, T.R.; Drmanac, R.; Ford, J
Biochem. Biophys. Res. Commun. 263, 702-706, 1999
A;Title: IL1HY1: A novel interleukin-1 receptor antagonist gene.
A;Reference number: JC7104; MUID:99443727
A;Accession: JC7104
A;Molecule type: mRNA
A;Residues: 1-155 <MUL>
A;Cross-references: GB:AF186094; NID:g6049804; PIDN:AAF02757.1; PID:g6049805
C;Genetics:
A;Gene: il1hy1
A;Map position: 2q14
C;Keywords: macrophage


  Query Match            22.3%;  Score 185.5;  DB 2;  Length 155;
  Best Local Similarity  44.8%;  Pred. No. 4.1e-11;
  Matches   43;  Conservative   13;  Mismatches   35;  Indels    5;  Gaps    3;

Qy      61 NPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFES 120
           :|: ||: | : || |  || :||| |:  :||:||   :  ||| ||    |  |:|||
Db      55 SPVILGVQGGSQCLSCG-VGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFES 113

Qy     121 VAFPGWFIAVSSEGGCPLILTQ--ELG--KANTTDF 152
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Db     114 AAYPGWFLCTVPEADQPVRLTQLPENGGWNAPITDF 149


RESULT   4
A30368
interleukin-1 receptor antagonist secreted form precursor - human
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-May-2000
C;Accession: A40956; I37894; A30368; S08160; S08159; A37822
R;Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thomps
Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A;Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene fami
A;Reference number: A40956; MUID:91271363
A;Accession: A40956
A;Molecule type: DNA
A;Residues: 1-177 <EIS>
A;Cross-references: GB:M63099; NID:g186385; PIDN:AAB41943.1; PID:g186386
R;Lennard, A.; Gorman, P.; Carrier, M.; Griffiths, S.; Scotney, H.; Sheer, D.; Solari
Cytokine 4, 83-89, 1992
A;Title: Cloning and chromosome mapping of the human interleukin-1 receptor antagonis
A;Reference number: I37894; MUID:92338323
A;Accession: I37894
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-177 <LEN>
A;Cross-references: EMBL:X64532; NID:g33798; PIDN:CAA45832.1; PID:g33799
R;Carter, D.B.; Deibel Jr., M.R.; Dunn, C.J.; Tomich, C.S.C.; Laborde, A.L.; Slightom
J.G.; Sieu, L.C.; Hardee, M.M.; Zurcher-Neely, H.A.; Reardon, I.M.; Heinrikson, R.L.;
Nature 344, 633-638, 1990
A;Title: Purification, cloning, expression and biological characterization of an inte
A;Reference number: A30368; MUID:90220867
A;Accession: A30368
A;Molecule type: mRNA
A;Residues: 1-177 <CAR>
A;Cross-references: GB:X53296; NID:g32578; PIDN:CAA37386.1; PID:g32579
A;Note: parts of this sequence, including the amino end of the mature protein, were c
R;Eisenberg, S.P.; Evans, R.J.; Arend, W.P.; Verderber, E.; Brewer, M.T.; Hannum, C.H
Nature 343, 341-346, 1990
A;Title: Primary structure and functional expression from complementary DNA of a huma
A;Reference number: S08160; MUID:90136921
A;Accession: S08160
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-177 <EI2>
A;Cross-references: GB:X52015; NID:g32576; PIDN:CAA36262.1; PID:g32577
R;Hannum, C.H.; Wilcox, C.J.; Arend, W.P.; Joslin, F.G.; Dripps, D.J.; Heimdal, P.L.;
Nature 343, 336-340, 1990
A;Title: Interleukin-1 receptor antagonist activity of a human interleukin-1 inhibito
A;Reference number: S08159; MUID:90136920
A;Accession: S08159
A;Molecule type: protein
A;Residues: 26-75;97-108;110-116;120-131;163-176 <HAN>
R;Bienkowski, M.J.; Eessalu, T.E.; Berger, A.E.; Truesdell, S.E.; Shelly, J.A.; Labor
J. Biol. Chem. 265, 14505-14511, 1990
A;Title: Purification and characterization of interleukin 1 receptor level antagonist
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A;Reference number: A37822; MUID:90354444
A;Accession: A37822
A;Molecule type: protein
A;Residues: 26-52;70-77;122-127;170-175 <BIE>
A;Experimental source: culture medium, PMA-stimulated THP-1 cells
C;Comment: For an alternative splice form, see PIR:A39386
C;Genetics:
A;Gene: GDB:IL1RN
A;Cross-references: GDB:125897; OMIM:147679
A;Map position: 2q14.2-2q14.2
A;Introns: 39/2; 69/1; 106/3
C;Superfamily: interleukin-1
C;Keywords: alternative splicing; cytokine receptor; extracellular protein; glycoprotein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-177/Product: interleukin-1 receptor antagonist #status experimental <MAT>
F;109/Binding site: carbohydrate (Asn) (covalent) #status experimental


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  Matches   45;  Conservative   26;  Mismatches   49;  Indels   27;  Gaps    3;

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Qy      68 NGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWF 127
           :|  :|| | | ||:  |||:  :| ||    :  | | |  | ||  ::||| | ||||
Db      86 HGGKMCLSCVKSGDETRLQLEAVNITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWF 145

Qy     128 IAVSSEGGCPLILTQELGKANTTDFGL 154
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Db     146 LCTAMEADQPVSLT------NMPDEGV 166


RESULT   5
A39386
interleukin-1 receptor antagonist, long intracellular splice form - human
N;Contains: interleukin-1 receptor antagonist, short intracellular splice form
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1992 #sequence_revision 11-Apr-1997 #text_change 26-May-2000
C;Accession: I37893; A39386
R;Muzio, M.; Polentarutti, N.; Sironi, M.; Poli, G.; De Gioia, L.; Introna, M.; Mantovan
J. Exp. Med. 182, 623-628, 1995
A;Title: Cloning and characterization of a new isoform of the interleukin 1 receptor ant
A;Reference number: I37893; MUID:95355865
A;Accession: I37893
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-180 <RES>
A;Cross-references: EMBL:X84348; NID:g1008970; PIDN:CAA59087.1; PID:g1008971
R;Haskill, S.; Martin, G.; Van Le, L.; Morris, J.; Peace, A.; Bigler, C.F.; Jaffe, G.J.;
Proc. Natl. Acad. Sci. U.S.A. 88, 3681-3685, 1991
A;Title: cDNA cloning of an intracellular form of the human interleukin 1 receptor antag
A;Reference number: A39386; MUID:91219436
A;Accession: A39386
A;Molecule type: mRNA
A;Residues: 1-3,25-180 <HAS>
A;Cross-references: GB:M55646; NID:g186291; PIDN:AAA59138.1; PID:g186292
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A;Gene: GDB:IL1RN
A;Cross-references: GDB:125897; OMIM:147679
A;Map position: 2q14.2-2q14.2
C;Superfamily: interleukin-1
C;Keywords: alternative splicing; cytokine receptor
F;1-180/Product: interleukin-1 receptor antagonist, long intracellular splice form #stat
F;1-3,25-180/Product: interleukin-1 receptor antagonist, short intracellular splice form


  Query Match             22.1%;  Score 183.5;  DB 2;  Length 180;
  Best Local Similarity   30.6%;  Pred. No. 7.8e-11;
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Qy      15 IQDINHRVWVLQDQTLIA-------VPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGL 67
           | |:| : : |::  |:|       |  ::::  | |                : ::||:
Db      43 IWDVNQKTFYLRNNQLVAGYLQGPNVNLEEKIDVVPI-------------EPHALFLGI 88

Qy      68 NGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWF 127
           :|  :|| | | ||:  |||:  :| ||    :  | | |  | ||  ::||| | ||||
Db      89 HGGKMCLSCVKSGDETRLQLEAVNITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWF 148

Qy     128 IAVSSEGGCPLILTQELGKANTTDFGL 154
           :  : |   |: ||      |  | |:
Db     149 LCTAMEADQPVSLT------NMPDEGV 169


RESULT   6
S23010
interleukin-1 beta precursor - sheep
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 08-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 15-Oct-1999
C;Accession: S23010; S43047; S13092; B61246
R;Seow, H.F.; Rothel, J.S.; David, M.J.; Wood, P.R.
DNA Seq. 1, 423-426, 1991
A;Title: Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.
A;Reference number: S23010; MUID:92119335
A;Accession: S23010
A;Molecule type: mRNA
A;Residues: 1-266 <SEO>
A;Cross-references: EMBL:X56972; NID:g1808; PIDN:CAA40293.1; PID:g1809
A;Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in having an a
R;Sargan, D.R.
submitted to the EMBL Data Library, May 1992
A;Reference number: S43047
A;Accession: S43047
A;Molecule type: mRNA
A;Residues: 1-13,'C',15-54,'K',56-63,'A',65-144,'L',146-266 <SAR>
A;Cross-references: EMBL:X54796; NID:g1273; PIDN:CAA38566.1; PID:g1274
R;Fiskerstrand, C.; Sargan, D.
Nucleic Acids Res. 18, 7165, 1990
A;Title: Nucleotide sequence of ovine interleukin-1 beta.
A;Reference number: S13092; MUID:91088326
A;Accession: S13092
A;Molecule type: mRNA
A;Residues: 1-13,'C',15-54,'K',56-61,'S',63,'A',65-144,'L',146-266 <FIS>
A;Cross-references: EMBL:X54796
A;Note: the authors translated the codon AGT for residue 62 as Arg
R;Andrews, A.E.; Barcham, G.J.; Brandon, M.R.; Nash, A.D.
Immunology 74, 453-460, 1991
A;Title: Molecular cloning and characterization of ovine IL-1alpha and IL-1beta.
A;Reference number: A61246; MUID:92120716
A;Accession: B61246
A;Molecule type: mRNA
A;Residues: 1-144,'L',146-266 <AND>
C;Comment: This protein lacks a conventional signal sequence for protein export. Clea
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin
C;Genetics:
A;Gene: IL-1-beta
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;114-266/Product: interleukin-1 beta #status predicted <MAT>


  Query Match             20.9%;  Score 173.5;  DB 1;  Length 266;
  Best Local Similarity   30.8%;  Pred. No. 1.2e-09;
  Matches   48;  Conservative   27;  Mismatches   62;  Indels   19;  Gaps    4;

Qy       2 EKALKIDTPQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGN 61
           :|:| :|:|           ||:    : :| ::    |   :     |:  |:|
Db     128 QKSLVLDSP-----------CVLK---ALHLPSQEMSREVVFCM---SFVQGEERDNKI 169

Qy      62 PIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESV 121
             |: ||:   || | | | || |||||:| |   :| :    | |:|| ::      ||||
```

```
Db    170 PVALGIRDKNLYLSCVKKGDTPTLQLEEVD-PKVYPKRNMEKRFVFYKTEIKNTVEFESV 228

Qy    122 AFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
          :| |:|: |     |: | :  |  : ||| :  |
Db    229 LYPNWYISTSQIEEKPVFLGRFRGGQDITDFRMETL 264


RESULT   7
A54377
interleukin-1 receptor antagonist secreted form precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C;Accession: A54377; I46729
R;Cominelli, F.; Bortolami, M.; Pizarro, T.T.; Monsacchi, L.; Ferretti, M.; Brewer, M.T.
J. Biol. Chem. 269, 6962-6971, 1994
A;Title: Rabbit interleukin-1 receptor antagonist. Cloning, expression, functional chara
A;Reference number: A54377; MUID:94165101
A;Accession: A54377
A;Molecule type: mRNA
A;Residues: 1-177 <COM>
A;Cross-references: GB:S68977; NID:g545740; PIDN:AAB30093.1; PID:g545741
A;Experimental source: colon tissue
A;Note: sequence extracted from NCBI backbone (NCBIN:144168, NCBIP:144169)
R;Goto, F.; Goto, K.; Miyata, T.; Ohkawara, S.; Takao, T.; Mori, S.; Furukawa, S.; Maeda
Immunology 77, 235-244, 1992
A;Title: Interleukin-1 recetor antagonist in inflammatory exudate cells of rabbits. Prod
A;Reference number: I46729; MUID:93052512
A;Accession: I46729
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-177 <GOT>
A;Cross-references: GB:D21832; NID:g425787; PIDN:BAA04860.1; PID:g452205
C;Superfamily: interleukin-1
C;Keywords: cytokine receptor; extracellular protein; glycoprotein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;109/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match             20.5%;  Score 170.5;  DB 2;  Length 177;
  Best Local Similarity   30.6%;  Pred. No. 1.5e-09;
  Matches   44;  Conservative   21;  Mismatches   52;  Indels   27;  Gaps    3;

Qy     15 IQDINHRVWVLQDQTLIA-------VPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGL 67
          | |:| : : |::  |:|         ::|:  | :                   ::||:
Db     40 IWDVNQKTFYLRNNQLVAGYLQGPNAKLEERIDVVPL-------------EPQLLFLGI 85

Qy     68 NGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWF 127
          ||| | | ||:  | |:  :| ||    |  | | |  | ||  :|||| : ||||
Db     86 QRGKLCLSCVKSGDKMKLHLEAVNITDLGKNKEQDKRFTFIRSNSGPTTTFESASCPGWF 145

Qy    128 IAVSSEGGCPLILTQELGKANTTD 151
          :  : |   |: ||      || |
Db    146 LCTALEADQPVSLT------NTPD 163


RESULT   8
ICBO1B
interleukin-1 beta precursor - bovine
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
C;Accession: JL0010; S01380
R;Maliszewski, C.R.; Baker, P.E.; Schoenborn, M.A.; Davis, B.S.; Cosman, D.; Gillis, S.;
Mol. Immunol. 25, 429-437, 1988
A;Title: Cloning, sequence and expression of bovine interleukin 1-alpha and interleukin
A;Reference number: A94695; MUID:88318652
A;Accession: JL0010
A;Molecule type: mRNA
A;Residues: 1-266 <MAL>
A;Cross-references: GB:M37211; NID:g163200; PIDN:AAA30584.1; PID:g163201
R;Leong, S.R.; Flaggs, G.M.; Lawman, M.; Gray, P.W.
Nucleic Acids Res. 16, 9054, 1988
A;Title: The nucleotide sequence for the cDNA of bovine interleukin-1 beta.
A;Reference number: S01380; MUID:89016591
A;Accession: S01380
A;Molecule type: mRNA
A;Residues: 1-251,'A',253-266 <LEO>
A;Cross-references: EMBL:X12498; NID:g448; PIDN:CAA31018.1; PID:g449
C;Comment: This protein is a cytokine that mediates a variety of immunoregulatory and
C;Comment: This protein lacks a conventional signal sequence for protein export. Clea
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;114-266/Product: interleukin-1 beta #status predicted <MAT>


  Query Match             20.5%;  Score 170;  DB 1;  Length 266;
  Best Local Similarity   31.6%;  Pred. No. 2.7e-09;
  Matches   49;  Conservative   23;  Mismatches   75;  Indels    8;  Gaps    4;

Qy      8 DTPQQG---SIQDINHRVWVLQDQTLIAVPR--KDRMSPVTIALISCRHVETLEKDRGNP 62
            | | |     :||   :  ||    ::         |:   :  :|   |:  |:|   |
Db    113 DAPVQSIKCKLQDREQKSLVLASPCVLKALHLLSQEMNREVVFCMS--FVQGEERDNKIP 170

Qy     63 IYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVA 122
          : ||:   || | | | || |||||:| |   :| :    | |:|| ::      ||||
Db    171 VALGIKDKNLYLSCVKKGDTPTLQLEEVD-PKVYPKRNMEKRFVFYKTEIKNTVEFESVL 229

Qy    123 FPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
          :| |:|: |     |: |    |  : ||| :  |
Db    230 YPNWYISTSQIEERPVFLGHFRGGQDITDFRMETL 264


RESULT   9
S38373
interleukin-1 beta precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 20-May-1994 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999
C;Accession: S38373
R;Vandenbroeck, K.; Fiten, P.; Beuken, E.; Martens, E.; Janssen, A.; van Damme, J.; O
Eur. J. Biochem. 217, 45-52, 1993
A;Title: Gene sequence, cDNA construction, expression in Escherichia coli and genetic
A;Reference number: S38373; MUID:94039070
A;Accession: S38373
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-267 <VAN>
A;Cross-references: EMBL:X74568; NID:g407899; PIDN:CAA52660.1; PID:g407900
C;Genetics:
A;Introns: 16/2; 33/3; 99/1; 154/1; 197/3
C;Superfamily: interleukin-1


  Query Match             19.3%;  Score 160;  DB 2;  Length 267;
  Best Local Similarity   29.0%;  Pred. No. 2.7e-08;
  Matches   45;  Conservative   27;  Mismatches   73;  Indels   10;  Gaps    4;

Qy      9 TPQQG---SIQDINHRVWVL---QDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNP 62
          || |     :|| : :  ||    :   : : : |    |   :     |:  : |   |
Db    115 TPVQSVDCKLQDKDEKALVLAGPHELKALHLLKGDLKREVVFCM---SFVQGDDSDDKIP 171

Qy     63 IYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVA 122
          : ||: | || | |    | ||||::|    | : :  | |:|| ::      |||
Db    172 VTLGIKGKNLYLSCVMKDDTPTLQLEDVDPKS-YPKRDMEKRFVFYKTEIKNRVEFESAL 230

Qy    123 FPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
          :| |:|: |     |: |  |: : ||| : :|
Db    231 YPNWYISTSQAEQKPVFLGNSKGRQDITDFTMEVL 265


RESULT  10
JN0724
interleukin-1 beta precursor - pig
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Sus scrofa domestica (domestic pig)
```

C;Date: 14-Jul-1994 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999
C;Accession: JN0724
R;Huether, M.J.; Lin, G.; Smith, D.M.; Murtaugh, M.P.; Molitor, T.W.
Gene 129, 285-289, 1993
A;Title: Cloning, sequencing and regulation of an mRNA encoding porcine interleukin-1 be
A;Reference number: JN0724; MUID:93314975
A;Accession: JN0724
A;Molecule type: mRNA
A;Residues: 1-267 <HUE>
A;Cross-references: GB:M86725; NID:g164607; PIDN:AAA02584.1; PID:g164608
A;Experimental source: alveolar macrophage
C;Comment: This protein is a pleiotropic cytokine that mediates a variety of processes i
C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavag
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophag
F;115-267/Product: interleukin-1 beta #status predicted <IL1>
F;77/Binding site: myristate (Lys) (covalent) #status predicted

Query Match 18.7%; Score 155; DB 1; Length 267;
Best Local Similarity 22.8%; Pred. No. 8.4e-08;
Matches 52; Conservative 34; Mismatches 66; Indels 76; Gaps 7;

```
Qy       5 LKIDTPQQGSIQ-DINHRVW---VLQDQTLIAVPRKDRMSPVT---------------- 43
           | : : : |||| |:|::|   : |  ::|    |   :| :
Db      39 LDLGSLRNGSIQLQISHQLWNKSIRQMVSVIVAVEKPMKNPSSQAFCDDDQKSIFSFIFE 98

Qy      44 ---IALISCR-------HVETLE---------------------------------- 56
               | | :|        :|:::|
Db      99 EEPIILETCNDDFVCDANVQSMECKLQDKDHKSLVLAGPHMLKALHLLTGDLKREVVFCM 158

Qy      57 -----KDRGN--PIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYH 109
                 |  |  |: ||: | || | |    : |||||:: |    | : :  | |:||
Db     159 SFVQGDDSNNKIPVTLGIKGKNLYLSCVMKDNTPTLQLEDID-PKRYPKRDMEKRFVFYK 217

Qy     110 SQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
             ::      |||  :| |:|: |     |: |    |: : ||| : :|
Db     218 TEIKNRVEFESALYPNWYISTSQAEQKPVFLGNSKGRQDITDFTMEVL 265
```

RESULT 11
ICHU1B
interleukin-1 beta precursor [validated] - human
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1986 #sequence_revision 15-May-1998 #text_change 15-Sep-2000
C;Accession: A25542; A29019; A94023; A93361; I51852; I65200; I38132; B27616; A01848; S19
R;Clark, B.D.; Collins, K.L.; Gandy, M.S.; Webb, A.C.; Auron, P.E.
Nucleic Acids Res. 14, 7897-7914, 1986
A;Title: Genomic sequence for human prointerleukin 1 beta: possible evolution from a rev
A;Reference number: A25542; MUID:87040762
A;Accession: A25542
A;Molecule type: DNA; mRNA
A;Residues: 1-5,'K',7-269 <CLA>
A;Cross-references: GB:X04500; NID:g33788
A;Note: the mRNA sequence had codon AAG for 6-Lys, the DNA sequence had GAG for 6-Glu
R;Bensi, G.; Raugei, G.; Palla, E.; Carinci, V.; Buonamassa, D.T.; Melli, M.
Gene 52, 95-101, 1987
A;Title: Human interleukin-1 beta gene.
A;Reference number: A29019; MUID:87248099
A;Accession: A29019
A;Molecule type: DNA
A;Residues: 1-269 <BEN>
A;Cross-references: GB:M15840; NID:g186281; PIDN:AAA74137.1; PID:g386816
R;Auron, P.E.; Webb, A.C.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Dinare
Proc. Natl. Acad. Sci. U.S.A. 81, 7907-7911, 1984
A;Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
A;Reference number: A94023; MUID:85088517
A;Accession: A94023
A;Molecule type: mRNA
A;Residues: 1-5,'K',7-269 <AUR>
A;Cross-references: GB:K02770; NID:g186268; PIDN:AAA36106.1; PID:g307043
R;March, C.J.; Mosley, B.; Larsen, A.; Cerretti, D.P.; Braedt, G.; Price, V.; Gillis,
Nature 315, 641-647, 1985
A;Title: Cloning, sequence and expression of two distinct human interleukin-1 complem
A;Reference number: A93361; MUID:85240547
A;Accession: A93361
A;Molecule type: mRNA
A;Residues: 1-269 <MAR>
A;Cross-references: GB:X02532; NID:g33789; PIDN:CAA26372.1; PID:g33790
A;Note: parts of this sequence, including the amino end of the mature form, were conf
R;Webb, A.C.; Dinarello, C.A.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.;
Adv. Gene Technol. 22, 339-340, 1985
A;Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
A;Reference number: I51852
A;Accession: I51852
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-5,'K',7-19,'H',21-110,'Q',112-176,'A',178-213,'P',215-269 <WEB>
A;Cross-references: GB:M54933; NID:g186287; PIDN:AAA59136.1; PID:g186288
R;Nishida, T.; Nishino, N.; Takano, M.; Kawai, K.; Bando, K.; Masui, Y.; Nakai, S.; H
Biochem. Biophys. Res. Commun. 143, 345-352, 1987
A;Title: cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell line.
A;Reference number: I52217; MUID:87156769
A;Accession: I65200
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-269 <NIS>
A;Cross-references: GB:M15330; NID:g186283; PIDN:AAA59135.1; PID:g307045
R;Kotenko, S.V.; Bulenkov, M.T.; Veiko, V.P.; Epishin, S.M.; Lomakin, I.B.; Emel'yano
ii, S.A.; Vinetskii, Y.P.
Dokl. Akad. Nauk SSSR 309, 1005-1008, 1989
A;Title: [Cloning of the cDNA coding for human prointerleukin-1 alpha and prointerleu
A;Reference number: I38131; MUID:90249285
A;Accession: I38132
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-269 <KOT>
A;Cross-references: EMBL:X56087; NID:g35662; PIDN:CAA39567.1; PID:g35663
R;Zsebo, K.M.; Wypych, J.; Yuschenkoff, V.N.; Lu, H.; Hunt, P.; Dukes, P.P.; Langley,
Blood 71, 962-968, 1988
A;Title: Effects of hematopoietin-1 and interleukin 1 activities on early hematopoiet
A;Reference number: A90732; MUID:88184226
A;Accession: B27616
A;Molecule type: protein
A;Residues: 117-123,'X',125-126,'X',128 <ZSE>
R;Stevenson, F.T.; Bursten, S.L.; Fanton, C.; Locksley, R.M.; Lovett, D.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 7245-7249, 1993
A;Title: The 31-kDa precursor of interleukin 1alpha is myristoylated on specific lysi
A;Reference number: A48293; MUID:93348250
A;Contents: annotation; myristylation of lysines
R;Nanduri, V.B.; Hulmes, J.D.; Pan, Y.C.E.; Kilian, P.L.; Stern, A.S.
Biochim. Biophys. Acta 1118, 25-35, 1991
A;Title: The role of arginine residues in interleukin 1 receptor binding.
A;Reference number: S19608; MUID:92110334
A;Contents: annotation; type 1 IL-1 receptor interaction site
A;Note: modification of Arg-120 by phenylglyoxal blocks receptor binding
R;Clore, G.M.; Gronenborn, A.M.
submitted to the Brookhaven Protein Data Bank, January 1991
A;Reference number: A50049; PDB:6I1B
A;Contents: annotation; conformation by (13)C- and (1)H-NMR, residues 117-269
R;Clore, G.M.; Wingfield, P.T.; Gronenborn, A.M.
Biochemistry 30, 2315-2323, 1991
A;Title: High-resolution three-dimensional structure of interleukin 1beta in solution
A;Reference number: A44675; MUID:91159409
A;Contents: annotation; (1)H-NMR structural determination
R;Hazuda, D.J.; Strickler, J.; Simon, P.; Young, P.R.
J. Biol. Chem. 266, 7081-7086, 1991
A;Title: Structure-function mapping of interleukin 1 precursors. Cleavage leads to a
A;Reference number: A39774; MUID:91201363
A;Contents: annotation
R;Finzel, B.C.; Watenpaugh, K.D.; Einspahr, H.M.
submitted to the Brookhaven Protein Data Bank, December 1989
A;Reference number: A50016; PDB:1I1B

```
A;Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 119-269
R;Finzel, B.C.; Clancy, L.L.; Holland, D.R.; Muchmore, S.W.; Watenpaugh, K.D.; Einspahr,
J. Mol. Biol. 209, 779-791, 1989
A;Title: Crystal structure of recombinant human interleukin-1beta at 2.0 angstrom resolu
A;Reference number: A44666; MUID:90064532
A;Contents: annotation; X-ray crystallography, 2.0 angstroms
C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavag
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a
C;Genetics:
A;Gene: GDB:IL1B
A;Cross-references: GDB:120094; OMIM:147720
A;Map position: 2q13-2q21
A;Introns: 16/2; 33/3; 101/1; 156/1; 199/3
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophag
F;117-269/Product: interleukin-1 beta #status experimental <IL1>
F;76/Binding site: myristate (Lys) (covalent) (partial) #status experimental
F;123/Binding site: carbohydrate (Asn) (covalent) #status absent


  Query Match             17.3%;  Score 143.5;  DB 1;  Length 269;
  Best Local Similarity   34.5%;  Pred. No. 1.2e-06;
  Matches   39;  Conservative   15;  Mismatches   56;  Indels    3;  Gaps    2;

Qy      46 LISCRHVETLEKDRGNPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSF 105
           : |   |:  | :   |: |||   || | |    |:|||||:  |  : | : :  | |
Db     157 VFSMSFVQGEESNDKIPVALGLKEKNLYLSCVLKDDKPTLQLESVDPKN-YPKKKMEKRF 215

Qy     106 LFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTMLF 158
           :|   :      |||  || |:|: |     |: |    |  : |||  || |
Db     216 VFNKIEINNKLEFESAQFPNWYISTSQAENMPVFLGGTKGGQDITDF--TMQF 266


RESULT  12
A30584
interleukin-1 beta precursor - rabbit
N;Alternate names: hematopoietin-1; IL-1 beta; lymphocyte proliferation potentiating fac
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 25-May-1989 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999
C;Accession: A27714; A30584; JU0082; A32166
R;Mori, S.; Goto, F.; Goto, K.; Ohkawara, S.; Maeda, S.; Shimada, K.; Yoshinaga, M.
Biochem. Biophys. Res. Commun. 150, 1237-1243, 1988
A;Title: Cloning and sequence analysis of a cDNA for lymphocyte proliferation potentiati
A;Reference number: A27714; MUID:88134238
A;Accession: A27714
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-268 <MOR>
R;Cannon, J.G.; Clark, B.D.; Wingfield, P.; Schmeissner, U.; Losberger, C.; Dinarello, C
J. Immunol. 142, 2299-2306, 1989
A;Title: Rabbit IL-1. Cloning, expression, biologic properties, and transcription during
A;Reference number: A30584; MUID:89176242
A;Accession: A30584
A;Molecule type: mRNA
A;Residues: 1-268 <CAN>
A;Cross-references: GB:M26295; NID:g516632; PIDN:AAA31373.1; PID:g516633
R;Young, P.R.; Sylvester, D.
Protein Eng. 2, 545-551, 1989
A;Title: Cloning of rabbit interleukin-1 beta: differential evolution of IL-1 alpha and
A;Reference number: A94230; MUID:89315718
A;Accession: JU0082
A;Molecule type: mRNA
A;Residues: 1-268 <YOU>
C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavag
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;117-268/Product: interleukin-1 beta #status predicted <ILB>


  Query Match             17.0%;  Score 141.5;  DB 1;  Length 268;
  Best Local Similarity   33.0%;  Pred. No. 1.9e-06;
  Matches   36;  Conservative   16;  Mismatches   56;  Indels    1;  Gaps    1;

Qy      46 LISCRHVETLEKDRGNPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSF 105
           : |   |:  | :   |: ||| | || | |    |:|||||:  |  : | : :  | |
Db     156 VFSMSFVQGEESNDKIPVALGLRGKNLYLSCVMKDDKPTLQLESVD-PNRYPKKKMEKRF 214

Qy     106 LFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGL 154
           :|   :      |||  || |:|: |     |: |    |  : |||
Db     215 VFNKIEIKDKLEFESAQFPNWYISTSQTEYMPVFLGNNSGGQDLIDFSM 263


RESULT  13
JC5646
interleukin-1 beta - horse
C;Species: Equus caballus (domestic horse)
C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 20-Jun-2000
C;Accession: JC5646
R;Kato, H.; Youn, H.Y.; Ohashi, T.; Watari, T.; Goitsuka, R.; Tsujimoto, H.; Hasegawa
Gene 177, 11-16, 1996
A;Title: Identification of an alternatively spliced transcript of equine interleukin-
A;Reference number: JC5646; MUID:97080493
A;Accession: JC5646
A;Molecule type: mRNA
A;Residues: 1-214 <KAT>
A;Cross-references: DDBJ:D42165; NID:g2463549; PIDN:BAA22528.1; PID:g2463550
C;Comment: This protein mediates a variety of physiological response to infections an
synthesis by hepatocytes, and stimulation of chondrocytes and synovial cells to produ
C;Superfamily: interleukin-1


  Query Match             16.7%;  Score 138.5;  DB 2;  Length 214;
  Best Local Similarity   28.8%;  Pred. No. 2.8e-06;
  Matches   44;  Conservative   21;  Mismatches   71;  Indels   17;  Gaps    3;

Qy       1 MEKALKIDTPQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISC-RHVETLEKDR 59
           :||  ||  |   : || : |                | :   :: |   |:  |:
Db      71 VEKLKKIPVPCSQAFQDDDLR--------------SLFSVIFEEVVFCMSFVQGEEETD 115

Qy      60 GNPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFE 119
             |: |||   || | |     :|||||:  |  : | : :  | |:|   :   |  ||
Db     116 KIPVALGLKEKNLYLSCGMKDGKPTLQLETVD-PNTYPKRKMEKRFVFNKMEIKGNVEFE 174

Qy     120 SVAFPGWFIAVSSEGGCPLILTQELGKANTTDF 152
           |  :| |:|: |     |: |    |  : |||
Db     175 SAMYPNWYISTSQAEKSPVFLGNTRGGRDITDF 207


RESULT  14
I55969
interleukin-1 beta precursor - mouse
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999
C;Accession: I55969; A24719; S13029
R;Gray, P.W.; Glaister, D.; Chen, E.; Goeddel, D.V.; Pennica, D.
J. Immunol. 137, 3644-3648, 1986
A;Title: Two interleukin 1 genes in the mouse: Cloning and expression of the cDNA for
A;Reference number: I55969; MUID:87058957
A;Accession: I55969
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-269 <RES>
A;Cross-references: GB:M15131; NID:g198293; PIDN:AAA39276.1; PID:g309398
R;Telford, J.L.; Macchia, G.; Massone, A.; Carinci, V.; Palla, E.; Melli, M.
Nucleic Acids Res. 14, 9955-9963, 1986
A;Title: The murine interleukin 1-beta gene: structure and evolution.
A;Reference number: A24719; MUID:87117546
A;Accession: A24719
A;Molecule type: mRNA
A;Residues: 1-269 <TEL>
A;Cross-references: GB:X04964; NID:g52666; PIDN:CAA28637.1; PID:g52667
R;Daumy, G.O.; Wilder, C.L.; Merenda, J.M.; McColl, A.S.; Geoghegan, K.F.; Otterness,
```

FEBS Lett. 278, 98-102, 1991
A;Title: Reduction of biological activity of murine recombinant interleukin-1beta by sel
A;Reference number: S13029; MUID:91130610
A;Accession: S13029
A;Status: preliminary
A;Molecule type: protein
A;Residues: 118-269 <DAU>
C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavag
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a
C;Genetics:
A;Gene: IL-1-beta
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;118-269/Product: interleukin-1 beta #status experimental <IL1>

Query Match 14.6%; Score 121; DB 1; Length 269;
Best Local Similarity 35.2%; Pred. No. 0.0002;
Matches 32; Conservative 11; Mismatches 46; Indels 2; Gaps 2;

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Qy      62 PIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESV 121
           |: ||| | || | |      |||||:  |    | : :  | |:|   :      |||
Db     174 PVALGLKGKNLYLSCVMKDGTPTLQLESVDPKQ-YPKKKMEKRFVFNKIEVKSKVEFESA 232

Qy     122 AFPGWFIAVSSEGGCPLILTQELGKANTTDF 152
           || |:|: |     |: |    |: :  ||
Db     233 EFPNWYISTSQAEHKPVFLGNNSGQ-DIIDF 262
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RESULT 15
F86463
hypothetical protein F12G12.19 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C;Accession: F86463
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: F86463
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-256 <STO>
A;Cross-references: GB:AE005172; NID:g10086476; PIDN:AAG12536.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1

Query Match 9.8%; Score 81; DB 2; Length 256;
Best Local Similarity 25.2%; Pred. No. 1.8;
Matches 32; Conservative 18; Mismatches 45; Indels 32; Gaps 6;

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Qy      30 LIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNGLNLCLMCAKVGDQPTLQLKE 89
           ::|   :  :||||: |  |                  | |:           ||:
Db      22 MVASLEESGLSPVTVDLTGC------------------GFNM----TDTNTVSTLEEYS 58

Qy      90 KDIMDLY-NQPEPVKSFLFYHSQSGRNSTFESVAFP-----GWFIAVS--SEGGCPL-IL 140
           | ::||  | ||  |  |  ||  | : ::    ||       |:  :  |:|  |  :
Db      59 KPLIDLLENLPEEEKVILVGHSTGGASISYALERFPEKISKAIFVCATMVSDGQRPFDVF 118

Qy     141 TQELGKA 147
           ::||| |
Db     119 SEELGSA 125
```

Search completed: June 20, 2002, 15:03:52
Job time: 162 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 20, 2002, 15:11:19 ; Search time 19.43 Seconds
(without alignments)
314.858 Million cell updates/sec

Title: US-09-763-498-8
Perfect score: 830
Sequence: 1 MEKALKIDTPQQGSIQDINH.....ILTQELGKANTTDFGLTMLF 158

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	195.5	23.6	178	1	IL1X_MOUSE	P25085 mus musculu
2	190.5	23.0	178	1	IL1X_RAT	P25086 rattus norv
3	186.5	22.5	177	1	IL1X_HORSE	O18999 equus cabal
4	183.5	22.1	177	1	IL1X_HUMAN	P18510 homo sapien
5	178.5	21.5	177	1	IL1X_PIG	Q29056 sus scrofa
6	173.5	20.9	266	1	IL1B_SHEEP	P21621 ovis aries
7	172.5	20.8	174	1	IL1X_BOVIN	O77482 bos taurus
8	170.5	20.5	177	1	IL1X_RABIT	P26890 oryctolagus
9	167	20.1	266	1	IL1B_CEREL	P51745 cervus elap
10	164	19.8	266	1	IL1B_BOVIN	P09428 bos taurus
11	162.5	19.6	266	1	IL1B_CAPHI	P79162 capra hircu
12	155	18.7	267	1	IL1B_PIG	P26889 sus scrofa
13	145.5	17.5	268	1	IL1B_MACFA	P79182 macaca fasc
14	145.5	17.5	269	1	IL1B_MACMU	P48090 macaca mula
15	143.5	17.3	269	1	IL1B_HUMAN	P01584 homo sapien
16	143.5	17.3	269	1	IL1B_MACNE	P51493 macaca neme
17	142.5	17.2	266	1	IL1B_CAVPO	Q9wvg1 cavia porce
18	141.5	17.0	268	1	IL1B_RABIT	P14628 oryctolagus
19	137.5	16.6	269	1	IL1B_CERTO	P46648 cercocebus
20	133.5	16.1	268	1	IL1B_HORSE	Q28386 equus cabal
21	128	15.4	268	1	IL1B_RAT	Q63264 rattus norv
22	127.5	15.4	267	1	IL1B_FELCA	P41687 felis silve
23	121	14.6	269	1	IL1B_MOUSE	P10749 mus musculu
24	120.5	14.5	269	1	IL1B_TRIVU	Q9xs77 trichosurus
25	82	9.9	270	1	IL1A_HORSE	Q28385 equus cabal
26	79	9.5	268	1	IL1A_CAPHI	P79161 capra hircu
27	79	9.5	270	1	IL1A_FELCA	O46613 felis silve
28	77	9.3	268	1	IL1A_BOVIN	P08831 bos taurus
29	77	9.3	501	1	GLPK_ECOLI	P08859 escherichia
30	75.5	9.1	270	1	IL1A_PIG	P18430 sus scrofa
31	75	9.0	1505	1	CUT2_HUMAN	O14529 homo sapien
32	74	8.9	268	1	IL1A_SHEEP	Q28579 ovis aries
33	73.5	8.9	1297	1	PUR4_HAEIN	P43847 haemophilus
34	72.5	8.7	325	1	RIR2_MYCLE	Q9cbq2 mycobacteri
35	72.5	8.7	421	1	CHDE_MUCRO	P50325 mucor rouxi
36	72.5	8.7	950	1	IF2_LACLC	Q9x764 lactococcus
37	72	8.7	1220	1	IF2P_HUMAN	O60841 homo sapien
38	72	8.7	1955	1	PC15_HUMAN	Q96qu1 homo sapien
39	71.5	8.6	194	1	IL18_RAT	P97636 rattus norv
40	71	8.6	872	1	MGR2_HUMAN	Q14416 homo sapien
41	71	8.6	1426	1	CUT2_MOUSE	P70298 mus musculu
42	71	8.6	1943	1	PC15_MOUSE	Q99pj1 mus musculu
43	70.5	8.5	271	1	IL1A_MACFA	P79340 macaca fasc
44	70.5	8.5	556	1	CD19_HUMAN	P15391 homo sapien
45	70.5	8.5	944	1	IF2_LACLA	P58002 lactococcus

ALIGNMENTS

RESULT 1
IL1X_MOUSE
ID IL1X_MOUSE STANDARD; PRT; 178 AA.
AC P25085; O70207;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE (IRAP).
GN IL1RN OR IL-1RA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=91250712; PubMed=1828262;
RA Zahedi K., Seldin M.F., Rits M., Ezekowitz R.A., Whitehead A.S.;
RT "Mouse IL-1 receptor antagonist protein. Molecular characterization,
RT gene mapping, and expression of mRNA in vitro and in vivo.";
RL J. Immunol. 146:4228-4233(1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=91316273; PubMed=1830498;
RA Matsushime H., Roussel M.F., Matsushima K., Hishinuma A., Sherr C.J.;
RT "Cloning and expression of murine interleukin-1 receptor antagonist
RT in macrophages stimulated by colony-stimulating factor 1.";
RL Blood 78:616-623(1991).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=SWISS;
RX MEDLINE=94271931; PubMed=8003626;
RA Zahedi K.A., Uhlar C.M., Rits M., Prada A.E., Whitehead A.S.;
RT "The mouse interleukin 1 receptor antagonist protein: gene structure
RT and regulation in vitro.";
RL Cytokine 6:1-9(1994).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=FVBXDBA/1 LACJ;
RX MEDLINE=98209757; PubMed=9550387;
RA Gabay C., Porter B., Fantuzzi G., Arend W.P.;
RT "Mouse IL-1 receptor antagonist isoforms: complementary DNA cloning
RT and protein expression of intracellular isoform and tissue
RT distribution of secreted and intracellular IL-1 receptor antagonist in
RT vivo.";
RL J. Immunol. 159:5905-5913(1997).
RN [5]
RP SEQUENCE OF 7-178 FROM N.A.
RX MEDLINE=91271363; PubMed=1828896;
RA Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
RA Brandhuber B.J., Thompson R.C.;
RT "Interleukin 1 receptor antagonist is a member of the interleukin 1
RT gene family: evolution of a cytokine control mechanism.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
RN [6]
RP SEQUENCE OF 23-178 FROM N.A.

```
RX   MEDLINE=92037824; PubMed=1834470;
RA   Shuck M.E., Eessalu T.E., Tracey D.E., Bienkowski M.J.;
RT   "Cloning, heterologous expression and characterization of murine
RT   interleukin 1 receptor antagonist protein.";
RL   Eur. J. Immunol. 21:2775-2780(1991).
CC   -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC       RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC   -!- SUBCELLULAR LOCATION: SECRETED (ISOFORM 1) OR INTRACELLULAR
CC       (ISOFORM 2).
CC   -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC       produced by alternative splicing.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M74294; AAA39309.1; -.
DR   EMBL; M64404; AAA39277.1; -.
DR   EMBL; L32838; AAA20576.1; -.
DR   EMBL; AF001795; AAC15251.1; -.
DR   EMBL; M57525; AAA39278.1; -.
DR   EMBL; M63100; AAA39310.1; -.
DR   EMBL; S64082; AAB20265.1; -.
DR   PIR; B40956; B40956.
DR   PIR; A44610; A44610.
DR   HSSP; P18510; 1IRA.
DR   MGD; MGI:96547; Il1rn.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Glycoprotein; Signal; Alternative splicing.
FT   SIGNAL        1     26       BY SIMILARITY.
FT   CHAIN        27    178       INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT                                 PROTEIN.
FT   DISULFID     92    142       BY SIMILARITY.
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC      1     21       MEICWGPYSHLISLLLLILLFH -> MA (IN ISOFORM
FT                                 2).
SQ   SEQUENCE   178 AA;  20274 MW;  84AA002A3119C024 CRC64;


  Query Match             23.6%;  Score 195.5;  DB 1;  Length 178;
  Best Local Similarity   35.1%;  Pred. No. 2.8e-13;
  Matches   47;  Conservative   21;  Mismatches   45;  Indels   21;  Gaps    2;

Qy      15 IQDINHRVWVLQDQTLIA-------VPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGL 67
           | | | : : |::  |||       :  ::::  | | | |              ::||:
Db      41 IWDTNQKTFYLRNNQLIAGYLQGPNIKLEEKIDMVPIDLHS-------------VFLGI 86

Qy      68 NGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWF 127
           :|  ||| ||| ||   |||:| :| ||    |  | | |  |: |  ::||| | ||||
Db      87 HGGKLCLSCAKSGDDIKLQLEEVNITDLSKNKEEDKRFTFIRSEKGPTTSFESAACPGWF 146

Qy     128 IAVSSEGGCPLILT 141
           :  : |   |: ||
Db     147 LCTTLEADRPVSLT 160


RESULT   2
IL1X_RAT
ID   IL1X_RAT       STANDARD;      PRT;   178 AA.
AC   P25086;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE   (IRAP).
GN   IL1RN OR IL-1RA.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91271363; PubMed=1828896;
RA   Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
RA   Brandhuber B.J., Thompson R.C.;
RT   "Interleukin 1 receptor antagonist is a member of the interleukin 1
RT   gene family: evolution of a cytokine control mechanism.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
CC   -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC       RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M63101; AAA41434.1; -.
DR   PIR; C40956; C40956.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Glycoprotein; Signal.
FT   SIGNAL        1     26       BY SIMILARITY.
FT   CHAIN        27    178       INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT                                 PROTEIN.
FT   DISULFID     92    142       BY SIMILARITY.
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   178 AA;  20282 MW;  F3A5754FB6C51B03 CRC64;


  Query Match             23.0%;  Score 190.5;  DB 1;  Length 178;
  Best Local Similarity   35.1%;  Pred. No. 9.3e-13;
  Matches   46;  Conservative   20;  Mismatches   50;  Indels   15;  Gaps    2;

Qy      15 IQDINHRVWVLQDQTLIA----VPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNGL 70
           | | | : : |::  |||     |       : :  |  |:|           :||::|
Db      41 IWDTNQKTFYLRNNQLIAGYLQGPNTKLEEKIDMVPIDFRNV----------FLGIHGG 89

Qy      71 NLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAV 130
           |||  | | ||   |||:| :| ||    |  | | |  |::|  ::|||:| ||||:
Db      90 KLCLSCVKSGDDTKLQLEEVNITDLNKNKEEDKRFTFIRSETGPTTSFESLACPGWFLCT 149

Qy     131 SSEGGCPLILT 141
           : |   |: ||
Db     150 TLEADHPVSLT 160


RESULT   3
IL1X_HORSE
ID   IL1X_HORSE     STANDARD;      PRT;   177 AA.
AC   O18999; O77745;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE   (IRAP).
GN   IL1RN OR IL1RA.
OS   Equus caballus (Horse).
```

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97366446; PubMed=9223227;
RA   Kato H., Ohashi T., Matsushiro H., Watari T., Goitsuka R.,
RA   Tsujimoto H., Hasegawa A.;
RT   "Molecular cloning and functional expression of equine interleukin-1
RT   receptor antagonist.";
RL   Vet. Immunol. Immunopathol. 56:221-231(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98285942; PubMed=9622739;
RA   Howard R.D., McIlwraith C.W., Trotter G.W., Nyborg J.K.;
RT   "Cloning of equine interleukin-1 receptor antagonist and
RT   determination of its full-length cDNA sequence.";
RL   Am. J. Vet. Res. 59:712-716(1998).
CC   -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC       RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D83714; BAA22529.1; -.
DR   EMBL; U92482; AAC39257.1; -.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Glycoprotein; Signal.
FT   SIGNAL        1     25       BY SIMILARITY.
FT   CHAIN        26    177       INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT                                PROTEIN.
FT   DISULFID     91    141       BY SIMILARITY.
FT   CARBOHYD    109    109       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     19     19       F -> L (IN REF. 2).
SQ   SEQUENCE   177 AA;  20459 MW;  1ABC377F1F1CF80B CRC64;


  Query Match             22.5%;  Score 186.5;  DB 1;  Length 177;
  Best Local Similarity   33.3%;  Pred. No. 2.4e-12;
  Matches   43;  Conservative   25;  Mismatches   54;  Indels    7;  Gaps    2;

Qy      15 IQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNGLNLCL 74
           | |:| : : :::  |:|   ::  : :   :     |  :| |    ::|||:|  |||
Db      40 IWDVNQKTFYMRNNQLVAGYLQESNTKLQEKI----DVVPIEPD---ALFLGLHGRKLCL 92

Qy      75 MCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEG 134
             | | ||:   ||:  :| ||    |  | | |  | ||  ::||| | ||||:  : |
Db      93 ACVKSGDEIRFQLEAVNITDLSKNKEENKRFTFIRSNSGPTTSFESAACPGWFLCTAQEA 152

Qy     135 GCPLILTQE 143
             |: || :
Db     153 DRPVSLTNK 161


RESULT   4
IL1X_HUMAN
ID   IL1X_HUMAN     STANDARD;      PRT;   177 AA.
AC   P18510; Q14628; Q9UPC0;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Interleukin-1 receptor antagonist protein precursor (IL-1RA) (ICIL-
DE   1RA) (IRAP) (IL-1RN).
GN   IL1RN OR IL1RA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=90220867; PubMed=2139180;
RA   Carter D.B., Deibel M.R. Jr., Dunn C.J., Tomich C.S.C., Laborde A.L.,
RA   Slightom J.L., Berger A.E., Bienkowski M.J., Sun F.F., McEwan R.N.,
RA   Harris P.K.W., Yem A.W., Waszak G.A., Chosay J.G., Sieu L.C.,
RA   Hardee M.M., Zurcher-Neely H.A., Reardon I.M., Heinrikson R.L.,
RA   Truesdell S.E., Shelly J.A., Eessalu T.E., Taylor B.M., Tracey D.E.;
RT   "Purification, cloning, expression and biological characterization of
RT   an interleukin-1 receptor antagonist protein.";
RL   Nature 344:633-638(1990).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=90136921; PubMed=2137201;
RA   Eisenberg S.P., Evans R.J., Arend W.P., Verderber E., Brewer M.T.,
RA   Hannum C.H., Thompson R.C.;
RT   "Primary structure and functional expression from complementary DNA
RT   of a human interleukin-1 receptor antagonist.";
RL   Nature 343:341-346(1990).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=91271363; PubMed=1828896;
RA   Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
RA   Brandhuber B.J., Thompson R.C.;
RT   "Interleukin 1 receptor antagonist is a member of the interleukin 1
RT   gene family: evolution of a cytokine control mechanism.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=92338323; PubMed=1385987;
RA   Lennard A., Gorman P., Carrier M., Griffiths S., Scotney H.,
RA   Sheer D., Solari R.;
RT   "Cloning and chromosome mapping of the human interleukin-1 receptor
RT   antagonist gene.";
RL   Cytokine 4:83-89(1992).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
RX   MEDLINE=97146044; PubMed=8992991;
RA   Jenkins J.K., Drong R.F., Shuck M.E., Bienkowski M.J., Slightom J.L.,
RA   Arend W.P., Smith M.F. Jr.;
RT   "Intracellular IL-1 receptor antagonist promoter: cell type-specific
RT   and inducible regulatory regions.";
RL   J. Immunol. 158:748-755(1997).
RN   [6]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RX   MEDLINE=91219436; PubMed=1827201;
RA   Haskill S., Martin G., van Le L., Morris J., Peace A., Bigler C.F.,
RA   Jaffe G.J., Hammerberg C., Sporn S.A., Fong S., Arend W.P., Ralph P.;
RT   "cDNA cloning of an intracellular form of the human interleukin 1
RT   receptor antagonist associated with epithelium.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:3681-3685(1991).
RN   [7]
RP   SEQUENCE FROM N.A. (ISOFORM 3).
RX   MEDLINE=95355865; PubMed=7629520;
RA   Muzio M., Polentarutti N., Sironi M., Poli G., De Gioia L.,
RA   Introna M., Mantovani A., Colotta F.;
RT   "Cloning and characterization of a new isoform of the interleukin 1
RT   receptor antagonist.";
RL   J. Exp. Med. 182:623-628(1995).
RN   [8]
RP   SEQUENCE OF 26-45.
RX   MEDLINE=90136920; PubMed=2137200;
RA   Hannum C.H., Wilcox C.J., Arend W.P., Joslin F.G., Dripps D.J.,
RA   Heimdal P.L., Armes L.G., Sommer A., Eisenberg S.P., Thompson R.C.;
RT   "Interleukin-1 receptor antagonist activity of a human interleukin-1
RT   inhibitor.";
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RL   Nature 343:336-340(1990).
RN   [9]
RP   SEQUENCE OF 26-52.
RX   MEDLINE=90354444; PubMed=2143761;
RA   Bienkowski M.J., Eessalu T.E., Berger A.E., Truesdell S.E.,
RA   Shelly J.A., Laborde A.L., Zurcher-Neely H.A., Reardon I.M.,
RA   Heinrikson R.L., Chosay J.G., Tracey D.E.;
RT   "Purification and characterization of interleukin 1 receptor level
RT   antagonist proteins from THP-1 cells.";
RL   J. Biol. Chem. 265:14505-14511(1990).
RN   [10]
RP   SEQUENCE OF 35-177 FROM N.A. (ISOFORM 4).
RX   MEDLINE=98183404; PubMed=9514884;
RA   Weissbach L., Tran K., Colquhoun S.A., Champliaud M.F., Towle C.A.;
RT   "Detection of an interleukin-1 intracellular receptor antagonist mRNA
RT   variant.";
RL   Biochem. Biophys. Res. Commun. 244:91-95(1998).
RN   [11]
RP   STRUCTURE BY NMR.
RX   MEDLINE=92297633; PubMed=1534997;
RA   Stockman B.J., Scahill T.A., Roy M., Ulrich E.L., Strakalaitis N.A.,
RA   Brunner D.P., Yem A.W., Deibel M.R. Jr.;
RT   "Secondary structure and topology of interleukin-1 receptor
RT   antagonist protein determined by heteronuclear three-dimensional NMR
RT   spectroscopy.";
RL   Biochemistry 31:5237-5244(1992).
RN   [12]
RP   STRUCTURE BY NMR.
RX   MEDLINE=94320651; PubMed=8045306;
RA   Stockman B.J., Scahill T.A., Strakalaitis N.A., Brunner D.P.,
RA   Yem A.W., Deibel M.R. Jr.;
RT   "Solution structure of human interleukin-1 receptor antagonist
RT   protein.";
RL   FEBS Lett. 349:79-83(1994).
RN   [13]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=94230368; PubMed=8175703;
RA   Vigers G.P.A., Caffes P., Evans R.J., Thompson R.C., Eisenberg S.P.,
RA   Brandhuber B.J.;
RT   "X-ray structure of interleukin-1 receptor antagonist at 2.0-A
RT   resolution.";
RL   J. Biol. Chem. 269:12874-12879(1994).
RN   [14]
RP   X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX   MEDLINE=95172072; PubMed=7867645;
RA   Schreuder H.A., Rondeau J.-M., Tardif C., Soffientini A., Sarubbi E.,
RA   Akeson A., Bowlin T.L., Yanofsky S., Barrett R.W.;
RT   "Refined crystal structure of the interleukin-1 receptor antagonist.
RT   Presence of a disulfide link and a cis-proline.";
RL   Eur. J. Biochem. 227:838-847(1995).
RN   [15]
RP   X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 32-177 IN COMPLEX WITH IL1R.
RX   MEDLINE=97215904; PubMed=9062194;
RA   Schreuder H., Tardif C., Trump-Kallmeyer S., Soffientini A.,
RA   Sarubbi E., Akeson A., Bowlin T., Yanofsky S., Barrett R.W.;
RT   "A new cytokine-receptor binding mode revealed by the crystal
RT   structure of the IL-1 receptor with an antagonist.";
RL   Nature 386:194-200(1997).
CC   -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC       RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC   -!- SUBCELLULAR LOCATION: SECRETED (ISOFORM 1) OR INTRACELLULAR
CC       (ISOFORMS 2, 3 AND 4).
CC   -!- ALTERNATIVE PRODUCTS: 4 isoforms; 1 (shown here), 2/icIL-1ra,
CC       3/icIL-1ra type II and 4; are produced by alternative splicing.
CC   -!- TISSUE SPECIFICITY: THE INTRACELLULAR FORM OF IL-1RA IS
CC       PREDOMINANTLY EXPRESSED IN EPITHELIAL CELLS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   -!- DATABASE: NAME=R&D Systems' cytokine source book: IL1RN;
CC       WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=205".
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M55646; AAA59138.1; -.
DR   EMBL; M63099; AAB41943.1; -.
DR   EMBL; X52015; CAA36262.1; -.
DR   EMBL; X53296; CAA37386.1; -.
DR   EMBL; X64532; CAA45832.1; -.
DR   EMBL; U65590; AAB92268.1; -.
DR   EMBL; U65590; AAB92270.1; -.
DR   EMBL; X84348; CAA59087.1; -.
DR   EMBL; U65590; AAB92269.1; -.
DR   EMBL; AF043143; AAC39672.1; -.
DR   PIR; A30368; A30368.
DR   PIR; A37822; A37822.
DR   PIR; S08160; S08160.
DR   PIR; S08159; S08159.
DR   PIR; A40956; A40956.
DR   PIR; A39386; A39386.
DR   PDB; 1ITN; 30-APR-94.
DR   PDB; 2IRT; 15-OCT-94.
DR   PDB; 1IRP; 27-FEB-95.
DR   PDB; 1ILR; 07-FEB-95.
DR   PDB; 1ILT; 01-APR-95.
DR   PDB; 1IRA; 17-JUN-98.
DR   Aarhus/Ghent-2DPAGE; 7104; IEF.
DR   Aarhus/Ghent-2DPAGE; 7105; IEF.
DR   MIM; 147679; -.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Glycoprotein; Signal; Alternative splicing; 3D-structure.
FT   SIGNAL        1     25
FT   CHAIN        26    177       INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT                                 PROTEIN.
FT   DISULFID      91    141
FT   CARBOHYD     109    109       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC       1     21       MEICRGLRSHLITLLLFLFHS -> MAL (IN
FT                                 ISOFORM 2).
FT   VARSPLIC       1     21       MEICRGLRSHLITLLLFLFHS -> MALADLYEEGGGGGGE
FT                                 GEDNADSK (IN ISOFORM 3).
FT   VARSPLIC       1     34       MISSING (IN ISOFORM 4).
SQ   SEQUENCE   177 AA;  20055 MW;  D1690776A7394057 CRC64;


  Query Match             22.1%;  Score 183.5;  DB 1;  Length 177;
  Best Local Similarity   30.6%;  Pred. No. 4.9e-12;
  Matches   45;  Conservative   26;  Mismatches   49;  Indels   27;  Gaps    3;

Qy      15 IQDINHRVWVLQDQTLIA-------VPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGL 67
           | |:| : : |::  |:|       |  ::::  | |              : ::||:
Db      40 IWDVNQKTFYLRNNQLVAGYLQGPNVNLEEKIDVVPI-------------EPHALFLGI 85

Qy      68 NGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWF 127
           :|  :|| | | ||:  |||:  :| ||    :  | | |  | ||  ::|:| | ||||
Db      86 HGGKMCLSCVKSGDETRLQLEAVNITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWF 145

Qy     128 IAVSSEGGCPLILTQELGKANTTDFGL 154
           :  : |   |: ||       |  | |:
Db     146 LCTAMEADQPVSLT------NMPDEGV 166


RESULT   5
IL1X_PIG
ID   IL1X_PIG       STANDARD;      PRT;   177 AA.
AC   Q29056;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
```

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DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE   (IRAP).
GN   IL1RN OR IRAP1.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CROSSBREED; TISSUE=Lung;
RA   Yin J., Murtaugh M.P.;
RT   "Characterization of IRAP in morphine treated pig.";
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC       RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L38849; AAA99424.1; -.
DR   HSSP; P18510; 1IRA.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Glycoprotein; Signal.
FT   SIGNAL        1     25       BY SIMILARITY.
FT   CHAIN        26    177       INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT                                 PROTEIN.
FT   DISULFID      91    141      BY SIMILARITY.
FT   CARBOHYD     109    109      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   177 AA;  20093 MW;  2114DC6119A9D5F9 CRC64;


  Query Match             21.5%;  Score 178.5;  DB 1;  Length 177;
  Best Local Similarity   32.4%;  Pred. No. 1.6e-11;
  Matches   44;  Conservative   20;  Mismatches   47;  Indels   25;  Gaps    2;

Qy      15 IQDINHRVWVLQDQTLIA---------VPRKDRMSPVTIALISCRHVETLEKDRGNPIYL 65
           | |:| : : |::  |:|         :  |  : ||                 : ::|
Db      40 IWDVNQKTFYLRNNQLVAGYLQGPNTKLEEKIDVVPV---------------EPHFVFL 83

Qy      66 GLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPG 125
           |::|  ||| | | ||:  |||   :| ||    |  | | |  | ||  ::||| | ||
Db      84 GIHGGKLCLSCVKSGDEMKLQLDAVNITDLRKNSEQDKRFTFIRSDSGPTTSFESAACPG 143

Qy     126 WFIAVSSEGGCPLILT 141
           ||:  : |   |: ||
Db     144 WFLCTALEADQPVGLT 159


RESULT   6
IL1B_SHEEP
ID   IL1B_SHEEP     STANDARD;      PRT;   266 AA.
AC   P21621;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Interleukin-1 beta precursor (IL-1 beta).
GN   IL1B.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92119335; PubMed=1840515;
RA   Seow H.F., Rothel J.S., David M.J., Wood P.R.;
RT   "Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.";
RL   DNA Seq. 1:423-426(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91088326; PubMed=2263490;
RA   Fiskerstrand C., Sargan D.;
RT   "Nucleotide sequence of ovine interleukin-1 beta.";
RL   Nucleic Acids Res. 18:7165-7165(1990).
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC   -!- SUBUNIT: MONOMER.
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X54796; CAA38566.1; -.
DR   EMBL; X56972; CAA40293.1; -.
DR   PIR; S13092; S13092.
DR   PIR; S13810; S13810.
DR   PIR; S23010; S23010.
DR   HSSP; P01584; 5I1B.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP        1    113
FT   CHAIN       114    266       INTERLEUKIN-1 BETA.
FT   CONFLICT     14     14       Y -> C (IN REF. 2).
FT   CONFLICT     55     55       Q -> K (IN REF. 2).
FT   CONFLICT     64     64       V -> A (IN REF. 2).
FT   CONFLICT    145    145       P -> L (IN REF. 2).
SQ   SEQUENCE   266 AA;  30717 MW;  BDED07B58224AB78 CRC64;


  Query Match             20.9%;  Score 173.5;  DB 1;  Length 266;
  Best Local Similarity   30.8%;  Pred. No. 9e-11;
  Matches   48;  Conservative   27;  Mismatches   62;  Indels   19;  Gaps    4;

Qy       2 EKALKIDTPQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGN 61
           :|:| :|:|              ||:    : :| ::    |   :     |:  |:|
Db     128 QKSLVLDSP-----------CVLK---ALHLPSQEMSREVVFCM---SFVQGEERDNKI 169

Qy      62 PIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESV 121
           |: ||:   || | | | || |||||:| |   :| :   | |:|| ::      ||||
Db     170 PVALGIRDKNLYLSCVKKGDTPTLQLEEVD-PKVYPKRNMEKRFVFYKTEIKNTVEFESV 228
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```
Qy    122 AFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
          :| |:|: |     |: | :  |  : ||| :  |
Db    229 LYPNWYISTSQIEEKPVFLGRFRGGQDITDFRMETL 264
```

```
RESULT   7
IL1X_BOVIN
ID   IL1X_BOVIN     STANDARD;      PRT;   174 AA.
AC   O77482;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE   (IRAP).
GN   IL1RN.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98305607; PubMed=9643454;
RA   Kirisawa R., Fukuda T., Yamanaka H., Hagiwara K., Goto M., Obata Y.,
RA   Yoshino T., Iwai H.;
RT   "Enzymatic amplification and expression of bovine interleukin-1
RT   receptor antagonist cDNA.";
RL   Vet. Immunol. Immunopathol. 62:197-208(1998).
CC   -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC       RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB005148; BAA31854.1; -.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Glycoprotein; Signal.
FT   SIGNAL        1     23       BY SIMILARITY.
FT   CHAIN        24    174       INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT                                PROTEIN.
FT   DISULFID     89    139       BY SIMILARITY.
FT   CARBOHYD    107    107       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   174 AA;  19926 MW;  1E56E7F224FF851F CRC64;
```

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  Query Match             20.8%;  Score 172.5;  DB 1;  Length 174;
  Best Local Similarity   30.6%;  Pred. No. 6.7e-11;
  Matches   41;  Conservative   25;  Mismatches   47;  Indels   21;  Gaps    2;

Qy     15 IQDINHRVWVLQDQTLIA-------VPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGL 67
          | |:| ::: |::  |:|          ::::  | |               : ::||:
Db     38 IWDVNQKIFYLRNNQLVAGYLQGPNTKLEEKIDVVPI-------------EPHTMFLGI 83

Qy     68 NGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWF 127
          :|  ||| | | ||:  |:|:  :| ||    |  | | |    :|  ::||| | ||||
Db     84 HGGKLCLACVKSGDEIKLKLEAVNITDLNQNREQDKRFAFIRFDNGPTTSFESAACPGWF 143

Qy    128 IAVSSEGGCPLILT 141
          :  | |   |: ||
Db    144 LCTSLEADQPVGLT 157
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RESULT   8
IL1X_RABIT
ID   IL1X_RABIT     STANDARD;      PRT;   177 AA.
AC   P26890;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE   (IRAP).
GN   IL1RN OR IL1RA.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94165101; PubMed=7509813;
RA   Cominelli F., Bortolami M., Pizarro T.T., Monsacchi L., Ferretti M.,
RA   Brewer M.T., Eisenberg S.P., Ng R.K.;
RT   "Rabbit interleukin-1 receptor antagonist. Cloning, expression,
RT   functional characterization, and regulation during intestinal
RT   inflammation.";
RL   J. Biol. Chem. 269:6962-6971(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Hamada H., Mulligan R.C.;
RL   Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93052512; PubMed=1427977;
RA   Goto F., Goto K., Miyata T., Ohkawara S., Takao T., Mori S.,
RA   Furukawa S., Maeda T., Iwanaga S., Shimonishi Y., Yoshinaga M.;
RT   "Interleukin-1 receptor antagonist in inflammatory exudate cells of
RT   rabbits. Production, purification and determination of primary
RT   structure.";
RL   Immunology 77:235-244(1992).
CC   -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC       RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S68977; AAB30093.1; -.
DR   EMBL; M57526; AAA31374.1; -.
DR   EMBL; D21832; BAA04860.1; -.
DR   PIR; A54377; A54377.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Glycoprotein; Signal.
FT   SIGNAL        1     25       BY SIMILARITY.
FT   CHAIN        26    177       INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT                                PROTEIN.
FT   DISULFID     91    141       BY SIMILARITY.
FT   CARBOHYD    109    109       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   177 AA;  20214 MW;  F5BC087F097FFEAF CRC64;
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  Query Match             20.5%;  Score 170.5;  DB 1;  Length 177;
  Best Local Similarity   30.6%;  Pred. No. 1.1e-10;
  Matches   44;  Conservative   21;  Mismatches   52;  Indels   27;  Gaps    3;
```

```
Qy      15 IQDINHRVWVLQDQTLIA-------VPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGL 67
           | |:|.:. : |::  |:|          ::|:  | :                  ::||:
Db      40 IWDVNQKTFYLRNNQLVAGYLQGPNAKLEERIDVVPL--------------EPQLLFLGI 85

Qy      68 NGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWF 127
           ||| | | ||:  | |:  :| ||    |  | | |  | ||  :|||| : ||||
Db      86 QRGKLCLSCVKSGDKMKLHLEAVNITDLGKNKEQDKRFTFIRSNSGPTTTFESASCPGWF 145

Qy     128 IAVSSEGGCPLILTQELGKANTTD 151
           :  : |   |: ||      || |
Db     146 LCTALEADQPVSLT------NTPD 163


RESULT   9
IL1B_CEREL
ID   IL1B_CEREL     STANDARD;      PRT;   266 AA.
AC   P51745;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Interleukin-1 beta precursor (IL-1 beta).
GN   IL1B.
OS   Cervus elaphus (Red deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Cervinae; Cervus.
OX   NCBI_TaxID=9860;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lockhart E.A.;
RL   Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION AND PROLIFERATION, AND FIBROBLAST GROWTH FACTOR
CC       ACTIVITY. IL-1S ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS
CC       (BY SIMILARITY).
CC   -!- SUBUNIT: MONOMER (By similarity).
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U20500; AAA62234.1; -.
DR   HSSP; P01584; 1HIB.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP        1    113       BY SIMILARITY.
FT   CHAIN       114    266       INTERLEUKIN-1 BETA.
SQ   SEQUENCE   266 AA;  30629 MW;  4F40B4E6F0D9F060 CRC64;

  Query Match             20.1%;  Score 167;  DB 1;  Length 266;
  Best Local Similarity   31.4%;  Pred. No. 4.3e-10;
  Matches   49;  Conservative   25;  Mismatches   64;  Indels   18;  Gaps    5;

Qy      14 SIQDINHRVWVLQDQ----TLIAVP--------RKDRMSPVTIALISCRHVETLEKDRGN 61
           ::| :| :   |||:     ::| |            ||   :  :|   |:  |:|
Db     115 AVQSVNCK---LQDREQNSLVLASPCVLKALHLLSQEMSREVVFCMS--FVQAEERDNKI 169

Qy      62 PIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESV 121
           |: ||:   |  | | | || |||||:| |   :| :    | |:|| ::      ||||
Db     170 PVALGIRDKNQYLSCVKKGDTPTLQLEEVD-PKVYPKRNMEKRFVFYKTEIKDTVEFESV 228

Qy     122 AFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
           :| |:|: |     |: |    |  : ||| :  |
Db     229 LYPNWYISTSHPEEKPVFLGHFRGGQDITDFRMETL 264


RESULT  10
IL1B_BOVIN
ID   IL1B_BOVIN     STANDARD;      PRT;   266 AA.
AC   P09428;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Interleukin-1 beta precursor (IL-1 beta).
GN   IL1B.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89016591; PubMed=3262866;
RA   Leong S.R., Flaggs G.M., Lawman M., Gray P.W.;
RT   "The nucleotide sequence for the cDNA of bovine interleukin-1 beta.";
RL   Nucleic Acids Res. 16:9054-9054(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88318652; PubMed=3261832;
RA   Maliszewski C.R., Baker P.E., Schoenborn M.A., Davis B.S., Cosman D.,
RA   Gillis S., Cerretti D.P.;
RT   "Cloning, sequence and expression of bovine interleukin 1 alpha and
RT   interleukin 1 beta complementary DNAs.";
RL   Mol. Immunol. 25:429-437(1988).
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC   -!- SUBUNIT: MONOMER.
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M35589; AAA30585.1; -.
DR   EMBL; X12498; CAA31018.1; -.
DR   EMBL; M37211; AAA30584.1; -.
DR   PIR; JL0010; ICBO1B.
DR   PIR; S01380; S01380.
DR   HSSP; P01584; 1HIB.
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DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP        1    113
FT   CHAIN       114    266       INTERLEUKIN-1 BETA.
FT   CONFLICT    252    252       A -> G (IN REF. 2).
SQ   SEQUENCE   266 AA;  30774 MW;  9D1EF8F575070586 CRC64;


  Query Match             19.8%;  Score 164;  DB 1;  Length 266;
  Best Local Similarity   31.0%;  Pred. No. 8.8e-10;
  Matches   48;  Conservative   23;  Mismatches   76;  Indels    8;  Gaps    4;

Qy       8 DTPQQG---SIQDINHRVWVLQDQTLIAVPR--KDRMSPVTIALISCRHVETLEKDRGNP 62
           | | |     :||   :  ||    ::         |:   :  :|   |:  |:|   |
Db     113 DAPVQSIKCKLQDREQKSLVLASPCVLKALHLLSQEMNREVVFCMS--FVQGEERDNKIP 170

Qy      63 IYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVA 122
           : ||:   || | | | || |||||:| |   :| :    | |:|| ::      ||||
Db     171 VALGIKDKNLYLSCVKKGDTPTLQLEEVD-PKVYPKRNMEKRFVFYKTEIKNTVEFESVL 229

Qy     123 FPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
           :| |:|: |     |: |       : ||| :  |
Db     230 YPNWYISTSQIEERPVFLGHFRAGQDITDFRMETL 264


RESULT  11
IL1B_CAPHI
ID   IL1B_CAPHI     STANDARD;      PRT;   266 AA.
AC   P79162;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Interleukin-1 beta precursor (IL-1 beta).
GN   IL1B.
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Capra.
OX   NCBI_TaxID=9925;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Takakura H., Hashimoto O., Mori Y., Tatsumi M.;
RT   "Molecular cloning and expression of caprine IL-1alpha and
RT   IL-1beta.";
RL   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS
CC       (BY SIMILARITY).
CC   -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D63351; BAA09675.1; -.
DR   HSSP; P01584; 1HIB.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP        1    113       BY SIMILARITY.
FT   CHAIN       114    266       INTERLEUKIN-1 BETA.
SQ   SEQUENCE   266 AA;  30769 MW;  59F7B39BD1D4DDA5 CRC64;


  Query Match             19.6%;  Score 162.5;  DB 1;  Length 266;
  Best Local Similarity   31.4%;  Pred. No. 1.3e-09;
  Matches   49;  Conservative   25;  Mismatches   63;  Indels   19;  Gaps    4;

Qy       2 EKALKIDTPQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGN 61
             :|:| :|:|             ||:   |::      ||   :  :|   |:  |:|
Db     128 QKSLVLDSP-----------CVLKALHLLS----QEMSREVVFCMS--FVQGEERDNKI 169

Qy      62 PIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESV 121
           |: ||:   || |   | || |||||:| |   :| :    | |:|| ::      ||||
Db     170 PVALGIRDKNLYLSWVKKGDTPTLQLEEVD-PKVYPKRNMEKRFVFYKTEIKNTVEFESV 228

Qy     122 AFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
           :| |:|: |     |: |    |  : ||| :  |
Db     229 LYPNWYISTSQIEEKPVFLGHFRGGQDITDFRMETL 264


RESULT  12
IL1B_PIG
ID   IL1B_PIG       STANDARD;      PRT;   267 AA.
AC   P26889;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Interleukin-1 beta precursor (IL-1 beta).
GN   IL1B.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93314975; PubMed=8325511;
RA   Huether M.J., Lin G., Smith D.M., Murtaugh M.P., Molitor T.W.;
RT   "Cloning, sequencing and regulation of an mRNA encoding porcine
RT   interleukin-1 beta.";
RL   Gene 129:285-289(1993).
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC   -!- SUBUNIT: MONOMER.
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M86725; AAA02584.1; -.
DR   PIR; JN0724; JN0724.
DR   HSSP; P01584; 1HIB.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP        1    114       BY SIMILARITY.
FT   CHAIN       115    267       INTERLEUKIN-1 BETA.
SQ   SEQUENCE   267 AA;  30404 MW;  7F6B92B784D5086F CRC64;


  Query Match             18.7%;  Score 155;  DB 1;  Length 267;
  Best Local Similarity   22.8%;  Pred. No. 7.6e-09;
  Matches   52;  Conservative   34;  Mismatches   66;  Indels   76;  Gaps    7;

Qy       5 LKIDTPQQGSIQ-DINHRVW---VLQDQTLIAVPRKDRMSPVT---------------- 43
           | : : : ||||  |:|::|   : |  ::|    |   :| :
Db      39 LDLGSLRNGSIQLQISHQLWNKSIRQMVSVIVAVEKPMKNPSSQAFCDDDQKSIFSFIFE 98

Qy      44 ---IALISCR-------HVETLE---------------------------------- 56
              | | :|        :|:::|
Db      99 EEPIILETCNDDFVCDANVQSMECKLQDKDHKSLVLAGPHMLKALHLLTGDLKREVVFCM 158

Qy      57 -----KDRGN--PIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYH 109
                 |  |  |: ||: | || | |    : |||||:: |    | : :  | |:||
Db     159 SFVQGDDSNNKIPVTLGIKGKNLYLSCVMKDNTPTLQLEDID-PKRYPKRDMEKRFVFYK 217

Qy     110 SQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
           ::      |||  :| |:|: |     |: |    |: : ||| : :|
Db     218 TEIKNRVEFESALYPNWYISTSQAEQKPVFLGNSKGRQDITDFTMEVL 265


RESULT  13
IL1B_MACFA
ID   IL1B_MACFA     STANDARD;      PRT;   268 AA.
AC   P79182;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Interleukin-1 beta precursor (IL-1 beta).
GN   IL1B.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Thymus;
RA   Totsuka K., Takakura H., Hashimoto O., Tatsumi M.;
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC   -!- SUBUNIT: MONOMER.
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; D63353; BAA09677.1; -.
DR   HSSP; P01584; 1HIB.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP        1    116       BY SIMILARITY.
FT   CHAIN       117    268       INTERLEUKIN-1 BETA.
SQ   SEQUENCE   268 AA;  30425 MW;  CFB7266E3E2C05B4 CRC64;


  Query Match             17.5%;  Score 145.5;  DB 1;  Length 268;
  Best Local Similarity   34.5%;  Pred. No. 7.5e-08;
  Matches   39;  Conservative   15;  Mismatches   56;  Indels    3;  Gaps    2;

Qy      46 LISCRHVETLEKDRGNPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSF 105
             :|   |:  | :   |: |||   || | |    |:|||||:  |  : | : :  | |
Db     157 VFSMSFVQGEESNDKIPVALGLKAKNLYLSCVLKDDKPTLQLESVDPKN-YPKKKMEKRF 215

Qy     106 LFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTMLF 158
           :|   :      |||  || |:|: |     |: |    |  : |||  || |
Db     216 VFNKIEINNKLEFESAQFPNWYISTSQAESMPVFLGGTRGGQDITDF--TMQF 266


RESULT  14
IL1B_MACMU
ID   IL1B_MACMU     STANDARD;      PRT;   269 AA.
AC   P48090;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Interleukin-1 beta precursor (IL-1 beta).
GN   IL1B.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and
RT   nonhuman primates.";
RL   J. Immunol. 155:3946-3954(1995).
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
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CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC   -!- SUBUNIT: MONOMER.
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
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CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U19845; AAA86709.1; -.
DR   HSSP; P01584; 1HIB.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP        1    116       BY SIMILARITY.
FT   CHAIN       117    269       INTERLEUKIN-1 BETA.
SQ   SEQUENCE   269 AA;  30481 MW;  A7CD59EBAC120EC7 CRC64;


  Query Match             17.5%;  Score 145.5;  DB 1;  Length 269;
  Best Local Similarity   34.5%;  Pred. No. 7.5e-08;
  Matches   39;  Conservative   15;  Mismatches   56;  Indels    3;  Gaps    2;

Qy      46 LISCRHVETLEKDRGNPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSF 105
           : |   |:  | :   |: |||   || | |    |:|||||:  |  : | : :  | |
Db     157 VFSMSFVQGEESNDKIPVALGLKAKNLYLSCVLKDDKPTLQLESVDPKN-YPKKKMEKRF 215

Qy     106 LFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTMLF 158
           :|   :      |||  || |:|: |     |: |    |  : |||  || |
Db     216 VFNKIEINNKLEFESAQFPNWYISTSQAENMPVFLGGTRGGQDITDF--TMQF 266


RESULT  15
IL1B_HUMAN
ID   IL1B_HUMAN     STANDARD;      PRT;   269 AA.
AC   P01584; Q96HE5; Q9UCT6;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Interleukin-1 beta precursor (IL-1 beta) (Catabolin).
GN   IL1B.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85088517; PubMed=6083565;
RA   Auron P.E., Webb A.C., Rosenwasser L.J., Mucci S.F., Rich A.,
RA   Wolff S.M., Dinarello C.A.;
RT   "Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:7907-7911(1984).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85240547; PubMed=2989698;
RA   March C.J., Mosley B., Larsen A., Cerretti D.P., Braedt G., Price V.,
RA   Gillis S., Henney C.S., Kronheim S.R., Grabstein K., Conlon P.J.,
RA   Hopp T.P., Cosman D.;
RT   "Cloning, sequence and expression of two distinct human interleukin-1
RT   complementary DNAs.";
RL   Nature 315:641-647(1985).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87040762; PubMed=3490654;
RA   Clark B.D., Collins K.L., Gandy M.S., Webb A.C., Auron P.E.;
RT   "Genomic sequence for human prointerleukin 1 beta: possible evolution
RT   from a reverse transcribed prointerleukin 1 alpha gene.";
RL   Nucleic Acids Res. 14:7897-7914(1986).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87248099; PubMed=2954882;
RA   Bensi G., Raugei G., Palla E., Carinci V., Buonamassa D.T., Melli M.;
RT   "Human interleukin-1 beta gene.";
RL   Gene 52:95-101(1987).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90249285; PubMed=2635664;
RA   Kotenko S.V., Bulenkov M.T., Veiko V.P., Epishin S.M., Lomakin I.B.,
RA   Emel'Yanov A.V., Kozlov A.P., Konusova V.G., Kotov A.Y.,
RA   Kurbatova T.V., Reshetnikov V.L., Simbirtsev A.S., Ketlinskii S.A.,
RA   Vinetskii Y.P.;
RT   "Cloning of the cDNA coding for human prointerleukin-1 alpha and
RT   prointerleukin-1 beta.";
RL   Dokl. Akad. Nauk SSSR 309:1005-1008(1989).
RN   [6]
RP   SEQUENCE FROM N.A.
RA   Webb A.C., Dinarello C.A., Rosenwasser L.J., Mucci S.F., Rich A.,
RA   Wolff S.M., Auron P.E.;
RT   "Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.";
RL   Adv. Gene Technol. 22:339-340(1985).
RN   [7]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87156769; PubMed=3493774;
RA   Nishida T., Nishino N., Takano M., Kawai K., Bando K., Masui Y.,
RA   Nakai S., Hirai Y.;
RT   "cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell
RT   line.";
RL   Biochem. Biophys. Res. Commun. 143:345-352(1987).
RN   [8]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
RN   [9]
RP   SEQUENCE OF 117-128.
RX   MEDLINE=88184226; PubMed=3281727;
RA   Zsebo K.M., Wypych J., Yuschenkoff V.N., Lu H., Hunt P., Dukes P.P.,
RA   Langley K.E.;
RT   "Effects of hematopoietin-1 and interleukin 1 activities on early
RT   hematopoietic cells of the bone marrow.";
RL   Blood 71:962-968(1988).
RN   [10]
RP   SEQUENCE OF 114-135.
RC   TISSUE=Skin;
RX   MEDLINE=92013781; PubMed=1919436;
RA   Mizutani H., Schechter N., Lazarus G., Black R.A., Kupper T.S.;
RT   "Rapid and specific conversion of precursor interleukin 1 beta (IL-1
RT   beta) to an active IL-1 species by human mast cell chymase.";
RL   J. Exp. Med. 174:821-825(1991).
RN   [11]
RP   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX   MEDLINE=88211543; PubMed=3259176;
RA   Priestle J.P., Schar H.-P., Grutter M.G.;
RT   "Crystal structure of the cytokine interleukin-1 beta.";
RL   EMBO J. 7:339-343(1988).
RN   [12]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=90099325; PubMed=2602367;
RA   Priestle J.P., Schar H.-P., Grutter M.G.;
RT   "Crystallographic refinement of interleukin 1 beta at 2.0-A
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RT   resolution.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:9667-9671(1989).
RN   [13]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=90064532; PubMed=2585509;
RA   Finzel B.C., Clancy L.L., Holland D.R., Muchmore S.W.,
RA   Watenpaugh K.D., Einspahr H.M.;
RT   "Crystal structure of recombinant human interleukin-1 beta at 2.0-A
RT   resolution.";
RL   J. Mol. Biol. 209:779-791(1989).
RN   [14]
RP   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF COMPLEX WITH RECEPTOR.
RX   MEDLINE=97215903; PubMed=9062193;
RA   Vigers G.P., Anderson L.J., Caffes P., Brandhuber B.J.;
RT   "Crystal structure of the type-I interleukin-1 receptor complexed
RT   with interleukin-1beta.";
RL   Nature 386:190-194(1997).
RN   [15]
RP   STRUCTURE BY NMR.
RX   MEDLINE=90321925; PubMed=2372550;
RA   Driscoll P.C., Gronenborn A.M., Wingfield P.T., Clore G.M.;
RT   "Determination of the secondary structure and molecular topology of
RT   interleukin-1 beta by use of two- and three-dimensional heteronuclear
RT   15N-1H NMR spectroscopy.";
RL   Biochemistry 29:4668-4682(1990).
RN   [16]
RP   STRUCTURE BY NMR.
RX   MEDLINE=91159409; PubMed=2001363;
RA   Clore G.M., Wingfield P.T., Gronenborn A.M.;
RT   "High-resolution three-dimensional structure of interleukin 1 beta in
RT   solution by three- and four-dimensional nuclear magnetic resonance
RT   spectroscopy.";
RL   Biochemistry 30:2315-2323(1991).
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
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CC   -!- SUBUNIT: MONOMER.
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
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CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
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CC   ---------------------------------------------------------------------
DR   EMBL; M15840; AAA74137.1; -.
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DR   EMBL; K02770; AAA36106.1; -.
DR   EMBL; X04500; CAA28185.1; -.
DR   EMBL; X56087; CAA39567.1; -.
DR   EMBL; M54933; AAA59136.1; -.
DR   EMBL; M15330; AAA59135.1; -.
DR   EMBL; BC008678; AAH08678.1; -.
DR   PIR; A01848; ICHU1B.
DR   PIR; A25542; A25542.
DR   PIR; A29019; A29019.
DR   PIR; B27616; B27616.
DR   PIR; S19626; S19626.
DR   PDB; 1I1B; 15-OCT-92.
DR   PDB; 2I1B; 15-JUL-93.
DR   PDB; 4I1B; 15-JAN-93.
DR   PDB; 5I1B; 15-OCT-94.
DR   PDB; 6I1B; 15-OCT-92.
DR   PDB; 7I1B; 15-OCT-92.
DR   PDB; 21BI; 15-APR-92.
DR   PDB; 31BI; 15-APR-92.
DR   PDB; 41BI; 15-JUL-92.
DR   PDB; 1HIB; 31-JAN-94.
DR   PDB; 1IOB; 17-AUG-96.
DR   PDB; 1ITB; 04-FEB-98.
DR   PDB; 9ILB; 06-JAN-99.
DR   MIM; 147720; -.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen;
KW   3D-structure.
FT   PROPEP        1    116
FT   CHAIN       117    269       INTERLEUKIN-1 BETA.
FT   CONFLICT      6      6       K -> E (IN REF. 2, 6 AND 8).
FT   CONFLICT     20     20       D -> H (IN REF. 7).
FT   CONFLICT    111    111       E -> Q (IN REF. 7).
FT   CONFLICT    177    177       G -> A (IN REF. 7).
FT   CONFLICT    214    214       R -> P (IN REF. 7).
FT   STRAND      121    128
FT   TURN        129    130
FT   STRAND      132    138

  Query Match             17.3%;  Score 143.5;  DB 1;  Length 269;
  Best Local Similarity   34.5%;  Pred. No. 1.2e-07;
  Matches   39;  Conservative   15;  Mismatches   56;  Indels    3;  Gaps    2;

Qy      46 LISCRHVETLEKDRGNPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSF 105
           : |   |:  | :   |: |||   || | |    |:|||||:  |  : | : :  | |
Db     157 VFSMSFVQGEESNDKIPVALGLKEKNLYLSCVLKDDKPTLQLESVDPKN-YPKKKMEKRF 215

Qy     106 LFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTMLF 158
           :|   :      |||  || |:|: |     |: |    |  : |||  || |
Db     216 VFNKIEINNKLEFESAQFPNWYISTSQAENMPVFLGGTKGGQDITDF--TMQF 266


Search completed: June 20, 2002, 15:11:20
Job time: 445 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 20, 2002, 15:10:54 ; Search time 61.16 Seconds
(without alignments)
446.913 Million cell updates/sec

Title: US-09-763-498-8
Perfect score: 830
Sequence: 1 MEKALKIDTPQQGSIQDINH.....ILTQELGKANTTDFGLTMLF 158

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	830	100.0	158	4	Q9UHA7	Q9uha7 homo sapien
2	466.5	56.2	169	4	Q9NZH8	Q9nzh8 homo sapien
3	463	55.8	160	11	Q9JLA2	Q9jla2 mus musculu
4	385	46.4	157	4	Q9UHA5	Q9uha5 homo sapien
5	333	40.1	183	11	Q9D6Z6	Q9d6z6 mus musculu
6	209	25.2	192	4	Q9UHA6	Q9uha6 homo sapien
7	209	25.2	218	4	Q9NZH6	Q9nzh6 homo sapien
8	209	25.2	218	4	Q9HBF3	Q9hbf3 homo sapien
9	202	24.3	164	4	Q9NZH7	Q9nzh7 homo sapien
10	185.5	22.3	155	4	Q9UBH0	Q9ubh0 homo sapien
11	185	22.3	267	13	O73909	O73909 gallus gall
12	183.5	22.1	159	4	Q96GD6	Q96gd6 homo sapien
13	180.5	21.7	176	6	Q9BEH0	Q9beh0 canis famil
14	172.5	20.8	177	6	Q9GMZ4	Q9gmz4 tursiops tr
15	170.5	20.5	176	6	Q9GKK2	Q9gkk2 canis famil
16	169	20.4	152	4	Q969H5	Q969h5 homo sapien
17	167.5	20.2	155	11	Q9QYY1	Q9qyy1 mus musculu
18	167.5	20.2	156	11	Q9JIG2	Q9jig2 mus musculu
19	166.5	20.1	144	4	Q9BYX1	Q9byx1 homo sapien
20	160	19.3	267	6	Q29082	Q29082 sus scrofa
21	154.5	18.6	260	13	Q9YGD3	Q9ygd3 oncorhynchu
22	151.5	18.3	178	4	Q9HBF2	Q9hbf2 homo sapien
23	147	17.7	261	13	Q90W84	Q90w84 dicentrarch
24	144.5	17.4	283	13	Q9PVZ5	Q9pvz5 xenopus lae
25	144	17.3	266	6	Q9TTK1	Q9ttk1 tursiops tr
26	143.5	17.3	153	4	O43645	O43645 homo sapien
27	143.5	17.3	269	4	Q96HE5	Q96he5 homo sapien
28	138	16.6	272	13	Q9DDF2	Q9ddf2 cyprinus ca
29	136	16.4	267	11	Q91ZL5	Q91zl5 sigmodon hi
30	136	16.4	276	13	O57398	O57398 cyprinus ca
31	136	16.4	276	13	Q9PW18	Q9pw18 cyprinus ca
32	133.5	16.1	272	13	Q9DDF3	Q9ddf3 cyprinus ca
33	124.5	15.0	254	13	Q9PT12	Q9pt12 oncorhynchu
34	121	14.6	253	13	Q90W32	Q90w32 sparus aura
35	121	14.6	599	11	Q91WP7	Q91wp7 mus musculu
36	107	12.9	72	6	O77771	O77771 equus cabal
37	94	11.3	118	6	Q9TSJ0	Q9tsj0 equus cabal
38	87	10.5	64	13	Q98SG5	Q98sg5 scophthalmu
39	82.5	9.9	65	6	Q9TV37	Q9tv37 equus cabal
40	81	9.8	256	10	Q9FX11	Q9fx11 arabidopsis
41	81	9.8	348	10	Q9FVW3	Q9fvw3 arabidopsis
42	79	9.5	747	5	Q9N9L5	Q9n9l5 leishmania
43	78	9.4	603	10	Q9SQT8	Q9sqt8 arabidopsis
44	76	9.2	728	4	Q9BRZ1	Q9brz1 homo sapien
45	76	9.2	1065	4	O94898	O94898 homo sapien

ALIGNMENTS

RESULT 1
Q9UHA7
ID Q9UHA7 PRELIMINARY; PRT; 158 AA.
AC Q9UHA7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE FIL1 EPSILON.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092888; PubMed=10625660;
RA Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
RA Sims J.E.;
RT "Four New Members Expand the IL-1 Superfamily.";
RL J. Biol. Chem. 275:1169-1175(2000).
DR EMBL; AF201831; AAF25211.1; -.
DR HSSP; P18510; 1ILR.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 158 AA; 17684 MW; 469AC84306B0E280 CRC64;

Query Match 100.0%; Score 830; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.1e-81;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MEKALKIDTPQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MEKALKIDTPQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRG 60

Qy      61 NPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFES 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 NPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFES 120
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Qy    121 VAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTMLF 158
          |||||||||||||||||||||||||||||||||||||||
Db    121 VAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTMLF 158


RESULT   2
Q9NZH8
ID   Q9NZH8      PRELIMINARY;      PRT;   169 AA.
AC   Q9NZH8;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN-1 HOMOLOG 1 (INTERLEUKIN-1 EPSILON).
GN   IL1E.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20209405; PubMed=10744718;
RA   Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA   Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA   Young P.R.;
RT   "Identification and initial characterization of four novel members of
RT   the interleukin-1 family.";
RL   J. Biol. Chem. 275:10308-10314(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=AIRWAY EPITHELIAL CELLS INDUCED WITH TNF ALPHA, AND IFN;
RA   Debets R., Timans J., Zurawski S., Bazan J.F., Kastelein R.A.;
RT   "Novel IL-1 family member IL-1e responds through the orphan IL-1R-
RT   related protein 2; response is antagonized by IL-1d.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF200492; AAF69248.1; -.
DR   EMBL; AF206696; AAG35670.1; -.
DR   HSSP; P18510; 1ITN.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
SQ   SEQUENCE   169 AA;  18721 MW;  F00A9243706F4154 CRC64;


  Query Match             56.2%;  Score 466.5;  DB 4;  Length 169;
  Best Local Similarity   59.9%;  Pred. No. 1.9e-42;
  Matches   88;  Conservative   24;  Mismatches   34;  Indels    1;  Gaps    1;

Qy     10 PQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNG 69
          |  |:| |:| :|| || | |:|||| | ::|||:|:|:|:: | ||: ||:|||||:
Db     22 PITGTINDLNQQVWTLQGQNLVAVPRSDSVTPVTVAVITCKYPEALEQGRGDPIYLGIQN 81

Qy     70 LNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIA 129
            :|| | |||:||||||||: ||||| |||||| |||| :::|| || |||||| ||||
Db     82 PEMCLYCEKVGEQPTLQLKEQKIMDLYGQPEPVKPFLFYRAKTGRTSTLESVAFPDWFIA 141

Qy    130 VSSEGGCPLILTQELGKANTTDFGLTM 156
           ||:   |:||| ||||:  | | | :
Db    142 -SSKRDQPIILTSELGKSYNTAFELNI 167


RESULT   3
Q9JLA2
ID   Q9JLA2      PRELIMINARY;      PRT;   160 AA.
AC   Q9JLA2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN-1 HOMOLOG 1 (INTERLEUKIN-1 EPSILON) (INTERLEUKIN 1
DE   SUPERFAMILY 1, EPSILON).
GN   IL1F6 OR FIL1 OR IL1E.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20209405; PubMed=10744718;
RA   Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA   Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA   Young P.R.;
RT   "Identification and initial characterization of four novel members of
RT   the interleukin-1 family.";
RL   J. Biol. Chem. 275:10308-10314(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Debets R., Timans J., Zurawski S., Bazan J.F., Kastelein R.A.;
RT   "Novel IL-1 family member IL-1e responds through the orphan IL-1R-
RT   related protein 2; response is antagonized by IL-1d.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AF200493; AAF69249.1; -.
DR   EMBL; AF206697; AAG35671.1; -.
DR   EMBL; AK004061; BAB23147.1; -.
DR   HSSP; P01584; 1HIB.
DR   MGD; MGI:1859324; Il1f6.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
SQ   SEQUENCE   160 AA;  18015 MW;  AA0434D68FF62F4A CRC64;


  Query Match             55.8%;  Score 463;  DB 11;  Length 160;
  Best Local Similarity   54.5%;  Pred. No. 4.2e-42;
  Matches   85;  Conservative   30;  Mismatches   41;  Indels    0;  Gaps    0;

Qy      2 EKALKIDTPQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGN 61
          || |:  :|    :||:: |||:||:  | |||||::  |||| |: |::::||| :||:
Db      4 EKELRAASPSLRHVQDLSSRVWILQNNILTAVPRKEQTVPVTITLLPCQYLDTLETNRGD 63

Qy     62 PIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESV 121
          | |:|:     || | | |:|| ||| | :||::||: |||| |||| :|| |||||
Db     64 PTYMGVQRPMSCLFCTKDGEQPVLQLGEGNIMEMYNKKEPVKASLFYHKKSGTTSTFESA 123

Qy    122 AFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
          ||||||||| |:| ||||||||||:   ||| : ::
Db    124 AFPGWFIAVCSKGSCPLILTQELGEIFITDFEMIVV 159


RESULT   4
Q9UHA5
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ID   Q9UHA5      PRELIMINARY;      PRT;   157 AA.
AC   Q9UHA5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   FIL1 ETA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20092888; PubMed=10625660;
RA   Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
RA   Sims J.E.;
RT   "Four New Members Expand the IL-1 Superfamily.";
RL   J. Biol. Chem. 275:1169-1175(2000).
DR   EMBL; AF201833; AAF25213.1; -.
DR   HSSP; P10749; 2MIB.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
SQ   SEQUENCE   157 AA;  17702 MW;  7A54F3D7557A3EE3 CRC64;


  Query Match             46.4%;  Score 385;  DB 4;  Length 157;
  Best Local Similarity   49.0%;  Pred. No. 1.1e-33;
  Matches   71;  Conservative   29;  Mismatches   45;  Indels    0;  Gaps    0;

Qy      10 PQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNG 69
           |:  :|:|    ||||   :||| |    : |||: ||:|| |  :|::|| :|||: |
Db       9 PKSYAIRDSRQMVWVLSGNSLIAAPLSRSIKPVTLHLIACRDTEFSDKEKGNMVYLGIKG 68

Qy      70 LNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIA 129
            :||| ||::  :||||||||:|||||| : :  | |||:|:: |  | |:||::|||||
Db      69 KDLCLFCAEIQGKPTLQLKEKNIMDLYVEKKAQKPFLFFHNKEGSTSVFQSVSYPGWFIA 128

Qy     130 VSSEGGCPLILTQELGKANTTDFGL 154
            |:  | |: ||:| |  | |:| |
Db     129 TSTTSGQPIFLTKERGITNNTNFYL 153


RESULT   5
Q9D6Z6
ID   Q9D6Z6      PRELIMINARY;      PRT;   183 AA.
AC   Q9D6Z6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   2310043N20RIK PROTEIN.
GN   2310043N20RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=TONGUE;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK009787; BAB26505.1; -.
DR   HSSP; P01584; 1HIB.
DR   MGD; MGI:1916927; 2310043N20Rik.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
SQ   SEQUENCE   183 AA;  20878 MW;  A3ACE339FB96F02F CRC64;


  Query Match             40.1%;  Score 333;  DB 11;  Length 183;
  Best Local Similarity   44.4%;  Pred. No. 5.2e-28;
  Matches   64;  Conservative   25;  Mismatches   55;  Indels    0;  Gaps    0;

Qy       9 TPQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLN 68
           :|:   : |    ||||   || |||  : : || ::|||:||  |  :  :|| ::|||:
Db      34 SPRNYRVHDSQQMVWVLTGNTLTAVPASNNVKPVILSLIACRDTEFQDVKKGNLVFLGIK 93

Qy      69 GLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFI 128
             |||  | ::  :|||||||| |||:|| : :  |:|||||   |  | |:|| :|||||
Db      94 NRNLCFCCVEMEGKPTLQLKEVDIMNLYKERKAQKAFLFYHGIEGSTSVFQSVLYPGWFI 153

Qy     129 AVSSEGGCPLILTQELGKANTTDF 152
           | ||     :||| : ||   |:|
Db     154 ATSSIERQTIILTHQRGKLVNTNF 177


RESULT   6
Q9UHA6
ID   Q9UHA6      PRELIMINARY;      PRT;   192 AA.
AC   Q9UHA6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   FIL1 ZETA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20092888; PubMed=10625660;
RA   Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
RA   Sims J.E.;
RT   "Four New Members Expand the IL-1 Superfamily.";
RL   J. Biol. Chem. 275:1169-1175(2000).
DR   EMBL; AF201832; AAF25212.1; -.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
SQ   SEQUENCE   192 AA;  21543 MW;  4AF584C81802F612 CRC64;


  Query Match             25.2%;  Score 209;  DB 4;  Length 192;
  Best Local Similarity   36.7%;  Pred. No. 1.3e-14;
  Matches   54;  Conservative   26;  Mismatches   61;  Indels    6;  Gaps    4;

Qy      10 PQQGSIQDINHRVWVLQDQTLIAVPRKDRMSP-VTIALISCRHVETLEKDRGNPIYLGLN 68
           |:: || | :|:| ||    ||||| |: : | :  || |   : :   ::|:|| ||::
Db      31 PKKFSIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALAS--SLSSASAEKGSPILLGVS 88

Qy      69 GLNLCLMCAKVGDQ--PTLQLKEKDIMDLYNQPEPV-KSFLFYHSQSGRNSTFESVAFPG 125
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              || | |   |  |:||||:: :| |  | |   : |:|| :| |  :  || | ||
Db     89 KGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPG 148

Qy    126 WFIAVSSEGGCPLILTQELGKANTTDF 152
          |||  |     |: :| :       :|
Db    149 WFICTSCNCNEPVGVTDKFENRKHIEF 175


RESULT   7
Q9NZH6
ID   Q9NZH6      PRELIMINARY;      PRT;   218 AA.
AC   Q9NZH6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN-1 HOMOLOG 4 (IL-1X PROTEIN) (INTERLEUKIN-1-RELATED PROTEIN
DE   LONG ISOFORM A).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=FETAL LUNG, FETAL TESTIS, FETAL B-CELL, AND FETAL COLON;
RX   MEDLINE=20209405; PubMed=10744718;
RA   Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA   Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA   Young P.R.;
RT   "Identification and initial characterization of four novel members of
RT   the interleukin-1 family.";
RL   J. Biol. Chem. 275:10308-10314(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON CARCINOMA;
RA   Manoj P.P., Mantovani A., Muzio M.;
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Pan G., Risser P., Mao W., Baldwin D.T., Zhong A.W., Yansura D.,
RA   Lewis L., Eigenbrot C., Henzle W.J., Vandlen R., Filvaroff E.;
RT.  "IL-1H, an interleukin-1-related protein that binds IL-18 receptor/IL-
RT   1Rrp.";
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF200496; AAF69252.1; -.
DR   EMBL; AF167368; AAG29344.1; -.
DR   EMBL; AF251118; AAG14420.1; -.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
SQ   SEQUENCE   218 AA;  24126 MW;  96E089310D2CEA68 CRC64;


  Query Match             25.2%;  Score 209;  DB 4;  Length 218;
  Best Local Similarity   36.7%;  Pred. No. 1.5e-14;
  Matches   54;  Conservative   26;  Mismatches   61;  Indels    6;  Gaps    4;

Qy      10 PQQGSIQDINHRVWVLQDQTLIAVPRKDRMSP-VTIALISCRHVETLEKDRGNPIYLGLN 68
           |:: || | :|:| ||    ||||| |: : | :  || |   : :   ::|:|| ||::
Db      57 PKKFSIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALAS--SLSSASAEKGSPILLGVS 114

Qy      69 GLNLCLMCAKVGDQ--PTLQLKEKDIMDLYNQPEPV-KSFLFYHSQSGRNSTFESVAFPG 125
              || | |   |  |:||||:: :| |  | |   : |:|| :| |  :  || | ||
Db     115 KGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPG 174

Qy     126 WFIAVSSEGGCPLILTQELGKANTTDF 152
           |||  |     |: :| :       :|
Db     175 WFICTSCNCNEPVGVTDKFENRKHIEF 201


RESULT   8
Q9HBF3
```

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ID   Q9HBF3      PRELIMINARY;      PRT;   218 AA.
AC   Q9HBF3;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN-1-RELATED PROTEIN LONG ISOFORM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21066552; PubMed=11145836;
RA   Pan G., Risser P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E.,
RA   Yansura D., Lewis L., Eigenbrot C., Henzel W.J., Vandlen R.;
RT   "IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-
RT   1Rrp.";
RL   Cytokine 13:1-7(2001).
DR   EMBL; AF251119; AAG14421.1; -.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
SQ   SEQUENCE   218 AA;  24138 MW;  76E09C35093DEA63 CRC64;


  Query Match             25.2%;  Score 209;  DB 4;  Length 218;
  Best Local Similarity   36.7%;  Pred. No. 1.5e-14;
  Matches   54;  Conservative   26;  Mismatches   61;  Indels    6;  Gaps    4;

Qy      10 PQQGSIQDINHRVWVLQDQTLIAVPRKDRMSP-VTIALISCRHVETLEKDRGNPIYLGLN 68
           |:: || | :|:| ||    ||||| |: : | :  || |   : :   ::|:|| ||::
Db      57 PKKFSIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALAS--SLSSASAEKGSPILLGVS 114

Qy      69 GLNLCLMCAKVGDQ--PTLQLKEKDIMDLYNQPEPV-KSFLFYHSQSGRNSTFESVAFPG 125
              || | |   |  |:||||:: :| |  | |   : |:|| :| |  :  || | ||
Db     115 KGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPG 174

Qy     126 WFIAVSSEGGCPLILTQELGKANTTDF 152
           |||  |     |: :| :       :|
Db     175 WFICTSCNCNEPVGVTDKFENRKHIEF 201


RESULT   9
Q9NZH7
ID   Q9NZH7      PRELIMINARY;      PRT;   164 AA.
AC   Q9NZH7;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   INTERLEUKIN-1 HOMOLOG 2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=OSTEOCLASTOMA;
RX   MEDLINE=20209405; PubMed=10744718;
RA   Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA   Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA   Young P.R.;
RT   "Identification and initial characterization of four novel members of
RT   the interleukin-1 family.";
RL   J. Biol. Chem. 275:10308-10314(2000).
DR   EMBL; AF200494; AAF69250.1; -.
DR   InterPro; IPR000975; Interleukin_1.
DR   SMART; SM00125; IL1; 1.
SQ   SEQUENCE   164 AA;  18521 MW;  F0D2099F4A357A0A CRC64;


  Query Match             24.3%;  Score 202;  DB 4;  Length 164;
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  Best Local Similarity   44.7%;  Pred. No. 6.1e-14;
  Matches   38;  Conservative   17;  Mismatches   30;  Indels    0;  Gaps    0;

Qy      10 PQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNG 69
           |:  :|:|    ||||   :||| |    : |||: ||:||  |  :|::|| :|||: |
Db       9 PKSYAIRDSRQMVWVLSGNSLIAAPLSRSIKPVTLHLIACRDTEFSDKEKGNMVYLGIKG 68

Qy      70 LNLCLMCAKVGDQPTLQLKEKDIMD 94
           :||| ||::  :|||||| :   |
Db      69 KDLCLFCAEIQGKPTLQLKLQGSQD 93


RESULT  10
Q9UBH0
ID   Q9UBH0      PRELIMINARY;      PRT;   155 AA.
AC   Q9UBH0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   FIL1 DELTA (INTERLEUKIN-1 LIKE PROTEIN 1) (INTERLEUKIN-1 RECEPTOR
DE   ANTAGONIST HOMOLOG 1) (INTERLEUKIN-1 DELTA).
GN   IL1HY1 OR IL1L1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20092888; PubMed=10625660;
RA   Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
RA   Sims J.E.;
RT   "Four New Members Expand the IL-1 Superfamily.";
RL   J. Biol. Chem. 275:1169-1175(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99443727; PubMed=10512743;
RA   Mulero J.J., Pace A.M., Nelken S.T., Loeb D.B., Correa T.R.,
RA   Drmanac R., Ford J.E.;
RT   "IL1HY1: A Novel Interleukin-1 Receptor Antagonist Gene.";
RL   Biochem. Biophys. Res. Commun. 263:702-706(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RA   Barton J.L., di Giovine F.S., Symons J.A., Nicklin M.J.H.;
RT   "A tissue specific interleukin-1 receptor antagonist homolog from the
RT   IL1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18ra activities.";
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Barton J.L., Herbst R., Bosisio D., Nicklin M.J.H.;
RT   "A tissue specific interleukin-1 receptor antagonist homolog from the
RT   IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18ra activities.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20322477; PubMed=10866108;
RA   Mulero J.J., Nelken S.T., Ford J.E.;
RT   "Organization of the Human Interleukin-1 Receptor Antagonist Gene
RT   IL1HY1.";
RL   Immunogenetics 51:425-428(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RA   Debets R., Timans J.C., Zurawski S., Sana T.R., Bazan F.,
RA   Kastelein R.A.;
RT   "Novel IL-1 ligands IL-1d and IL-1e use IL-1R related protein 2.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF201830; AAF25210.1; -.
DR   EMBL; AF186094; AAF02757.1; -.
DR   EMBL; AJ242737; CAB59822.1; -.
DR   EMBL; AJ242738; CAB59823.1; -.
DR   EMBL; AJ271338; CAB67704.1; -.
DR   EMBL; AF216693; AAF76981.1; -.
DR   EMBL; AF230377; AAF91274.1; -.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
KW   Receptor.
SQ   SEQUENCE   155 AA;  16962 MW;  B96DB5EFA2612E25 CRC64;


  Query Match             22.3%;  Score 185.5;  DB 4;  Length 155;
  Best Local Similarity   44.8%;  Pred. No. 3.4e-12;
  Matches   43;  Conservative   13;  Mismatches   35;  Indels    5;  Gaps    3;

Qy      61 NPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFES 120
           :|: ||: | : || |  || :||| |:  :||:||   :  ||| ||    |  |:|||
Db      55 SPVILGVQGGSQCLSCG-VGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFES 113

Qy     121 VAFPGWFIAVSSEGGCPLILTQ--ELG--KANTTDF 152
           |:||||:    |   |: |||  | |   |  |||
Db     114 AAYPGWFLCTVPEADQPVRLTQLPENGGWNAPITDF 149


RESULT  11
O73909
ID   O73909      PRELIMINARY;      PRT;   267 AA.
AC   O73909;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   INTERLEUKIN-1BETA.
GN   IL-1BETA OR IL1B.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Weining K.C., Sick C., Kaspers B., Staeheli P.;
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LINE N;
RA   Kaiser P., Rothwell L., Goodchild M., Bumstead N.;
RT   "Chicken interleukin-1b: an evolutionary bridge between fish and
RT   mammals.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Y15006; CAA75239.1; -.
DR   EMBL; AJ245728; CAC04510.1; -.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
FT   CHAIN       106    267       INTERLEUKIN-1BETA.
SQ   SEQUENCE   267 AA;  29822 MW;  3EF72164E4D40B64 CRC64;


  Query Match             22.3%;  Score 185;  DB 13;  Length 267;
  Best Local Similarity   32.7%;  Pred. No. 7.5e-12;
  Matches   54;  Conservative   25;  Mismatches   66;  Indels   20;  Gaps    6;

Qy       4 ALKIDTPQQGSIQDINHRVWVLQDQT-LIAV----PRKDRMSPVTIALISCRHVETLEKD 58
           | :    |   | ||| : :||:  | |:|:    |   :   : |||   |
Db     108 AFRYTRSQSFDIFDINQKCFVLESPTQLVALHLQGPSSSQKVRLNIALYRPR------GP 161

Qy      59 RGN------PIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQS 112
           ||:      |: ||: |  | : |   | :|||||:| |:|   :  | :  |:||   |
Db     162 RGSAGTGQMPVALGIKGYKLYMSCVMSGTEPTLQLEEADVMRDIDSVE-LTRFIFYRLDS 220
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Qy    113 GRNST--FESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLT 155
          |  ||| |||||||  | :   |: :| :  : |   : |:
Db    221 PTEGTTRFESAAFPGWFICTSLQPRQPVGITNQPDQVNIATYKLS 265
```

RESULT 12
Q96GD6
ID Q96GD6 PRELIMINARY; PRT; 159 AA.
AC Q96GD6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INTERLEUKIN 1 RECEPTOR ANTAGONIST.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PANCREATIC ADENOCARCINOMA;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC009745; AAH09745.1; -.
KW Receptor.
SQ SEQUENCE 159 AA; 17888 MW; C1D66CDF0D2F7B44 CRC64;

Query Match 22.1%; Score 183.5; DB 4; Length 159;
Best Local Similarity 30.6%; Pred. No. 5.8e-12;
Matches 45; Conservative 26; Mismatches 49; Indels 27; Gaps 3;

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Qy     15 IQDINHRVWVLQDQTLIA-------VPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGL 67
          | |:| : : |::  |:|       |  ::::  | |              : ::||:
Db     22 IWDVNQKTFYLRNNQLVAGYLQGPNVNLEEKIDVVPI--------------EPHALFLGI 67

Qy     68 NGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWF 127
          :|  :|| | | ||:  |||:  :| ||    :  | | |  | ||  ::||| | ||||
Db     68 HGGKMCLSCVKSGDETRLQLEAVNITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWF 127

Qy    128 IAVSSEGGCPLILTQELGKANTTDFGL 154
          :  : |   |: ||      |  | |:
Db    128 LCTAMEADQPVSLT------NMPDEGV 148
```

RESULT 13
Q9BEH0
ID Q9BEH0 PRELIMINARY; PRT; 176 AA.
AC Q9BEH0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INTERLEUKIN-1 RECEPTOR ANTAGONIST.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Shin I.-S., Youn H.-Y.;
RT "Molecular cloning of canine interleukin-1 receptor antagonist (IL-
RT 1ra).";
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY026462; AAK01472.1; -.
DR HSSP; P18510; 1ILR.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Receptor.
SQ SEQUENCE 176 AA; 19922 MW; 8486CA54A240212B CRC64;

Query Match 21.7%; Score 180.5; DB 6; Length 176;
Best Local Similarity 30.6%; Pred. No. 1.4e-11;
Matches 41; Conservative 25; Mismatches 47; Indels 21; Gaps 2;

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Qy     15 IQDINHRVWVLQDQTLIA-------VPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGL 67
          | |:| : : |::  |:|         ::::  | :                : ::||:
Db     40 IWDVNQKTFYLRNNQLVAGYLQGSNTKLEEKLDVVPV--------------EPHAVFLGI 85

Qy     68 NGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWF 127
          :|  ||| | | ||:  |||:  :| ||    :  | | |  | ||  ::||| | ||||
Db     86 HGGKLCLACVKSGDETRLQLEAVNITDLSKNKDQDKRFTFILSDSGPTTSFESAACPGWF 145

Qy    128 IAVSSEGGCPLILT 141
          :  : |   |: ||
Db    146 LCTALEADRPVSLT 159
```

RESULT 14
Q9GMZ4
ID Q9GMZ4 PRELIMINARY; PRT; 177 AA.
AC Q9GMZ4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INTERLEUKIN-1 RECEPTOR ANTAGONIST.
GN IL-1RA.
OS Tursiops truncatus (Atlantic bottle-nosed dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Tursiops.
OX NCBI_TaxID=9739;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21109087; PubMed=11182153;
RA Inoue Y., Itou T., Jimbo T., Syouji Y., Ueda K., Sakai T.;
RT "Molecular cloning and functional expression of bottle-nosed dolphin
RT (Tursiops truncatus) interleukin-1 receptor antagonist.";
RL Vet. Immunol. Immunopathol. 78:131-141(2001).
DR EMBL; AB038268; BAB11806.1; -.
DR HSSP; P18510; 1IRA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Receptor.
SQ SEQUENCE 177 AA; 19923 MW; 6FD19A06C09B131B CRC64;

Query Match 20.8%; Score 172.5; DB 6; Length 177;
Best Local Similarity 31.3%; Pred. No. 1e-10;
Matches 42; Conservative 24; Mismatches 47; Indels 21; Gaps 2;

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Qy     15 IQDINHRVWVLQDQTLIA-------VPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGL 67
          | |:| : : |::  |:|         ::::  | |                : ::||:
Db     40 IWDVNQKTFYLRNNQLVAGYLQGPNTKLEEKIDVVPI--------------EPHAMFLGI 85

Qy     68 NGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWF 127
          :|  ||| | | ||:  | |:  :| || :  |  | | |  | ||  ::||| | ||||
Db     86 HGGKLCLACVKSGDEIKLGLEPVNITDLNSSKEEDKRFAFIRSDSGPTTSFESAACPGWF 145

Qy    128 IAVSSEGGCPLILT 141
          :  : |   |: ||
Db    146 LCTALETDQPVGLT 159
```

RESULT 15
Q9GKK2
ID Q9GKK2 PRELIMINARY; PRT; 176 AA.
AC Q9GKK2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

```
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN-1 RECEPTOR ANTAGONIST.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21109092; PubMed=11182158;
RA   Campbell S.E., Nasir L., Argyle D.J., Gault E.A., Duthie S.,
RA   Bennett D.;
RT   "Cloning of canine IL-1ra, TNFR and TIMP-2.";
RL   Vet. Immunol. Immunopathol. 78:207-214(2001).
DR   EMBL; AF216526; AAG36777.1; -.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
KW   Receptor.
SQ   SEQUENCE   176 AA;  19938 MW;  8486CA54A254206B CRC64;


  Query Match             20.5%;  Score 170.5;  DB 6;  Length 176;
  Best Local Similarity   29.9%;  Pred. No. 1.7e-10;
  Matches   40;  Conservative   25;  Mismatches   48;  Indels   21;  Gaps    2;

Qy      15 IQDINHRVWVLQDQTLIA-------VPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGL 67
           | |:| : : |::  |:|          ::::  | :                : ::||:
Db      40 IWDVNQKTFYLRNNQLVAGYLQGSNTKLEEKLDVVPV--------------EPHAVFLGI 85

Qy      68 NGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWF 127
           :|  ||| | | ||:  |||:  :| ||    :  | | |  | ||  ::||| | ||||
Db      86 HGGKLCLACVKSGDETRLQLEAVNITDLSKNKDQDKRFTFILSDSGPTTSFESAACPGWF 145

Qy     128 IAVSSEGGCPLILT 141
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Db     146 LCTALEADRLVSLT 159


Search completed: June 20, 2002, 15:10:54
Job time: 465 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: June 21, 2002, 11:56:23 ; Search time 2781.56 Seconds
(without alignments)
3588.619 Million cell updates/sec

Title: US-09-763-498-12
Perfect score: 477
Sequence: 1 atggaaaaagcattgaaaat.....ggttaactatgctgttttaa 477

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
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14: gb_vi:*
15: em_ba:*
16: em_fun:*
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	475.4	99.7	477	9	AF201831	AF201831 Homo sapi
2	349.8	73.3	391	6	AX193589	AX193589 Sequence
3	238.6	50.0	483	10	AF200493	AF200493 Mus muscu
4	238.6	50.0	795	10	AF206697	AF206697 Mus muscu
5	222	46.5	244	6	AX193660	AX193660 Sequence
6	215.8	45.2	197308	9	AC016724	AC016724 Homo sapi
7	202	42.3	1073	6	AX207820	AX207820 Sequence
8	202	42.3	1177	9	AF206696	AF206696 Homo sapi
9	202	42.3	1183	6	E54910	E54910 Interleukin
10	202	42.3	1183	9	AF200492	AF200492 Homo sapi
11	134.2	28.1	520	6	AX193587	AX193587 Sequence
12	134.2	28.1	585	6	AX052581	AX052581 Sequence
13	134.2	28.1	585	9	AF201833	AF201833 Homo sapi
14	134.2	28.1	1244	6	AX167128	AX167128 Sequence
15	129.2	27.1	746	6	AR137703	AR137703 Sequence
16	127	26.6	243	6	AR137705	AR137705 Sequence
17	127	26.6	294	6	AR137704	AR137704 Sequence
18	112	23.5	329	6	AX193643	AX193643 Sequence
19	106.4	22.3	186587	2	AC106686	AC106686 Rattus no
c 20	79.4	16.6	184626	2	AC096974	AC096974 Rattus no
21	78.8	16.5	1036	4	AY026462	AY026462 Canis fam
22	77.2	16.2	563	4	AF216526	AF216526 Canis fam
23	74.8	15.7	520	10	MUSILRA	M63100 M.musculus
24	74.8	15.7	542	10	S64082	S64082 interleukin
25	74.8	15.7	604	10	AF001795	AF001795 Mus muscu
26	74.8	15.7	1576	10	MUSIL1RAA	M57525 Mouse inter
27	74.8	15.7	1877	6	E55194	E55194 Interleukin
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29	74.8	15.7	1940	10	MUSIL1RA	M64404 Mus domesti
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32	71.8	15.1	1590	4	D83714	D83714 Equus cabal
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34	71.8	15.1	1614	4	ECU92482	U92482 Equus cabal
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37	71	14.9	574	4	S68977	S68977 sIL-1ra=int
38	70.8	14.8	462	6	AR105636	AR105636 Sequence
39	70.8	14.8	474	6	A50276	A50276 Sequence 10
40	70.8	14.8	474	6	AR001464	AR001464 Sequence
41	70.8	14.8	474	6	AR055509	AR055509 Sequence
42	70.8	14.8	474	6	AR085392	AR085392 Sequence
43	70.8	14.8	514	6	I42450	I42450 Sequence 41
44	70.8	14.8	531	6	A49726	A49726 Sequence 1
45	70.8	14.8	531	6	A50144	A50144 Sequence 1

ALIGNMENTS

RESULT 1
AF201831
LOCUS AF201831 477 bp mRNA linear PRI 16-JAN-2000
DEFINITION Homo sapiens FIL1 epsilon mRNA, complete cds.
ACCESSION AF201831
VERSION AF201831.1 GI:6694389
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 477)
AUTHORS Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garka,K.E. and Sims,J.E.
TITLE Four new members expand the interleukin-1 superfamily
JOURNAL J. Biol. Chem. 275 (2), 1169-1175 (2000)
MEDLINE 20092888
REFERENCE 2 (bases 1 to 477)
AUTHORS Sims,J.E.
TITLE Direct Submission
JOURNAL Submitted (04-NOV-1999) Molecular Genetics, Immunex Corporation, 51 University Street, Seattle, WA 98101, USA
FEATURES Location/Qualifiers

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     CDS             1. .477
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                     /db_xref="GI:6694390"
                     /translation="MEKALKIDTPQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTI
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BASE COUNT      124 a    123 c    117 g    113 t
ORIGIN
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Best Local Similarity 99.8%; Pred. No. 2.3e-134;
Matches 476; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      61 cgggtgtgggttcttcaggaccagacgctcatagcagtcccgaggaaggaccgtatgtct 120
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Db      61 CGGGTGTGGGTTCTTCAGGACCAGACGCTCATAGCAGTCCCGAGGAAGGACCGTATGTCT 120

Qy     121 ccagtcactattgccttaatctcatgccgacatgtggagacccttgagaaagacagaggg 180
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Qy     181 aaccccatctacctgggcctgaatggactcaatctctgcctgatgtgtgctaaagtcggg 240
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Qy     241 gaccagcccacactgcagctgaaggaaaaggatataatggatttgtacaaccaacccgag 300
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Qy     301 cctgtgaagtcctttctcttctaccacagccagagtggcaggaactccaccttcgagtct 360
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Qy     361 gtggctttccctggctggttcatcgctgtcagctctgaaggaggctgtcctctcatcctt 420
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Qy     421 acccaagaactggggaaagccaacactactgactttgggttaactatgctgttttaa 477
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Db     421 ACCCAAGAACTGGGGAAAGCCAACACTACTGACTTTGGGTTAACTATGCTGTTTTAA 477
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RESULT   2
AX193589
LOCUS       AX193589                391 bp    DNA     linear   PAT 15-AUG-2001
DEFINITION  Sequence 11 from Patent WO0140291.
ACCESSION   AX193589
VERSION     AX193589.1  GI:15211518
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 391)
  AUTHORS   Burgess,C.E., Prayaga,S.K., Shimkets,R.A., Rastelli,L.,
            Zerhusen,B.D. and Mezes,P.S.
  TITLE     Proteins and nucleic acids encoding the same
  JOURNAL   Patent: WO 0140291-A 11 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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Best Local Similarity 96.5%; Pred. No. 6e-96;
Matches 383; Conservative 0; Mismatches 2; Indels 12; Gaps 2;

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Db       1 GATATCAATCATCGGGTGTGGGTTCTTCAGGACCAGACGCTCATAGCAGTCCCGAGGAAG 60

Qy     109 gaccgtatgtctccagtcactattgccttaatctcatgccgacatgtggagacccttgag 168
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Db      61 G------TGTTCCCAGTCACTATTGCCTTAATCTCATGCCGACATGTGGAGACCCTTGAG 114

Qy     169 aaagacagagggaaccccatctacctgggcctgaatggactcaatctctgcctgatgtgt 228
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Qy     229 gctaaagtcggggaccagcccacactgcagctga------aggaaaaggatataatggat 282
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Db     175 GCTAAAGTCGGGGACCAGCCCACACTGCAGCTGAAGCTTCAGGAAAAGGATATAATGGAT 234

Qy     283 ttgtacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcagg 342
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Qy     343 aactccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaagga 402
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Db     295 AACTCCACCTTCGAGTCTGTGGCTTTCCCTGGCTGGTTCATCGCTGTCAGCTCTGAAGGA 354

Qy     403 ggctgtcctctcatccttacccaagaactggggaaag 439
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RESULT   3
AF200493
LOCUS       AF200493                483 bp    mRNA    linear   ROD 11-MAY-2000
DEFINITION  Mus musculus interleukin-1 homolog 1 mRNA, complete cds.
ACCESSION   AF200493
VERSION     AF200493.1  GI:7769113
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 483)
  AUTHORS   Kumar,S., McDonnell,P.C., Lehr,R., Tierney,L., Tzimas,M.N.,
            Griswold,D.E., Capper,E.A., Tal-Singer,R., Wells,G.I., Doyle,M.L.
            and Young,P.R.
  TITLE     Identification and initial characterization of four novel members
            of the interleukin-1 family
  JOURNAL   J. Biol. Chem. 275 (14), 10308-10314 (2000)
  MEDLINE   20209405
   PUBMED   10744718
REFERENCE   2  (bases 1 to 483)
  AUTHORS   Kumar,S., McDonnell,P.C. and Young,P.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-NOV-1999) Bone and Cartilage Biology, UW 2109,
            SmithKline Beecham Pharmaceuticals, 709 Swedeland Rd., King of
            Prussia, PA 19406, USA
FEATURES             Location/Qualifiers
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  Best Local Similarity   68.8%;  Pred. No. 6.4e-62;
  Matches  328;  Conservative    0;  Mismatches  149;  Indels    0;  Gaps    0;

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Qy     61 cgggtgtgggttcttcaggaccagacgctcatagcagtcccgaggaaggaccgtatgtct 120
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Qy    121 ccagtcactattgccttaatctcatgccgacatgtggagacccttgagaaagacagaggg 180
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Qy    181 aaccccatctacctgggcctgaatggactcaatctctgcctgatgtgtgctaaagtcggg 240
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Qy    301 cctgtgaagtcctttctcttctaccacagccagagtggcaggaactccaccttcgagtct 360
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Qy    361 gtggctttccctggctggttcatcgctgtcagctctgaaggaggctgtcctctcatcctt 420
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Db    427 ACCCAAGAACTGGGGGAAATCTTCATCACTGACTTCGAGATGATTGTGGTTCATTAA 483


RESULT   4
AF206697
LOCUS       AF206697                 795 bp    mRNA    linear   ROD 01-NOV-2001
DEFINITION  Mus musculus interleukin-1 epsilon (Ille) mRNA, complete cds.
ACCESSION   AF206697
VERSION     AF206697.1  GI:11493849
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 795)
  AUTHORS   Debets,R., Timans,J.C., Homey,B., Zurawski,S., Sana,T.R., Lo,S.,
            Wagner,J., Edwards,G., Clifford,T., Menon,S., Bazan,J.F. and
            Kastelein,R.A.
  TITLE     Two novel IL-1 family members, IL-1 delta and IL-1 epsilon,
            function as an antagonist and agonist of NF-kappa B activation
            through the orphan IL-1 receptor-related protein 2
  JOURNAL   J. Immunol. 167 (3), 1440-1446 (2001)
  MEDLINE   21359532
   PUBMED   11466363
REFERENCE   2  (bases 1 to 795)
  AUTHORS   Debets,R., Timans,J.C., Zurawski,S., Bazan,J.F. and Kastelein,R.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-NOV-1999) Molecular Biology, DNAX Research Institute
            of Molecular and Cellular Biology, Inc., 901 California Avenue,
            Palo Alto, CA 94304-1104, USA
FEATURES             Location/Qualifiers
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                     and IL-1ra; highly expressed in skin tissue; acts through
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                     signaling cascade; antagonized by IL-1d"
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                     /product="interleukin-1 epsilon"
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BASE COUNT      237 a    177 c    174 g    207 t
ORIGIN


  Query Match             50.0%;  Score 238.6;  DB 10;  Length 795;
  Best Local Similarity   68.8%;  Pred. No. 6.8e-62;
  Matches  328;  Conservative    0;  Mismatches  149;  Indels    0;  Gaps    0;

Qy      1 atggaaaaagcattgaaaattgacacacctcagcgggggagcattcaggatatcaatcat 60
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Db     82 AAGGAGAAAGAACTAAGAGCAGCATCACCTTCGCTTAGACATGTTCAGGATCTTAGTAGT 141

Qy     61 cgggtgtgggttcttcaggaccagacgctcatagcagtcccgaggaaggaccgtatgtct 120
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Db    142 CGTGTGTGGATCCTGCAGAACAATATCCTCACTGCAGTCCCAAGGAAAGAGCAAACAGTT 201

Qy    121 ccagtcactattgccttaatctcatgccgacatgtggagacccttgagaaagacagaggg 180
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Db    202 CCAGTCACTATTACCTTGCTCCCATGCCAATATCTGGACACTCTTGAGACGAACAGGGGG 261

Qy    181 aaccccatctacctgggcctgaatggactcaatctctgcctgatgtgtgctaaagtcggg 240
           | ||||  ||| ||||  || |  | |  |    ||||||| | ||  | || |  |||
Db    262 GATCCCACGTACATGGGAGTGCAAAGGCCGATGAGCTGCCTGTTCTGCACAAAGGATGGG 321

Qy    241 gaccagcccacactgcagctgaaggaaaaggatataatggatttgtacaaccaacccgag 300
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Qy    301 cctgtgaagtcctttctcttctaccacagccagagtggcaggaactccaccttcgagtct 360
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Qy    361 gtggctttccctggctggttcatcgctgtcagctctgaaggaggctgtcctctcatcctt 420
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Qy    421 acccaagaactggggaaagccaacactactgactttgggttaactatgctgttttaa 477
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Db    502 ACCCAAGAACTGGGGGAAATCTTCATCACTGACTTCGAGATGATTGTGGTACATTAA 558


RESULT   5
AX193660
LOCUS       AX193660                 244 bp    DNA     linear   PAT 15-AUG-2001
DEFINITION  Sequence 82 from Patent WO0140291.
ACCESSION   AX193660
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VERSION     AX193660.1  GI:15211539
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 244)
  AUTHORS   Burgess,C.E., Prayaga,S.K., Shimkets,R.A., Rastelli,L.,
            Zerhusen,B.D. and Mezes,P.S.
  TITLE     Proteins and nucleic acids encoding the same
  JOURNAL   Patent: WO 0140291-A 82 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .244
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT       53 a     71 c     58 g     62 t
ORIGIN
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Query Match 46.5%; Score 222; DB 6; Length 244;
Best Local Similarity 97.5%; Pred. No. 7.1e-57;
Matches 238; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

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Qy     188 tctacctgggcctgaatggactcaatctctgcctgatgtgtgctaaagtcggggaccagc 247
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TCTACCTGGGCCTGAATGGACTCAATCTCTGCCTGATGTGTGCTAAAGTCGGGGACCAGC 60

Qy     248 ccacactgcagctga------aggaaaaggatataatggatttgtacaaccaacccgagc 301
           |||||||||||||||      ||||||||||||||||||||||||||||||||||||||
Db      61 CCACACTGCAGCTGAAGCTTCAGGAAAAGGATATAATGGATTTGTACAACCAACCCGAGC 120

Qy     302 ctgtgaagtcctttctcttctaccacagccagagtggcaggaactccaccttcgagtctg 361
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CTGTGAAGTCCTTTCTCTTCTACCACAGCCAGAGTGGCAGGAACTCCACCTTCGAGTCTG 180

Qy     362 tggctttccctggctggttcatcgctgtcagctctgaaggaggctgtcctctcatcctta 421
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TGGCTTTCCCTGGCTGGTTCATCGCTGTCAGCTCTGAAGGAGGCTGTCCTCTCATCCTTA 240

Qy     422 ccca 425
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Db     241 CCCA 244
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RESULT   6
AC016724
LOCUS       AC016724              197308 bp    DNA     linear   PRI 09-JAN-2002
DEFINITION  Homo sapiens BAC clone RP11-339F22 from 2, complete sequence.
ACCESSION   AC016724
VERSION     AC016724.11  GI:14718389
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 197308)
  AUTHORS   Sulston,J.E. and Waterston,R.
  TITLE     Toward a complete human genome sequence
  JOURNAL   Genome Res. 8 (11), 1097-1108 (1998)
  MEDLINE   99063792
REFERENCE   2  (bases 1 to 197308)
  AUTHORS   Armstrong,J. and Haakenson,W.
  TITLE     The sequence of Homo sapiens BAC clone RP11-339F22
  JOURNAL   Unpublished (2001)
REFERENCE   3  (bases 1 to 197308)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-DEC-1999) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   4  (bases 1 to 197308)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JUL-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   5  (bases 1 to 197308)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JAN-2002) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT     On Jul 14, 2001 this sequence version replaced gi:13431151.
            -------------- Genome Center
               Center: Washington University Genome Sequencing Center
               Center code: WUGSC
               Web site: http://genome.wustl.edu/gsc
               Contact: sapiens@watson.wustl.edu
            -------------- Summary Statistics
               Center project name: H_NH0339F22
            --------------.

            NOTICE:  This sequence may not represent the entire insert of this
            clone.  It may be shorter because we only sequence overlapping
            clone sections once, or longer because we provide a small overlap
            between neighboring data submissions.

            This sequence was finished as follows unless otherwise noted:
            all regions were double stranded, sequenced with an alternate
            chemistry, or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by sequence
            from more than one subclone; and the assembly was confirmed by
            restriction digest.

            MAPPING INFORMATION:
            Mapping information for this clone was provided by Dr. John D.
            McPherson, Department of Genetics, Washington University, St. Louis
            MO.  For additional information about the map position of this
            sequence, see http://genome.wustl.edu/gsc

            SOURCE INFORMATION:
            The RPCI-11 human BAC library was made from the blood of one male
            donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
            Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
            approach for construction of bacterial artificial chromosome
            libraries.  Genomics 51:1-8.  The clone may be obtained either from
            Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
            and coworkers at the Roswell Park Cancer Institute
            (http://bacpac.med.buffalo.edu)
            VECTOR:  pBACe3.6
            NEIGHBORING SEQUENCE INFORMATION:
            The clone sequenced to the left is RP11-725J3; the clone sequenced
            to the right is RP11-97J14.  Actual start of this clone is at base
            position 1 of RP11-339F22; actual end is at base position 197308 of
            RP11-339F22.

            Data from AC084280 and AC024704 was used to finish this clone,
            AC016724.  Polymorphisms have been identified between AC024704 and
            AC016724.

            Sequence derived from pcr from base position 148683 to 149264.
FEATURES             Location/Qualifiers
     source          1. .197308
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="2"
                     /map="2"
                     /clone="RP11-339F22"
                     /clone_lib="RPCI-11"
     repeat_region   6. .275
                     /rpt_family="L1"
     repeat_region   274. .740
                     /rpt_family="L1"
     repeat_region   744. .907
                     /rpt_family="ERV1"
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repeat_region      917. .1361
                     /rpt_family="L1"
repeat_region     1362. .1814
                     /rpt_family="L1"
repeat_region     1838. .1952
                     /rpt_family="ERV1"
repeat_region     2105. .2161
                     /rpt_family="ERV1"
repeat_region     2245. .2587
                     /rpt_family="L1"
repeat_region     2588. .2877
                     /rpt_family="Alu"
repeat_region     2878. .3244
                     /rpt_family="L1"
repeat_region     3235. .4195
                     /rpt_family="L1"
repeat_region     3460. .3481
                     /rpt_family="AT_rich"
repeat_region     4311. .4450
                     /rpt_family="MIR"
repeat_region     4822. .4957
                     /rpt_family="MER1_type"
repeat_region     5152. .5337
                     /rpt_family="MER1_type"
repeat_region     6118. .7901
                     /rpt_family="L2"
repeat_region     8008. .8145
                     /rpt_family="L2"
repeat_region     8146. .8343
                     /rpt_family="MER1_type"
repeat_region     8344. .8429
                     /rpt_family="L2"
repeat_region     8661. .8827
                     /rpt_family="ERV1"
repeat_region     8999. .9029
                     /rpt_family="(T)n"
misc_feature      9003. .9030
                     /note="similar to Homo sapiens EST BI091273
                     (NID:g14509603)"
misc_feature      9011. .9031
                     /note="similar to Homo sapiens EST AA587127 (NID:g2397941)
                     nn70c01.s1"
misc_feature      9013. .9031
                     /note="similar to Homo sapiens EST AI034379 (NID:g3255332)
                     ox20g11.x1"
repeat_region     9167. .9564
                     /rpt_family="L2"
repeat_region    10187. .10267
                     /rpt_family="MIR"
repeat_region    11074. .11122
                     /rpt_family="(CTG)n"
repeat_region    11587. .11611
                     /rpt_family="(TG)n"
repeat_region    11651. .11884
                     /rpt_family="MALR"
repeat_region    12198. .12353
                     /rpt_family="MIR"
repeat_region    12578. .12714
                     /rpt_family="MER1_type"
repeat_region    13540. .13855
                     /rpt_family="Alu"
repeat_region    13985. .14843
                     /rpt_family="L1"
repeat_region    14923. .15243
                     /rpt_family="MER2_type"
repeat_region    15980. .16836
                     /rpt_family="L1"
repeat_region    17526. .17822
                     /rpt_family="Alu"
repeat_region    18067. .18089
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Matches 217; Conservative   0; Mismatches    2; Indels    0; Gaps    0;

Qy    259 ctgaaggaaaaggatataatggatttgtacaaccaaccgagccctgtgaagtccttctc 318
          ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   57056 CTTCAGGAAAAGGATATAATTGTACAACCAAGCCCGAGCCCTGTGAAGTCCTTTCTC 57115

Qy    319 ttctaccacagccagagtggcaggaactccaccttcgagtctgtggcttcccctggctgg 378
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   57116 TTCTACCACAGCCAGAGTGGCAGGAACTCCACCTTCGAGTCTGTGGCTTTCCCTGGCTGG 57175

Qy    379 ttcatcgctgtcagctctgaaggaggctgtcctctctcatcctaccaagaactgggaaa 438
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   57176 TTCATCGCTGTCAGCTCTGAAGGAGGCTGTCCTCTCATCCTTACCCAAGAACTGGGAAA 57235

Qy    439 gccaacactgacttgggttaactatgctgtttaa 477
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Db   57236 GCCAACACTGACTTGGGTTAACTATGCTGTTTAA 57274

RESULT  7
AX207820
LOCUS       AX207820              1073 bp    DNA     linear   PAT 31-AUG-2001
DEFINITION  Sequence 3 from Patent WO0157219.
ACCESSION   AX207820
VERSION     AX207820.1  GI:15422467
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   Debets,J.E., Timans,J.C., Bazan,J.F. and Kastelein,R.A.
  TITLE     Mammalian interleukin-1-delta and -epsilon. Their use in
            therapeutic and diagnostic methods
  JOURNAL   Patent: WO 0157219-A 3 09-AUG-2001;
            SCHERING CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .1073
                     /organism="unidentified"
                     /db_xref="taxon:32644"
                     /note="Description of Unknown Organism: primate; surmised
                     Homo sapiens"
     CDS             67. .576

Query Match         45.2%; Score 215.8; DB 9; Length 197308;
Best Local Similarity   99.1%; Pred. No. 1.2e-54;
Matches 217; Conservative   0; Mismatches    2; Indels    0; Gaps    0;

Qy    259 ctgaaggaaaaggatataatggatttgtacaaccaaccgagccctgtgaagtccttctc 318
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Db   19604 CTTCAGGAAAAGGATATAATTGTACAACCAAGCCCGAGCCCTGTGAAGTCCTTTCTC 19663

repeat_region    19604. .20083
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repeat_region    20084. .20447
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repeat_region    20448. .21020
                     /rpt_family="ERVL"
repeat_region    21033. .21306
                     /rpt_family="L1"
repeat_region    21315. .21656
                     /rpt_family="ERVL"
repeat_region    21906. .22079
                     /rpt_family="ERVL"
repeat_region    22533. .22637
                     /rpt_family="MER2_type"
repeat_region    22668. .22977
                     /rpt_family="ERVL"
repeat_region    23349. .23852
                     /rpt_family="L1"
repeat_region    25801. .25931
                     /rpt_family="ERVL"
misc_feature     27616. .28020
                     /note="match to EST AW937349 (NID:g8112771)"
repeat_region    28055. .28149
                     /rpt_family="L2"
repeat_region    28743. .28984
                     /rpt_family="CR1"
repeat_region    29010. .29092
                     /rpt_family="L2"
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                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC60373.1"
                     /db_xref="GI:15422468"
                     /translation="MRGTPGDADGGGRAVYQSMCKPITGTINDLNQQVWTLQGQNLVA
                     VPRSDSVTPVTVAVITCKYPEALEQGRGDPIYLGIQNPEMCLYCEKVGEQPTLQLKEQ
                     KIMDLYGQPEPVKPFLFYRAKTGRTSTLESVAFPDWFIASSKRDQPIILTSELGKSYN
                     TAFELNIND"
BASE COUNT      281 a    241 c    255 g    296 t
ORIGIN


  Query Match             42.3%;  Score 202;  DB 6;  Length 1073;
  Best Local Similarity   67.1%;  Pred. No. 1.1e-50;
  Matches  302;  Conservative    0;  Mismatches  145;  Indels    3;  Gaps    1;

Qy      18 aattgacacacctcagcgggggagcattcaggatatcaatcatcgggtgtgggttcttca 77
           |||    | ||||      ||||  ||| | ||| | ||||| |  ||||||   |||||
Db     120 AATGTGTAAACCTATTACTGGGACTATTAATGATTTGAATCAGCAAGTGTGGACCCTTCA 179

Qy      78 ggaccagacgctcatagcagtcccgaggaaggaccgtatgtctccagtcactattgcctt 137
           ||  ||||  ||  | ||||| ||  | |  ||| || || | ||||||||| ||||  |
Db     180 GGGTCAGAACCTTGTGGCAGTTCCACGAAGTGACAGTGTGACCCCAGTCACTGTTGCTGT 239

Qy     138 aatctcatgccgacatgtggagacccttgagaaagacagagggaaccccatctacctggg 197
           ||| |||||    ||   ||| | |||||| ||| |||||||| | |||||  ||  ||||
Db     240 TATCACATGCAAGTATCCAGAGGCTCTTGAGCAAGGCAGAGGGGATCCCATTTATTTGGG 299

Qy     198 cctgaatggactcaatctctgcctgatgtgtgctaaagtcggggaccagcccacactgca 257
             |  |    |   | | ||  ||   ||||  || || || || |||||||| ||||
Db     300 AATCCAGAATCCAGAAATGTGTTTGTATTGTGAGAAGGTTGGAGAACAGCCCACATTGCA 359

Qy     258 gctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttct 317
           ||| || ||  || | || ||||||  ||||   |||||||||||| |||||  |||| ||
Db     360 GCTAAAAGAGCAGAAGATCATGGATCTGTATGGCCAACCCGAGCCCGTGAAACCCTTCCT 419

Qy     318 cttctaccacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctg 377
           |||||||    | ||| ||| |||| ||||||| | ||||||||||| ||||| | |||
Db     420 TTTCTACCGTGCCAAGACTGGTAGGACCTCCACCCTTGAGTCTGTGGCCTTCCCGGACTG 479

Qy     378 gttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaa 437
           ||||||   || |  |||  |  ||| |   ||  |||| || ||   |||||| |||||
Db     480 GTTCAT---TGCCTCCTCCAAGAGAGACCAGCCCATCATTCTGACTTCAGAACTTGGGAA 536

Qy     438 agccaacactactgactttgggttaactat 467
           |  |||  |||| |||||  |||| |||
Db     537 GTCATACAACACTGCCTTTGAATTAAATAT 566


RESULT   8
AF206696
LOCUS       AF206696               1177 bp    mRNA    linear   PRI 01-NOV-2001
DEFINITION  Homo sapiens interleukin-1 epsilon (IL1E) mRNA, complete cds.
ACCESSION   AF206696
VERSION     AF206696.1  GI:11493847
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1177)
  AUTHORS   Debets,R., Timans,J.C., Homey,B., Zurawski,S., Sana,T.R., Lo,S.,
            Wagner,J., Edwards,G., Clifford,T., Menon,S., Bazan,J.F. and
            Kastelein,R.A.
  TITLE     Two novel IL-1 family members, IL-1 delta and IL-1 epsilon,
            function as an antagonist and agonist of NF-kappa B activation
            through the orphan IL-1 receptor-related protein 2
  JOURNAL   J. Immunol. 167 (3), 1440-1446 (2001)
  MEDLINE   21359532
   PUBMED   11466363
REFERENCE   2  (bases 1 to 1177)
  AUTHORS   Debets,R., Timans,J.C., Zurawski,S., Bazan,J.F. and Kastelein,R.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-NOV-1999) Molecular Biology, DNAX Research Institute
            of Molecular and Cellular Biology, Inc., 901 California Avenue,
            Palo Alto, CA 94304-1104, USA
FEATURES             Location/Qualifiers
     source          1. .1177
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /tissue_type="airway epithelial cells induced with TNF
                     alpha and IFN"
     gene            1. .1177
                     /gene="IL1E"
     CDS             67. .576
                     /gene="IL1E"
                     /note="interleukin-1-like protein; similar to IL-1a, IL-1b
                     and IL-1ra; highly expressed in skin tissue; acts through
                     an IL-1-like receptor IL-1Rrp2 resulting in IL-1-like
                     signaling cascade; antagonized by IL-1d"
                     /codon_start=1
                     /product="interleukin-1 epsilon"
                     /protein_id="AAG35670.1"
                     /db_xref="GI:11493848"
                     /translation="MRGTPGDADGGGRAVYQSMCKPITGTINDLNQQVWTLQGQNLVA
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                     KIMDLYGQPEPVKPFLFYRAKTGRTSTLESVAFPDWFIASSKRDQPIILTSELGKSYN
                     TAFELNIND"
BASE COUNT      320 a    249 c    267 g    341 t
ORIGIN


  Query Match             42.3%;  Score 202;  DB 9;  Length 1177;
  Best Local Similarity   67.1%;  Pred. No. 1.1e-50;
  Matches  302;  Conservative    0;  Mismatches  145;  Indels    3;  Gaps    1;

Qy      18 aattgacacacctcagcgggggagcattcaggatatcaatcatcgggtgtgggttcttca 77
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Db     120 AATGTGTAAACCTATTACTGGGACTATTAATGATTTGAATCAGCAAGTGTGGACCCTTCA 179

Qy      78 ggaccagacgctcatagcagtcccgaggaaggaccgtatgtctccagtcactattgcctt 137
           ||  ||||  ||  | ||||| ||  | |  ||| || || | ||||||||| ||||  |
Db     180 GGGTCAGAACCTTGTGGCAGTTCCACGAAGTGACAGTGTGACCCCAGTCACTGTTGCTGT 239

Qy     138 aatctcatgccgacatgtggagacccttgagaaagacagagggaaccccatctacctggg 197
           ||| |||||    ||   ||| | |||||| ||| |||||||| | |||||  ||  ||||
Db     240 TATCACATGCAAGTATCCAGAGGCTCTTGAGCAAGGCAGAGGGGATCCCATTTATTTGGG 299

Qy     198 cctgaatggactcaatctctgcctgatgtgtgctaaagtcggggaccagcccacactgca 257
             |  |    |   | | ||  ||   ||||  || || || || |||||||| ||||
Db     300 AATCCAGAATCCAGAAATGTGTTTGTATTGTGAGAAGGTTGGAGAACAGCCCACATTGCA 359

Qy     258 gctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttct 317
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Db     360 GCTAAAAGAGCAGAAGATCATGGATCTGTATGGCCAACCCGAGCCCGTGAAACCCTTCCT 419

Qy     318 cttctaccacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctg 377
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Db     420 TTTCTACCGTGCCAAGACTGGTAGGACCTCCACCCTTGAGTCTGTGGCCTTCCCGGACTG 479

Qy     378 gttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaa 437
           ||||||   || |  |||  |  ||| |   ||  |||| || ||   |||||| |||||
Db     480 GTTCAT---TGCCTCCTCCAAGAGAGACCAGCCCATCATTCTGACTTCAGAACTTGGGAA 536

Qy     438 agccaacactactgactttgggttaactat 467
           |  |||  |||| |||||  |||| |||
Db     537 GTCATACAACACTGCCTTTGAATTAAATAT 566


RESULT   9
E54910
LOCUS       E54910                 1183 bp    DNA     linear   PAT 07-FEB-2001
DEFINITION  Interleukin-1 receptor antagonist beta (IL-1RA-beta) polypeptide.
ACCESSION   E54910
VERSION     E54910.1  GI:13019313
KEYWORDS    JP 2000032990-A/1.
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SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1183)
  AUTHORS   Peter,R.Y.
  TITLE     Interleukin-1 receptor antagonist beta (IL-1RA-beta) polypeptide
  JOURNAL   Patent: JP 2000032990-A 1 02-FEB-2000;
            SMITHKLINE BEECHAM CORP
COMMENT     OS   Unidentified
            PN   JP 2000032990-A/1
            PD   02-FEB-2000
            PF   14-MAY-1999 JP 1999134172
            PR   28-JAN-1997 US    08/790032
            PI   PETER R YOUNG
            PC   C12N15/09,A61K38/00,A61K39/395,A61K45/00,C07K14/545,C07K16/24,
            PC   C12P21/02,
            PC   C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53//A61K31/00, PC
              A61K31/00,
            PC   A61K31/00,A61K31/00,C12N15/00,A61K37/02
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .1183
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .1183
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT      329 a    249 c    269 g    336 t
ORIGIN


  Query Match             42.3%;  Score 202;  DB 6;  Length 1183;
  Best Local Similarity   67.1%;  Pred. No. 1.1e-50;
  Matches  302;  Conservative    0;  Mismatches  145;  Indels    3;  Gaps    1;

Qy      18 aattgacacacctcagcgggggagcattcaggatatcaatcatcgggtgtgggttcttca 77
           |||    | ||||      ||||  ||| | ||| | ||||| |  ||||||   |||||
Db     128 AATGTGTAAACCTATTACTGGGACTATTAATGATTTGAATCAGCAAGTGTGGACCCTTCA 187

Qy      78 ggaccagacgctcatagcagtcccgaggaaggaccgtatgtctccagtcactattgcctt 137
           ||  ||||  ||  | ||||| ||  | |  ||| || || | ||||||||| ||||  |
Db     188 GGGTCAGAACCTTGTGGCAGTTCCACGAAGTGACAGTGTGACCCCAGTCACTGTTGCTGT 247

Qy     138 aatctcatgccgacatgtggagacccttgagaaagacagagggaaccccatctacctggg 197
           ||| |||||    ||   ||| | |||||| ||| ||||||| | |||||  ||  ||||
Db     248 TATCACATGCAAGTATCCAGAGGCTCTTGAGCAAGGCAGAGGGGATCCCATTTATTTGGG 307

Qy     198 cctgaatggactcaatctctgcctgatgtgtgctaaagtcggggaccagcccacactgca 257
           |  |    |   |  | ||  ||   |||  || || || ||||||||| ||||
Db     308 AATCCAGAATCCAGAAATGTGTTTGTATTGTGAGAAGGTTGGAGAACAGCCCACATTGCA 367

Qy     258 gctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttct 317
           ||| || ||  || | || |||||| ||||   |||||||||||| |||||  |||| ||
Db     368 GCTAAAAGAGCAGAAGATCATGGATCTGTATGGCCAACCCGAGCCCGTGAAACCCTTCCT 427

Qy     318 cttctaccacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctg 377
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Db     428 TTTCTACCGTGCCAAGACTGGTAGGACCTCCACCCTTGAGTCTGTGGCCTTCCCGGACTG 487

Qy     378 gttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaa 437
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Db     488 GTTCAT---TGCCTCCTCCAAGAGAGACCAGCCCATCATTCTGACTTCAGAACTTGGGAA 544

Qy     438 agccaacactactgactttgggttaactat 467
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Db     545 GTCATACAACACTGCCTTTGAATTAAATAT 574


RESULT  10
AF200492
LOCUS       AF200492               1183 bp    mRNA    linear   PRI 11-MAY-2000
DEFINITION  Homo sapiens interleukin-1 homolog 1 mRNA, complete cds.
ACCESSION   AF200492
VERSION     AF200492.1  GI:7769111
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1183)
  AUTHORS   Kumar,S., McDonnell,P.C., Lehr,R., Tierney,L., Tzimas,M.N.,
            Griswold,D.E., Capper,E.A., Tal-Singer,R., Wells,G.I., Doyle,M.L.
            and Young,P.R.
  TITLE     Identification and initial characterization of four novel members
            of the interleukin-1 family
  JOURNAL   J. Biol. Chem. 275 (14), 10308-10314 (2000)
  MEDLINE   20209405
   PUBMED   10744718
REFERENCE   2  (bases 1 to 1183)
  AUTHORS   Kumar,S., McDonnell,P.C. and Young,P.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-NOV-1999) Bone and Cartilage Biology, UW 2109,
            SmithKline Beecham Pharmaceuticals, 709 Swedeland Rd., King of
            Prussia, PA 19406, USA
FEATURES             Location/Qualifiers
     source          1. .1183
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /cell_type="primary keratinocytes; epithelial"
     CDS             75. .584
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                     KIMDLYGQPEPVKPFLFYRAKTGRTSTLESVAFPDWFIASSKRDQPIILTSELGKSYN
                     TAFELNIND"
BASE COUNT      329 a    249 c    269 g    336 t
ORIGIN


  Query Match             42.3%;  Score 202;  DB 9;  Length 1183;
  Best Local Similarity   67.1%;  Pred. No. 1.1e-50;
  Matches  302;  Conservative    0;  Mismatches  145;  Indels    3;  Gaps    1;

Qy      18 aattgacacacctcagcgggggagcattcaggatatcaatcatcgggtgtgggttcttca 77
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Db     128 AATGTGTAAACCTATTACTGGGACTATTAATGATTTGAATCAGCAAGTGTGGACCCTTCA 187

Qy      78 ggaccagacgctcatagcagtcccgaggaaggaccgtatgtctccagtcactattgcctt 137
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Db     188 GGGTCAGAACCTTGTGGCAGTTCCACGAAGTGACAGTGTGACCCCAGTCACTGTTGCTGT 247

Qy     138 aatctcatgccgacatgtggagacccttgagaaagacagagggaaccccatctacctggg 197
           ||| |||||    ||   ||| | |||||| ||| ||||||| | |||||  ||  ||||
Db     248 TATCACATGCAAGTATCCAGAGGCTCTTGAGCAAGGCAGAGGGGATCCCATTTATTTGGG 307

Qy     198 cctgaatggactcaatctctgcctgatgtgtgctaaagtcggggaccagcccacactgca 257
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Db     308 AATCCAGAATCCAGAAATGTGTTTGTATTGTGAGAAGGTTGGAGAACAGCCCACATTGCA 367

Qy     258 gctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttct 317
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Db     368 GCTAAAAGAGCAGAAGATCATGGATCTGTATGGCCAACCCGAGCCCGTGAAACCCTTCCT 427

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Db     428 TTTCTACCGTGCCAAGACTGGTAGGACCTCCACCCTTGAGTCTGTGGCCTTCCCGGACTG 487

Qy     378 gttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaa 437
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Db    488 GTTCAT---TGCCTCCTCCAAGAGAGACCAGCCCATCATTCTGACTTCAGAACTTGGGAA 544

Qy    438 agccaacactactgactttgggttaactat 467
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RESULT  11
AX193587
LOCUS       AX193587                520 bp    DNA     linear   PAT 15-AUG-2001
DEFINITION  Sequence 9 from Patent WO0140291.
ACCESSION   AX193587
VERSION     AX193587.1  GI:15211517
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 520)
  AUTHORS   Burgess,C.E., Prayaga,S.K., Shimkets,R.A., Rastelli,L.,
            Zerhusen,B.D. and Mezes,P.S.
  TITLE     Proteins and nucleic acids encoding the same
  JOURNAL   Patent: WO 0140291-A 9 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .520
                     /organism="Homo sapiens"
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BASE COUNT      147 a    127 c    112 g    134 t
ORIGIN


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  Best Local Similarity   56.8%;  Pred. No. 5.6e-30;
  Matches  247;  Conservative    0;  Mismatches  188;  Indels    0;  Gaps    0;

Qy     43 attcaggatatcaatcatcgggtgtgggttcttcaggaccagacgctcatagcagtcccg 102
Db     79 ATTCGTGATTCTCGACAGATGGTGTGGGTCCTGAGTGGAAATTCTTTAATAGCAGCTCCT 138

Qy    103 aggaaggaccgtatgtctccagtcactattgccttaatctcatgccgacatgtggagacc 162
Db    139 CTTAGCCGCAGCATTAAGCCTGTCACTCTTCATTTAATAGCCTGTAGAGACACAGAATTC 198

Qy    163 cttgagaaagacagagggaaccccatctacctgggcctgaatggactcaatctctgcctg 222
Db    199 AGTGACAAGGAAAAGGGTAATATGGTTTACCTGGGAATCAAGGGAAAAGATCTCTGTCTC 258

Qy    223 atgtgtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggatataatggat 282
Db    259 TTCTGTGCAGAAATTCAGGGCAAGCCTACTTTGCAGCTTAAGGAAAAAAATATCATGGAC 318

Qy    283 ttgtacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcagg 342
Db    319 CTGTATGTGGAGAAGAAAGCACAGAAGCCCTTTCTCTTTTTCCACAATAAAGAAGGCTCC 378

Qy    343 aactccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaagga 402
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Qy    403 ggctgtcctctcatccttacccaagaactggggaaagccaacactactgactttgggtta 462
Db    439 GGACAGCCCATCTTTCTCACCAAGGAGAGAGGCATAACTAATAACACTAACTTCTACTTA 498

Qy    463 actatgctgttttaa 477
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RESULT  12
AX052581
LOCUS       AX052581                585 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 1 from Patent WO0071720.
ACCESSION   AX052581
VERSION     AX052581.1  GI:12226796
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 585)
  AUTHORS   Sims,J.E. and Renshaw,B.R.
  TITLE     Il-1 eta dna and polypeptides
  JOURNAL   Patent: WO 0071720-A 1 30-NOV-2000;
            IMMUNEX CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .585
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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BASE COUNT      161 a    154 c    110 g    160 t
ORIGIN


  Query Match             28.1%;  Score 134.2;  DB 6;  Length 585;
  Best Local Similarity   56.8%;  Pred. No. 5.6e-30;
  Matches  247;  Conservative    0;  Mismatches  188;  Indels    0;  Gaps    0;

Qy     43 attcaggatatcaatcatcgggtgtgggttcttcaggaccagacgctcatagcagtcccg 102
Db    151 ATTCGTGATTCTCGACAGATGGTGTGGGTCCTGAGTGGAAATTCTTTAATAGCAGCTCCT 210

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Qy    223 atgtgtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggatataatggat 282
Db    331 TTCTGTGCAGAAATTCAGGGCAAGCCTACTTTGCAGCTTAAGGAAAAAAATATCATGGAC 390

Qy    283 ttgtacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcagg 342
Db    391 CTGTATGTGGAGAAGAAAGCACAGAAGCCCTTTCTCTTTTTCCACAATAAAGAAGGCTCC 450

Qy    343 aactccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaagga 402
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Qy    403 ggctgtcctctcatccttacccaagaactggggaaagccaacactactgactttgggtta 462
Db    511 GGACAGCCCATCTTTCTCACCAAGGAGAGAGGCATAACTAATAACACTAACTTCTACTTA 570

Qy    463 actatgctgttttaa 477
Db    571 GATTCTGTGGAATAA 585


RESULT  13
AF201833
LOCUS       AF201833                585 bp    mRNA    linear   PRI 16-JAN-2000
DEFINITION  Homo sapiens FIL1 eta mRNA, complete cds.
ACCESSION   AF201833
VERSION     AF201833.1  GI:6694393
KEYWORDS    .
SOURCE      human.
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 585)
  AUTHORS   Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garka,K.E. and
            Sims,J.E.
  TITLE     Four new members expand the interleukin-1 superfamily
  JOURNAL   J. Biol. Chem. 275 (2), 1169-1175 (2000)
  MEDLINE   20092888
REFERENCE   2  (bases 1 to 585)
  AUTHORS   Sims,J.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-NOV-1999) Molecular Genetics, Immunex Corporation, 51
            University Street, Seattle, WA 98101, USA
FEATURES             Location/Qualifiers
     source          1. .585
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BASE COUNT      161 a    154 c    110 g    160 t
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  Best Local Similarity 56.8%;  Pred. No. 5.6e-30;
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Qy     163 cttgagaaagacagagggaaccccatctacctgggcctgaatggactcaatctctgcctg 222
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Qy     403 ggctgtcctctcatccttacccaagaactggggaaagccaacactactgactttgggtta 462
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Qy     463 actatgctgttttaa 477
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RESULT  14
AX167128
LOCUS       AX167128                1244 bp    DNA     linear   PAT 03-JUL-2001
DEFINITION  Sequence 1 from Patent WO0142305.
ACCESSION   AX167128
VERSION     AX167128.1  GI:14596616
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1244)
  AUTHORS   Welcher,A.A., Luethy,R. and Jing,S.
  TITLE     Interleukin-1 receptor antagonist-like molecules and uses thereof
  JOURNAL   Patent: WO 0142305-A 1 14-JUN-2001;
            Amgen Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN


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  Best Local Similarity 56.8%;  Pred. No. 6.1e-30;
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Qy      43 attcaggatatcaatcatcgggtgtgggttcttcaggaccagacgctcatagcagtcccg 102
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Db     340 ATTCGTGATTCTCGACAGATGGTGTGGGTCCTGAGTGGAAATTCTTTAATAGCAGCTCCT 399

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Db     400 CTTAGCCGCAGCATTAAGCCTGTCACTCTTCATTTAATAGCCTGTAGAGACACAGAATTC 459

Qy     163 cttgagaaagacagagggaaccccatctacctgggcctgaatggactcaatctctgcctg 222
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Qy     343 aactccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaagga 402
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Qy     403 ggctgtcctctcatccttacccaagaactggggaaagccaacactactgactttgggtta 462
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Db     700 GGACAGCCCATCTTTCTCACCAAGGAGAGAGGCATAACTAATAACACTAACTTCTACTTA 759

Qy     463 actatgctgttttaa 477
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Db     760 GATTCTGTGGAATAA 774


RESULT  15
AR137703
LOCUS       AR137703                746 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 1 from patent US 6197551.
ACCESSION   AR137703
VERSION     AR137703.1  GI:14479212
KEYWORDS    .
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 746)
  AUTHORS   Busfield,S.J.
  TITLE     Spoil-1 protein and nucleic acid molecules and uses therefor
  JOURNAL   Patent: US 6197551-A 1 06-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .746
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Best Local Similarity 73.9%; Pred. No. 2e-28;
Matches 164; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

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Db    390 GAAATCTTCATCACTGACTTCGAGATGATTGTGGTACATTAA 431
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: June 21, 2002, 12:02:58 ; Search time 338.08 Seconds
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Title: US-09-763-498-12
Perfect score: 477
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

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23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	477	100.0	477	21	AAZ51248	Polymorphic human
2	475.4	99.7	477	21	AAZ51247	Human Interleukin-
3	462.8	97.0	819	22	AAD06911	Human interleukin-
4	349.8	73.3	391	22	AAF83870	Human interleukin-
5	238.6	50.0	809	19	AAV71960	Rodent interleukin
6	238.6	50.0	838	20	AAX86460	cDNA encoding a mu
7	213	44.7	213	21	AAZ51246	3' exon of human I
8	202	42.3	1073	22	AAD12296	Human interleukin-
9	202	42.3	1183	19	AAV42659	cDNA encoding Inte
10	202	42.3	1183	20	AAX90135	Human interleukin-
11	202	42.3	1183	22	AAS26842	Human cDNA encodin
12	202	42.3	1291	20	AAX86458	cDNA encoding a hu
13	201.6	42.3	673	22	AAS26915	Human cDNA encodin
14	201.6	42.3	673	22	AAD16762	Human novel protei
15	201.4	42.2	1377	20	AAX86459	cDNA encoding a hu
16	161.4	33.8	1321	21	AAA96351	cDNA encoding a no
17	161.4	33.8	1321	21	AAA51595	Human IL-1 recepto
18	134.2	28.1	520	22	AAF83869	Human interleukin-
19	134.2	28.1	585	22	AAC90487	Human IL-1 eta cDN
20	134.2	28.1	1244	22	AAD08531	Human Interleukin-
21	129.2	27.1	746	20	AAX86455	cDNA encoding a mu
22	127	26.6	219	19	AAV71959	Rodent interleukin
23	86.6	18.2	174	21	AAZ51249	Mouse Interleukin-
24	78.8	16.5	1710	20	AAV99953	Nucleotide sequenc
25	74.8	15.7	1877	21	AAA99192	Mouse interleukin-
26	72.6	15.2	654	21	AAD00213	Human zilla4 degen
27	71.8	15.1	531	22	AAF85156	Nucleotide sequenc
28	71.8	15.1	603	22	AAF85157	Nucleotide sequenc
29	71.8	15.1	1577	19	AAV21578	Equine interleukin
30	71.8	15.1	1614	22	AAF85155	Nucleotide sequenc
31	71	14.9	654	21	AAD00214	Human zilla4-E200K
32	70.8	14.8	456	14	AAQ40754	IL-1 inhibitor (IL
33	70.8	14.8	462	18	AAT38808	Recombinant human
34	70.8	14.8	462	19	AAV36455	Recombinant human
35	70.8	14.8	462	22	AAI70513	Human interleukin-
36	70.8	14.8	514	16	AAQ83763	Plasmid 15424. Sy
37	70.8	14.8	514	18	AAT72210	DNA encoding leade
38	70.8	14.8	514	20	AAX82158	Leaderless IL-1 re
39	70.8	14.8	531	17	AAT35255	Human interleukin-
40	70.8	14.8	531	17	AAT35256	Human interleukin-
41	70.8	14.8	531	17	AAT30157	Interleukin-1 rece
42	70.8	14.8	531	17	AAT30158	Interleukin-1 rece
43	70.8	14.8	531	17	AAT30159	Interleukin-1 rece
44	70.8	14.8	532	12	AAQ14693	IRAP gene. Homo s
45	70.8	14.8	540	10	AAN92441	Sequence of bps 61

ALIGNMENTS

RESULT 1
AAZ51248
ID AAZ51248 standard; DNA; 477 BP.
XX
AC AAZ51248;
XX
DT 06-JUN-2000 (first entry)
XX
DE Polymorphic human Interleukin-1 epsilon DNA.
XX
KW Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;
KW gene mapping; immune system; treatment; inflammatory disease;
KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
KW psoriasis; human; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..477
FT /*tag= a
FT /product= "Interleukin-1 epsilon polymorphic variant"
FT /note= "Homologous to mouse IL-1 epsilon protein"
FT variation replace (35, A)
FT /*tag= b
XX
PN WO200011174-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US18771.
XX

PR 21-AUG-1998; 98US-0097413.
PR 31-AUG-1998; 98US-0098595.
PR 11-SEP-1998; 98US-0099974.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Sims JE, Smith DE;
XX
DR WPI; 2000-237653/20.
DR P-PSDB; AAY70218.
XX
PT Nucleotide sequences encoding human interleukin -1 epsilon, useful to
PT treat inflammatory and immune system-related diseases such as
PT rheumatoid arthritis and inflammatory bowel disease -
XX
PS Claim 1a; Fig 1; 76pp; English.
XX
CC The present sequence is the polymorphic human Interleukin-1 (IL-1)
CC epsilon DNA. This gene is mapped to chromosome 2q and is mainly
CC expressed in spleen, lymph node, thymus, tonsil and leucocyte
CC tissues. IL-1 epsilon is a cytokine, with antiinflammatory,
CC immunosuppressant, antirheumatic, antiarthritic and antipsoriatic
CC activity. The DNA sequence can be used in chromosome identification,
CC gene mapping and study of immune system. IL-1 epsilon can be used in the
CC treatment of inflammatory or autoimmune diseases such as rheumatoid
CC arthritis, inflammatory bowel disease and psoriasis.
XX
SQ Sequence 477 BP; 123 A; 123 C; 118 G; 113 T; 0 other;

Query Match 100.0%; Score 477; DB 21; Length 477;
Best Local Similarity 100.0%; Pred. No. 2e-137;
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 cgggtgtgggttcttcaggaccagacgctcatagcagtcccgaggaaggaccgtatgtct 120
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Db     61 cgggtgtgggttcttcaggaccagacgctcatagcagtcccgaggaaggaccgtatgtct 120

Qy    121 ccagtcactattgccttaatctcatgccgacatgtggagacccttgagaaagacagaggg 180
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Qy    181 aaccccatctacctgggcctgaatggactcaatctctgcctgatgtgtgctaaagtcggg 240
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Qy    241 gaccagcccacactgcagctgaaggaaaaggatataatggatttgtacaaccaacccgag 300
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Qy    301 cctgtgaagtcctttctcttctaccacagccagagtggcaggaactccaccttcgagtct 360
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Db    301 cctgtgaagtcctttctcttctaccacagccagagtggcaggaactccaccttcgagtct 360

Qy    361 gtggctttccctggctggttcatcgctgtcagctctgaaggaggctgtcctctcatcctt 420
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Db    361 gtggctttccctggctggttcatcgctgtcagctctgaaggaggctgtcctctcatcctt 420

Qy    421 acccaagaactggggaaagccaacactactgactttgggttaactatgctgttttaa 477
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 acccaagaactggggaaagccaacactactgactttgggttaactatgctgttttaa 477
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RESULT 2
AAZ51247
ID AAZ51247 standard; DNA; 477 BP.
XX
AC AAZ51247;
XX
DT 06-JUN-2000 (first entry)
XX
DE Human Interleukin-1 epsilon DNA.
XX
KW Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;
KW gene mapping; immune system; treatment; inflammatory disease;
KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
KW psoriasis; human; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..477
FT /*tag= a
FT /product= "Interleukin-1 epsilon protein"
FT /note= "Homologous to mouse IL-1 epsilon protein"
XX
PN WO200011174-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US18771.
XX
PR 21-AUG-1998; 98US-0097413.
PR 31-AUG-1998; 98US-0098595.
PR 11-SEP-1998; 98US-0099974.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Sims JE, Smith DE;
XX
DR WPI; 2000-237653/20.
DR P-PSDB; AAY70217.
XX
PT Nucleotide sequences encoding human interleukin -1 epsilon, useful to
PT treat inflammatory and immune system-related diseases such as
PT rheumatoid arthritis and inflammatory bowel disease -
XX
PS Claim 1a; Fig 1; 76pp; English.
XX
CC The present sequence is the human Interleukin-1 (IL-1) epsilon DNA
CC encoding IL-1 epsilon protein. This gene is mapped to chromosome 2q and
CC is mainly expressed in spleen, lymph node, thymus, tonsil and leucocyte
CC tissues. IL-1 epsilon is a cytokine, with antiinflammatory,
CC immunosuppressant, antirheumatic, antiarthritic and antipsoriatic
CC activity. The DNA sequence can be used in chromosome identification,
CC gene mapping and study of immune system. IL-1 epsilon can be used in the
CC treatment of inflammatory or autoimmune diseases such as rheumatoid
CC arthritis, inflammatory bowel disease and psoriasis.
XX
SQ Sequence 477 BP; 124 A; 123 C; 117 G; 113 T; 0 other;

Query Match 99.7%; Score 475.4; DB 21; Length 477;
Best Local Similarity 99.8%; Pred. No. 6.3e-137;
Matches 476; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db    121 ccagtcactattgccttaatctcatgccgacatgtggagacccttgagaaagacagaggg 180

Qy    181 aaccccatctacctgggcctgaatggactcaatctctgcctgatgtgtgctaaagtcggg 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| .
Db    181 aaccccatctacctgggcctgaatggactcaatctctgcctgatgtgtgctaaagtcggg 240
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Db     241 gaccagcccacactgcagctgaaggaaaaggatataatggatttgtacaaccaacccgag 300

Qy     301 cctgtgaagtcctttctcttctaccacagccagagtggcaggaactccaccttcgagtct 360
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Db     301 cctgtgaagtcctttctcttctaccacagccagagtggcaggaactccaccttcgagtct 360

Qy     361 gtggctttccctggctggttcatcgctgtcagctctgaaggaggctgtcctctcatcctt 420
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Db     361 gtggctttccctggctggttcatcgctgtcagctctgaaggaggctgtcctctcatcctt 420

Qy     421 acccaagaactggggaaagccaacactactgactttgggttaactatgctgttttaa 477
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 acccaagaactggggaaagccaacactactgactttgggttaactatgctgttttaa 477
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RESULT 3
AAD06911
ID AAD06911 standard; cDNA; 819 BP.
XX
AC AAD06911;
XX
DT 03-AUG-2001 (first entry)
XX
DE Human interleukin-1 receptor antagonist-like (IL-1ra-L) cDNA.
XX
KW Human; interleukin-1 receptor antagonist-like protein; IL-1ra-L; therapy;
KW rheumatoid arthritis; psoriatic arthritis; inflammatory arthritis; lupus;
KW joint disease; autoimmune disease; multiple sclerosis; diabetes; obesity;
KW transplant rejection; graft versus host disease; strain; sprain; leprosy;
KW cartilage damage; hepatitis; human immunodeficiency virus; HIV; anorexia;
KW clostridium-associated diarrhoea; pulmonary tuberculosis; septic shock;
KW myopathy; Alzheimer's disease; Parkinson's disease; memory disorder;
KW acute respiratory disease syndrome; cystic fibrosis; asthma; psoriasis;
KW eczema; glomerulonephritis; osteoporosis; Paget's disease; lymphoma;
KW hypercalcaemia; haemorrhage; ischaemia; atherosclerosis; leukaemia;
KW infertility; endometriosis; retinal neuropathy; acute pancreatitis;
KW Kawasaki's disease; cancer; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
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FT		/product= "Human interleukin-1 receptor antagonist-like
FT		(IL-1ra-L) protein"
FT		/note= "CDS does not include stop codon"
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XX
PN WO200141792-A1.
XX
PD 14-JUN-2001.
XX
PF 04-DEC-2000; 2000WO-US32891.
XX
PR 10-DEC-1999; 99US-0170105.
PR 28-NOV-2000; 2000US-0724859.
XX
PA (AMGE-) AMGEN INC.
XX
PI Calzone FJ, Luethy R, Boedigheimer MJ, Zhu J, Chung Y, Jing S;
XX
DR WPI; 2001-381495/40.
DR P-PSDB; AAE03417.
XX
PT Novel Interleukin-1 Receptor Antagonist-Like nucleic acid molecule, the
PT polypeptide encoded by the nucleic acid is useful diagnosis, treatment,
PT and prevention of diseases such as arthritis, diabetes, transplant
PT rejection -
XX
PS Claim 1; Fig 1A; 127pp; English.
XX
CC The present sequence is human interleukin-1 receptor antagonist-like
CC (IL-1ra-L) cDNA. IL-1ra-L is useful for treating, preventing or
CC ameliorating IL-1ra-L polypeptide-related disease, condition or disorder
CC which include rheumatoid arthritis, psoriatic arthritis, inflammatory
CC arthritis, osteoarthritis, autoimmune disease, multiple sclerosis,
CC lupus, diabetes, transplant rejection, inflammatory joint disease, graft
CC versus host disease and inflammatory conditions resulting from strain,
CC sprain, cartilage damage, trauma, orthopaedic surgery, hepatitis, human
CC immunodeficiency virus (HIV) infection, clostridium-associated
CC diarrhoea, leprosy, pulmonary tuberculosis, septic shock, obesity,
CC anorexia, myopathies, Alzheimer's disease, Parkinson's disease, memory
CC disorders, acute respiratory disease syndrome, cystic fibrosis, asthma,
CC psoriasis, eczema, acute and chronic glomerulonephritis, osteoporosis,
CC Paget's disease, hypercalcaemia, haemorrhage, ischaemia, atherosclerosis,
CC lymphomas, lung and breast cancer, leukaemias, infertility,
CC endometriosis, retinal degeneration, retinal neuropathy, acute
CC pancreatitis and Kawasaki's disease.
XX
SQ Sequence 819 BP; 202 A; 196 C; 204 G; 217 T; 0 other;

Query Match 97.0%; Score 462.8; DB 22; Length 819;
Best Local Similarity 99.6%; Pred. No. 6.4e-133;
Matches 464; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      69 ggttcttcaggaccagacgctcatagcagtcccgaggaaggaccgtatgtctccagtcac 128
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Db     414 ggttcttcaggaccagacgctcatagcagtcccgaggaaggaccgtatgtctccagtcac 473

Qy     129 tattgccttaatctcatgccgacatgtggagacccttgagaaagacagagggaaccccat 188
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db     474 tattgccttaatctcatgccgacatgtggagacccttgagaaagacagaggggaccccat 533

Qy     189 ctacctgggcctgaatggactcaatctctgcctgatgtgtgctaaagtcggggaccagcc 248
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Qy     249 cacactgcagctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaa 308
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Db     594 cacactgcagctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaa 653

Qy     309 gtcctttctcttctaccacagccagagtggcaggaactccaccttcgagtctgtggcttt 368
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Db     654 gtcctttctcttctaccacagccagagtggcaggaactccaccttcgagtctgtggcttt 713

Qy     369 ccctggctggttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaaga 428
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Qy     429 actggggaaagccaacactactgactttgggttaactatgctgttt 474
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Db     774 actggggaaagccaacactactgactttgggttaactatgctgttt 819
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RESULT 4
AAF83870
ID AAF83870 standard; cDNA; 391 BP.
XX
AC AAF83870;
XX
DT 06-AUG-2001 (first entry)
XX
DE Human interleukin-1 receptor antagonist (NOVINTRA C) encoding cDNA.
XX
KW NOVX; transmembrane protein; NOVTRAN; neuromedin peptide; NOVNEUR;
KW gonadotropin-like protein; NOVGON; interleukin-1; NOVINTRA; human;
KW cytostatic; neuroprotective; reproductive; antiinflammatory; cancer;
KW antibacterial; cerebroprotective; antidiabetic; antiarthritic;

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KW   antiasthmatic; antiallergic; ss.
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OS   Homo sapiens.
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FT                   /product= "NOVINTRA C"
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PN   WO200140291-A2.
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PD   07-JUN-2001.
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PF   06-DEC-2000; 2000WO-US33029.
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PR   06-DEC-1999;   99US-0169056.
PR   09-DEC-1999;   99US-0169866.
PR   09-DEC-1999;   99US-0169886.
PR   10-DEC-1999;   99US-0170252.
PR   12-JAN-2000; 2000US-0175740.
PR   05-DEC-2000; 2000US-0170252.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Burgess CE,  Prayaga SK,  Shimkets RA,  Rastelli L,  Zerhusen BD;
PI   Mezes PS;
XX
DR   WPI; 2001-374790/39.
DR   P-PSDB; AAB85001.
XX
PT   Novel isolated human transmembrane, neuromedin peptide
PT   gonadotropin-like protein and interleukin-1 receptor antagonist
PT   proteins, useful for treating cancer, immune response disorder,
PT   metabolic function disorders  -
XX
PS   Claim 50; Fig 15A; 138pp; English.
XX
CC   The invention provides novel polypeptides (NOVX) selected from human
CC   transmembrane protein (NOVTRAN), neuromedin peptide (NOVNEUR),
CC   gonadotropin-like protein (NOVGON) and two interleukin-1 receptor
CC   antagonist proteins (NOVINTRA A and B). The invention also provides
CC   methods in which a NOVX polypeptide, polynucleotide and antibody are
CC   used in the detection, prevention and treatment of a broad range of
CC   pathological states. NOVTRAN can be used to treat is a cell signaling
CC   disorder such as cancer, immune response disorder, hematopoietic
CC   disorder, neurodegenerative disorder. NOVNEUR can be used to treat
CC   endocrine disorder, muscle disorder, neurologic disorder, cancers of
CC   central nervous system, breast, colon, ovary, kidney, prostate and
CC   thyroid. NOVGON can be used to treat reproductive development disorder,
CC   metabolic function disorder and melanoma. NOVINTRA A and B can be used
CC   to treat bone metabolism or structure disorder, inflammatory response
CC   disorder, immune regulation disorder, septic shock, stroke, diabetes,
CC   arthritis and cancer. The present sequence represents a cDNA encoding
CC   the NOVINTRA C polypeptide.
XX
SQ   Sequence 391 BP; 94 A; 106 C; 99 G; 92 T; 0 other;


  Query Match             73.3%;  Score 349.8;  DB 22;  Length 391;
  Best Local Similarity   96.5%;  Pred. No. 4e-98;
  Matches  383;  Conservative    0;  Mismatches    2;  Indels   12;  Gaps    2;

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Qy     109 gaccgtatgtctccagtcactattgccttaatctcatgccgacatgtggagacccttgag 168
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Qy     169 aaagacagagggaaccccatctacctgggcctgaatggactcaatctctgcctgatgtgt 228
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Qy     229 gctaaagtcggggaccagcccacactgcagctga------aggaaaaggatataatggat 282
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Qy     283 ttgtacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcagg 342
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Qy     343 aactccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaagga 402
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Qy     403 ggctgtcctctcatccttacccaagaactggggaaag 439
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RESULT   5
AAV71960
ID   AAV71960 standard; cDNA; 809 BP.
XX
AC   AAV71960;
XX
DT   19-FEB-1999  (first entry)
XX
DE   Rodent interleukin (IL)-1 epsilon polypeptide encoding cDNA.
XX
KW   Interleukin; IL-1 delta; polyclonal antibody; IL-1 epsilon; cytokine;
KW   inflammatory response; immune system; diagnosis; agonist; antagonist;
KW   chemokine; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
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FT                   /product= "IL-1 epsilon polypeptide"
XX
PN   WO9847921-A1.
XX
PD   29-OCT-1998.
XX
PF   17-APR-1998;   98WO-US06879.
XX
PR   06-AUG-1997;   97US-0055111.
PR   21-APR-1997;   97US-0837627.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Bazan JF,  Hedrick JA,  Kastelein RA,  Sana TR;
XX
DR   WPI; 1998-609976/51.
DR   P-PSDB; AAW86286.
XX
PT   Mammalian interleukin 1-delta and 1-epsilon - useful for, e.g.
PT   regulating the immune system and inflammatory responses
XX
PS   Claim 14; Pages 92-93; 113pp; English.
XX
CC   This cDNA encodes a rodent interleukin (IL)-1 epsilon polypeptide. The
CC   invention relates to a recombinant polypeptide that specifically binds
CC   polyclonal antibodies (Abs) generated against a 12 consecutive amino acid
CC   segment of IL-1 delta or IL-1 epsilon. Agonists or antagonists of these
CC   IL polypeptides are used to regulate a cell involved in an inflammatory
CC   response. The IL-1 delta or IL-1 epsilon polypeptides and peptides are
CC   used to produce Abs and antigen-Ab complexes. The polypeptides, Abs and
CC   the corresponding nucleic acids regulate development and/or the immune
CC   system, and can be used to diagnose and treat conditions associated with
CC   abnormal expression of IL. Agonists or antagonists of IL-1 delta or IL-1
CC   epsilon polypeptides are used with agonists or antagonists of IL-1 alpha,
CC   IL-1RA, IL-1 beta, IL-1 gamma, IL-2 and/or IL-12. The IL-1 delta or IL-1
CC   epsilon polypeptides may be used as a soluble polypeptide or as a fusion
```

CC protein with another cytokine or chemokine.
XX
SQ Sequence 809 BP; 241 A; 180 C; 179 G; 209 T; 0 other;

Query Match 50.0%; Score 238.6; DB 19; Length 809;
Best Local Similarity 68.8%; Pred. No. 1.3e-63;
Matches 328; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

```
Qy      1 atggaaaaagcattgaaaattgacacacctcagcgggggagcattcaggatatcaatcat 60
          | ||| |||| | | | |   |   |||||  ||   |     |||||||| | | |  |
Db     96 aaggagaaagaactaagagcagcatcaccttcgcttagacatgttcaggatcttagtagt 155

Qy     61 cgggtgtgggttcttcaggaccagacgctcatagcagtcccgaggaaggaccgtatgtct 120
          || |||||| | || ||| || | |  |||| |||||||| ||||| || |  |    |
Db    156 cgtgtgtggatcctgcagaacaatatcctcactgcagtcccaaggaaagagcaaacagtt 215

Qy    121 ccagtcactattgccttaatctcatgccgacatgtggagacccttgagaaagacagaggg 180
          |||||||||||| |||| || |||||| | || |||| || |||||||   |||| |||
Db    216 ccagtcactattaccttgctcccatgccaatatctggacactcttgagacgaacaggggg 275

Qy    181 aaccccatctacctgggcctgaatggactcaatctctgcctgatgtgtgctaaagtcggg 240
          | ||||  ||| ||||  || |  | |  |    ||||||| | ||  | || |  |||
Db    276 gatcccacgtacatgggagtgcaaaggccgatgagctgcctgttctgcacaaaggatggg 335

Qy    241 gaccagcccacactgcagctgaaggaaaaggatataatggatttgtacaaccaacccgag 300
          || |||||    || |||||   ||||  | | ||||||||  ||||||||  ||   ||
Db    336 gagcagcctgtgctacagcttggggaagggaacataatggaaatgtacaacaaaaaggaa 395

Qy    301 cctgtgaagtcctttctcttctaccacagccagagtggcaggaactccaccttcgagtct 360
          ||||| ||  ||| |||||||||| ||||   ||||||| |  | ||| || || ||||||
Db    396 cctgtaaaagcctctctcttctatcacaagaagagtggtacaacctctacatttgagtct 455

Qy    361 gtggctttccctggctggttcatcgctgtcagctctgaaggaggctgtcctctcatcctt 420
          |  || |||||||| |||||||||||||||| ||||| ||||  |||| || ||||| ||
Db    456 gcagccttccctggttggttcatcgctgtctgctctaaagggagctgcccactcattctg 515

Qy    421 acccaagaactgggggaaagccaacactactgactttgggttaactatgctgttttaa 477
          |||||||||||||||| ||  |  ||  |||||||| | | | | | || |   ||||
Db    516 acccaagaactgggggaaatcttcatcactgacttcgagatgattgtggtacattaa 572
```

RESULT 6
AAX86460
ID AAX86460 standard; cDNA; 838 BP.
XX
AC AAX86460;
XX
DT 30-SEP-1999 (first entry)
XX
DE cDNA encoding a murine SPOIL-II protein.
XX
KW SPOIL-II; interleukin-1 receptor antagonist; IL-1ra; modulating agent;
KW bone metabolism disorder; proinflammatory disorder; immune disorder;
KW inflammatory disease; septic shock; stroke; diabetes; arthritis;
KW intercolitis; pneumonitis; epithelial cell; skin disease;
KW proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;
KW epithelial cancer; squamous cell carcinoma; bone resorption disorder;
KW osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;
KW osteogenesis imperfecta; fibrous displasia; hypophosphatasia;
KW bone sarcoma; myeloma bone disorder; osteolytic bone lesion;
KW hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;
KW bone fracture; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 96..578
FT /*tag= a
FT /product= SPOIL-II
XX
PN WO9937662-A1.
XX

PD 29-JUL-1999.
XX
PF 26-JAN-1999; 99WO-US01575.
XX
PR 27-JAN-1998; 98US-0013810.
XX
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI Busfield SJ;
XX
DR WPI; 1999-458675/38.
DR P-PSDB; AAY24049.
XX
PT New isolated SPOIL proteins, used to develop products for treating,
PT e.g. inflammatory and immune disorders
XX
PS Claim 1; Fig 6; 126pp; English.
XX
CC The present sequence encodes a SPOIL-II protein. The SPOIL proteins have
CC homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.
CC The SPOIL proteins are used as modulating agents in regulating a variety
CC of cellular processes. The products can be used for treating disorders
CC characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone
CC metabolism disorder, a proinflammatory disorder or an immune disorder.
CC They can be used for treating e.g. inflammatory diseases and disorders
CC e.g. inflammation, septic shock, stroke, diabetes, arthritis,
CC intercolitis and pneumonitis, epithelial cell and/or skin diseases and
CC disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma
CC and Kaposi's sarcoma and other epithelial cancers including squamous cell
CC carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and
CC bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's
CC disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,
CC fibrous displasia, hypophosphatasia, bone sarcoma, myeloma bone disorder
CC (e.g. osteolytic bone lesions) and hypercalcemia. SPOIL molecules and
CC SPOIL modulators are useful for regulation of bone mass (e.g. increase in
CC bone mass and/or inhibit bone loss), management of bone fragility (e.g.
CC decrease bone fragility); and prevention and/or treatment of bone pain,
CC bone deformities and/or bone fractures. The products can also be used for
CC detection, diagnosis and screening assays.
XX
SQ Sequence 838 BP; 256 A; 188 C; 184 G; 210 T; 0 other;

Query Match 50.0%; Score 238.6; DB 20; Length 838;
Best Local Similarity 68.8%; Pred. No. 1.4e-63;
Matches 328; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

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Qy      1 atggaaaaagcattgaaaattgacacacctcagcgggggagcattcaggatatcaatcat 60
          | ||| |||| | | | |   |   |||||  ||   |     |||||||| | | |  |
Db    102 aaggagaaagaactaagagcagcatcaccttcgcttagacatgttcaggatcttagtagt 161

Qy     61 cgggtgtgggttcttcaggaccagacgctcatagcagtcccgaggaaggaccgtatgtct 120
          || |||||| | || ||| || | |  |||| |||||||| ||||| || |  |    |
Db    162 cgtgtgtggatcctgcagaacaatatcctcactgcagtcccaaggaaagagcaaacagtt 221

Qy    121 ccagtcactattgccttaatctcatgccgacatgtggagacccttgagaaagacagaggg 180
          |||||||||||| |||| || |||||| | || |||| || |||||||   |||| |||
Db    222 ccagtcactattaccttgctcccatgccaatatctggacactcttgagacgaacaggggg 281

Qy    181 aaccccatctacctgggcctgaatggactcaatctctgcctgatgtgtgctaaagtcggg 240
          | ||||  ||| ||||  || |  | |  |    ||||||| | ||  | || |  |||
Db    282 gatcccacgtacatgggagtgcaaaggccgatgagctgcctgttctgcacaaaggatggg 341

Qy    241 gaccagcccacactgcagctgaaggaaaaggatataatggatttgtacaaccaacccgag 300
          || |||||    || |||||   ||||  | | ||||||||  ||||||||  ||   ||
Db    342 gagcagcctgtgctacagcttggggaagggaacataatggaaatgtacaacaaaaaggaa 401

Qy    301 cctgtgaagtcctttctcttctaccacagccagagtggcaggaactccaccttcgagtct 360
          ||||| ||  ||| |||||||||| ||||   ||||||| |  | ||| || || ||||||
Db    402 cctgtaaaagcctctctcttctatcacaagaagagtggtacaacctctacatttgagtct 461

Qy    361 gtggctttccctggctggttcatcgctgtcagctctgaaggaggctgtcctctcatcctt 420
          |  || |||||||| |||||||||||||||| ||||| ||||  |||| || ||||| ||
Db    462 gcagccttccctggttggttcatcgctgtctgctctaaagggagctgcccactcattctg 521
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Db    462 gcagccttccctggttggttcatcgctgtctgctctaaagggagctgcccactcattctg 521

Qy    421 acccaagaactggggaaagccaacactactgactttgggttaactatgctgttttaa 477
          ||||||||||||||| ||  |  ||  |||||||| | | | | | || |   ||||
Db    522 acccaagaactgggggaaatcttcatcactgacttcgagatgattgtggtacattaa 578


RESULT   7
AAZ51246
ID   AAZ51246 standard; DNA; 213 BP.
XX
AC   AAZ51246;
XX
DT   06-JUN-2000  (first entry)
XX
DE   3' exon of human Interleukin-1 epsilon DNA.
XX
KW   Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
KW   immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;
KW   gene mapping; immune system; treatment; inflammatory disease;
KW   autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
KW   psoriasis; human; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..213
FT                   /*tag=  a
FT                   /partial
FT                   /product= "Partial human IL-1 epsilon protein"
FT                   /note= "Homologous to mouse IL-1 epsilon protein"
XX
PN   WO200011174-A1.
XX
PD   02-MAR-2000.
XX
PF   20-AUG-1999;   99WO-US18771.
XX
PR   21-AUG-1998;   98US-0097413.
PR   31-AUG-1998;   98US-0098595.
PR   11-SEP-1998;   98US-0099974.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Sims JE,  Smith DE;
XX
DR   WPI; 2000-237653/20.
DR   P-PSDB; AAY70216.
XX
PT   Nucleotide sequences encoding human interleukin -1 epsilon, useful to
PT   treat inflammatory and immune system-related diseases such as
PT   rheumatoid arthritis and inflammatory bowel disease -
XX
PS   Claim 1a; Fig 1; 76pp; English.
XX
CC   The present sequence is the 3' exon of human Interleukin-1 (IL-1)
CC   epsilon DNA. IL-1 epsilon gene is mapped to chromosome 2q and is mainly
CC   expressed in spleen, lymph node, thymus, tonsil and leucocyte tissues.
CC   IL-1 epsilon is a cytokine, with antiinflammatory, immunosuppressant,
CC   antirheumatic, antiarthritic and antipsoriatic activity. The DNA
CC   sequence can be used in chromosome identification, gene mapping and
CC   study of immune system. IL-1 epsilon can be used in the treatment of
CC   inflammatory or autoimmune diseases such as rheumatoid arthritis,
CC   inflammatory bowel disease and psoriasis.
XX
SQ   Sequence 213 BP; 51 A; 56 C; 48 G; 58 T; 0 other;


  Query Match             44.7%;  Score 213;  DB 21;  Length 213;
  Best Local Similarity   100.0%;  Pred. No. 6e-56;
  Matches  213;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    265 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 324
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 60

Qy    325 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 384
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 120

Qy    385 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 444
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 180

Qy    445 actactgactttgggttaactatgctgttttaa 477
          |||||||||||||||||||||||||||||||||
Db    181 actactgactttgggttaactatgctgttttaa 213


RESULT   8
AAD12296
ID   AAD12296 standard; DNA; 1073 BP.
XX
AC   AAD12296;
XX
DT   16-OCT-2001  (first entry)
XX
DE   Human interleukin-1epsilon (IL-1epsilon) protein DNA.
XX
KW   Human; interleukin-1epsilon; IL-1epsilon; virucide; hepatotropic; fever;
KW   immunological disorder; tumour; inflammatory disorder; hypoglycaemia;
KW   autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;
KW   psoriasis; viral infection; allergy; cytokine; HIV; drug screening; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             67..576
FT                   /*tag=  a
FT                   /product= "Human interleukin-1epsilon (IL-1epsilon)
FT                   protein"
XX
PN   WO200157219-A2.
XX
PD   09-AUG-2001.
XX
PF   01-FEB-2001; 2001WO-US03285.
XX
PR   02-FEB-2000; 2000US-0179638.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Debets JEMA,  Timans JC,  Bazan JF,  Kastelein RA;
XX
DR   WPI; 2001-488886/53.
DR   P-PSDB; AAE06656.
XX
PT   Novel isolated or recombinant antigenic interleukin-1 delta or epsilon
PT   polypeptide useful for treating conditions exhibiting abnormal
PT   expression of interleukin such as immunological disorders, tumor and
PT   allergy  -
XX
PS   Claim 18; Page 86-87; 103pp; English.
XX
CC   The invention relates to recombinant antigenic interleukin-1 like
CC   molecules and their corresponding nucleic acid sequences, designated
CC   as interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon).
CC   IL-1delta and IL-1epsilon are useful for treating conditions exhibiting
CC   abnormal expression of the interleukin such as immunological disorders,
CC   tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis,
CC   allergy, autoimmune diseases and infectious diseases (e.g., pulmonary
CC   tuberculosis, leprosy, fulminant hepatitis, and viral infections such as
CC   HIV). The invention also relates to methods of using the composition
CC   containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic
CC   utilities. IL-1delta is used as an immunogen for the production of
CC   antisera or antibodies specific, e.g., capable of distinguishing between
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CC   IL-1 family members and an IL-1delta, for the interleukin or its
CC   fragment. The purified interleukin is used as a reagent to detect any
CC   antibodies generated in response to the presence of elevated levels of
CC   expression, or immunological disorders which lead to antibody production
CC   to the endogenous cytokine. The invention also contemplates the use of
CC   competitive drug screening assays. The present DNA sequence encodes human
CC   interleukin-1epsilon (IL-1epsilon) protein.
XX
SQ   Sequence 1073 BP; 281 A; 241 C; 255 G; 296 T; 0 other;


  Query Match             42.3%;  Score 202;  DB 22;  Length 1073;
  Best Local Similarity   67.1%;  Pred. No. 3.1e-52;
  Matches  302;  Conservative    0;  Mismatches  145;  Indels    3;  Gaps    1;

Qy      18 aattgacacacctcagcgggggagcattcaggatatcaatcatcgggtgtgggttcttca 77
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Db     120 aatgtgtaaacctattactgggactattaatgatttgaatcagcaagtgtggacccttca 179

Qy      78 ggaccagacgctcatagcagtcccgaggaaggaccgtatgtctccagtcactattgcctt 137
           ||  ||||  ||  | ||||| ||  | |  ||| || || | ||||||||| ||||  |
Db     180 gggtcagaaccttgtggcagttccacgaagtgacagtgtgaccccagtcactgttgctgt 239

Qy     138 aatctcatgccgacatgtggagacccttgagaaagacagagggaaccccatctacctggg 197
            ||| |||||    ||   ||| | |||||| ||| ||||||| | |||||  ||  ||||
Db     240 tatcacatgcaagtatccagaggctcttgagcaaggcagaggggatcccatttatttggg 299

Qy     198 cctgaatggactcaatctctgcctgatgtgtgctaaagtcggggaccagcccacactgca 257
             |  |   |  | | ||  ||   ||||  || || || || |||||||| ||||
Db     300 aatccagaatccagaaatgtgtttgtattgtgagaaggttggagaacagcccacattgca 359

Qy     258 gctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttct 317
           ||| || ||  || | || |||||| ||||   |||||||||| |||||  |||| ||
Db     360 gctaaaagagcagaagatcatggatctgtatggccaacccgagcccgtgaaacccttcct 419

Qy     318 cttctaccacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctg 377
           |||||||    | ||| ||| |||| ||||||| | |||||||||| ||||| | |||
Db     420 tttctaccgtgccaagactggtaggacctccacccttgagtctgtggccttcccggactg 479

Qy     378 gttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaa 437
           ||||||   || |  |||  |  ||| |   ||  |||| || ||   |||||| |||||
Db     480 gttcat---tgcctcctccaagagagaccagcccatcattctgacttcagaacttgggaa 536

Qy     438 agccaacactactgactttgggttaactat 467
             |  |||  |||| |||||  |||| |||
Db     537 gtcatacaacactgcctttgaattaaatat 566


RESULT   9
AAV42659
ID   AAV42659 standard; cDNA; 1183 BP.
XX
AC   AAV42659;
XX
DT   14-OCT-1998  (first entry)
XX
DE   cDNA encoding Interleukin-1 receptor antagonist beta (IL-1ra-beta).
XX
KW   Interleukin-1 receptor antagonist beta; IL-1ra-beta; IL-1 alpha;
KW   IL-1 beta; inflammatory response; treatment; inflammation; septicaemia;
KW   cancer; anaemia; arthritis; inflammatory bowel disease;
KW   graft vs. host rejection; autoimmunity; stroke; cardiac ischaemia;
KW   acute respiratory disease syndrome; psoriasis; restenosis;
KW   traumatic brain injury; acquired immune deficiency syndrome;
KW   cachexia; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             75..584
FT                   /*tag=  a
FT                   /product= IL-1ra-beta
XX
PN   EP855404-A1.
XX
PD   29-JUL-1998.
XX
PF   27-JAN-1998;   98EP-0300572.
XX
PR   28-JAN-1997;   97US-0790032.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Young PR;
XX
DR   WPI; 1998-389778/34.
DR   P-PSDB; AAW63136.
XX
PT   New nucleic acid encoding human interleukin-1 receptor antagonist
PT   beta polypeptides - and related expression systems, transformed
PT   cells, proteins, antibodies, agonists and antagonists, useful for
PT   treatment, prevention and diagnosis of inflammation, septicaemia,
PT   cancer etc
XX
PS   Claim 3; Fig 1; 20pp; English.
XX
CC   The present sequence encodes human Interleukin-1 receptor antagonist
CC   beta (IL-ra-beta). IL-1 alpha and IL-1 beta play key roles in
CC   inflammatory responses, and are produced as zymogens which are cleaved
CC   upon secretion to yield mature carboxyl terminal 17 kD fragments.
CC   IL-1ra-beta polypeptides and polynucleotides are useful in treatment of
CC   chronic and acute inflammation, septicaemia, cancer, anaemia, arthritis,
CC   inflammatory bowel disease, graft vs. host rejection, autoimmunity,
CC   stroke, cardiac ischaemia, acute respiratory disease syndrome (ARDS),
CC   psoriasis, restenosis, traumatic brain injury, acquired immune
CC   deficiency syndrome (AIDS) and cachexia. These conditions (or
CC   susceptibility to them) may be diagnosed by detecting mutations in the
CC   IL-1ra-beta coding sequence analysing a sample for presence or amount
CC   of IL-1ra-beta.
XX
SQ   Sequence 1183 BP; 329 A; 249 C; 269 G; 336 T; 0 other;


  Query Match             42.3%;  Score 202;  DB 19;  Length 1183;
  Best Local Similarity   67.1%;  Pred. No. 3.3e-52;
  Matches  302;  Conservative    0;  Mismatches  145;  Indels    3;  Gaps    1;

Qy      18 aattgacacacctcagcgggggagcattcaggatatcaatcatcgggtgtgggttcttca 77
           |||    | ||||      ||||  ||| | ||| | ||||| |  ||||||   |||||
Db     128 aatgtgtaaacctattactgggactattaatgatttgaatcagcaagtgtggacccttca 187

Qy      78 ggaccagacgctcatagcagtcccgaggaaggaccgtatgtctccagtcactattgcctt 137
           ||  ||||  ||  | ||||| ||  | |  ||| || || | ||||||||| ||||  |
Db     188 gggtcagaaccttgtggcagttccacgaagtgacagtgtgaccccagtcactgttgctgt 247

Qy     138 aatctcatgccgacatgtggagacccttgagaaagacagagggaaccccatctacctggg 197
            ||| |||||    ||   ||| | |||||| ||| ||||||| | |||||  ||  ||||
Db     248 tatcacatgcaagtatccagaggctcttgagcaaggcagaggggatcccatttatttggg 307

Qy     198 cctgaatggactcaatctctgcctgatgtgtgctaaagtcggggaccagcccacactgca 257
             |  |   |  | | ||  ||   ||||  || || || || |||||||| ||||
Db     308 aatccagaatccagaaatgtgtttgtattgtgagaaggttggagaacagcccacattgca 367

Qy     258 gctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttct 317
           ||| || ||  || | || |||||| ||||   |||||||||| |||||  |||| ||
Db     368 gctaaaagagcagaagatcatggatctgtatggccaacccgagcccgtgaaacccttcct 427

Qy     318 cttctaccacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctg 377
           |||||||    | ||| ||| |||| ||||||| | |||||||||| ||||| | |||
Db     428 tttctaccgtgccaagactggtaggacctccacccttgagtctgtggccttcccggactg 487

Qy     378 gttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaa 437
           ||||||   || |  |||  |  ||| |   ||  |||| || ||   |||||| |||||
Db     488 gttcat---tgcctcctccaagagagaccagcccatcattctgacttcagaacttgggaa 544

Qy     438 agccaacactactgactttgggttaactat 467
```

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           |  |||  |||| |||||  |||| |||
Db    545 gtcatacaacactgcctttgaattaaatat 574


RESULT  10
AAX90135
ID   AAX90135 standard; cDNA; 1183 BP.
XX
AC   AAX90135;
XX
DT   20-SEP-1999  (first entry)
XX
DE   Human interleukin-1 receptor antagonist beta encoding cDNA.
XX
KW   Human; interleukin-1 receptor antagonist beta; IL-1RA beta; septicemia;
KW   chronic inflammation; acute inflammation; arthritis; autoimmunity;
KW   inflammatory bowel disease; graft vs. host disease; stroke; psoriasis;
KW   cardiac ischaemia; acute respiratory disease syndrome; ARDS; restenosis;
KW   traumatic brain injury; AIDS; cachexia; allergy; parasite infection;
KW   allergic rhinitis; allergic asthma; atopic dermatitis; gene therapy;
KW   allergic inflammatory disease; delayed hypersensitivity; vaccine; ss.
XX
OS   Homo sapiens.
XX
PN   WO9936541-A1.
XX
PD   22-JUL-1999.
XX
PF   14-JAN-1999;   99WO-US00847.
XX
PR   29-APR-1998;   98US-0069619.
PR   14-JAN-1998;   98US-0007464.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Marshall L,  Young PR;
XX
DR   WPI; 1999-430615/36.
DR   P-PSDB; AAY24395.
XX
PT   New interleukin-1 receptor antagonist beta, useful for treating
PT   inflammation and autoimmune diseases
XX
PS   Claim 5; Fig 1; 34pp; English.
XX
CC   The present sequence encodes human interleukin-1 receptor antagonist
CC   beta (IL-1RA beta). IL-1RA beta polypeptides and polynucleotides are
CC   useful for diagnosing diseases (or susceptibility to diseases) related
CC   to the expression or activity of IL-1RA beta, by determining mutations
CC   in the IL-1RA beta nucleic acid sequences and/or analysing for the
CC   presence or amount of IL-1RA beta polypeptide. IL-1RA beta polypeptides
CC   are also useful for screening for compounds which affect activity of the
CC   protein. These can be used in treatment to inhibit (antagonist) or
CC   enhance (agonist) IL-1RA beta activity, in addition to direct
CC   administration of IL-1RA beta polypeptides to treat conditions, or
CC   direct administration of antisense sequences to prevent expression.
CC   IL-1RA beta polypeptides (administered directly, in a vector i.e. gene
CC   therapy, and as a vaccine) and antibodies induce an immune response to
CC   immunise and prevent disease. Diseases diagnosed, prevented or treated
CC   include chronic and acute inflammation, septicemia, arthritis,
CC   inflammatory bowel disease, graft vs. host disease, autoimmunity,
CC   stroke, cardiac ischaemia, acute respiratory disease syndrome (ARDS),
CC   psoriasis, restenosis, traumatic brain injury, AIDS, cachexia, allergy,
CC   parasite infection, allergic rhinitis, allergic asthma, atopic
CC   dermatitis, allergic inflammatory diseases and delayed hypersensitivity.
XX
SQ   Sequence 1183 BP; 329 A; 249 C; 269 G; 336 T; 0 other;

  Query Match           42.3%;  Score 202;  DB 20;  Length 1183;
  Best Local Similarity 67.1%;  Pred. No. 3.3e-52;
  Matches  302;  Conservative    0;  Mismatches  145;  Indels    3;  Gaps    1;

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Db     128 aatgtgtaaacctattactgggactattaatgatttgaatcagcaagtgtggacccttca 187

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Db     188 gggtcagaaccttgtggcagttccacgaagtgacagtgtgaccccagtcactgttgctgt 247

Qy     138 aatctcatgccgacatgtggagacccttgagaaagacagagggaaccccatctacctggg 197
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Qy     198 cctgaatggactcaatctctgcctgatgtgtgctaaagtcggggaccagcccacactgca 257
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Db     308 aatccagaatccagaaatgtgtttgtattgtgagaaggttggagaacagcccacattgca 367

Qy     258 gctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttct 317
           ||| || ||  || | || |||||| ||||   ||||||||||| |||||  |||| ||
Db     368 gctaaaagagcagaagatcatggatctgtatggccaacccgagcccgtgaaaccttcct 427

Qy     318 cttctaccacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctg 377
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Db     428 tttctaccgtgccaagactggtaggacctccaccttgagtctgtggccttcccggactg 487

Qy     378 gttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaa 437
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Db     488 gttcat---tgcctcctccaagagagaccagcccatcattctgacttcagaacttgggaa 544

Qy     438 agccaacactactgactttgggttaactat 467
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Db     545 gtcatacaacactgcctttgaattaaatat 574


RESULT  11
AAS26842
ID   AAS26842 standard; cDNA; 1183 BP.
XX
AC   AAS26842;
XX
DT   07-NOV-2001  (first entry)
XX
DE   Human cDNA encoding a novel secreted protein, SEQ ID 34.
XX
KW   Human; immunosuppressive; antiarthritic; ss; antirheumatic;
KW   cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;
KW   neuroprotective; antibacterial; virucide; fungicide; opthalmalogical;
KW   vulnerary; secreted protein; rheumatoid arthritis;
KW   hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
KW   cerebrovascular disorder; cerebral ischaemia; angiogenesis;
KW   nervous system disorder; Alzheimer's disease; infection; ocular disorder;
KW   corneal infection; wound healing; epithelial cell proliferation;
KW   skin ageing; food additive; preservative; antiproliferative.
XX
OS   Homo sapiens.
XX
PN   WO200155441-A2.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US01320.
XX
PR   31-JAN-2000; 2000US-0179065.
PR   04-FEB-2000; 2000US-0180628.
PR   24-FEB-2000; 2000US-0184664.
PR   02-MAR-2000; 2000US-0186350.
PR   16-MAR-2000; 2000US-0189874.
PR   17-MAR-2000; 2000US-0190076.
PR   18-APR-2000; 2000US-0198123.
PR   19-MAY-2000; 2000US-0205515.
PR   07-JUN-2000; 2000US-0209467.
PR   28-JUN-2000; 2000US-0214886.
PR   30-JUN-2000; 2000US-0215135.
PR   07-JUL-2000; 2000US-0216647.
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PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
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PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
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PR 20-OCT-2000; 2000US-0240960.
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PR 20-OCT-2000; 2000US-0241785.
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PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
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PR 08-NOV-2000; 2000US-0246610.
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PR 17-NOV-2000; 2000US-0249207.
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PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-476222/51.
DR P-PSDB; AAU16937.
XX
PT Novel polypeptides and polynucleotides useful as diagnostic reagents to
PT diagnose diseases or disorders associated with aberrant expression or
PT activity of polypeptides, for treating blood clotting disorder,
PT haemophilia -
XX
PS Claim 1; SEQ ID No 34; 601pp; English.
XX
CC The invention relates to isolated nucleic acid molecules and their
CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They
CC are also used in diagnosing a pathological condition or susceptibility
CC to a pathological condition. Antibodies to the proteins can also
CC be used in alleviating symptoms associated with the disorders and in

CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked
CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated
CC include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi
CC and ocular disorders e.g. corneal infection, and many other
CC disorders listed in the specification. The polypeptides can also
CC be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present

Query Match 42.3%; Score 202; DB 22; Length 1183;
Best Local Similarity 67.1%; Pred. No. 3.3e-52;
Matches 302; Conservative 0; Mismatches 145; Indels 3; Gaps 1;

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Db     128 aatgtgtaaacctattactgggactattaatgatttgaatcagcaagtgtggacccttca 187

Qy      78 ggaccagacgctcatagcagtcccgaggaaggaccgtatgtctccagtcactattgcctt 137
           ||  ||||  ||  | ||||| ||  | |  ||| || || | |||||||| ||||  |
Db     188 gggtcagaaccttgtggcagttccacgaagtgacagtgtgaccccagtcactgttgctgt 247

Qy     138 aatctcatgccgacatgtggagacccttgagaaagacagagggaacccccatctacctggg 197
            ||| |||||    ||   ||| | |||||| ||| ||||||| | ||||| ||  ||||
Db     248 tatcacatgcaagtatccagaggctcttgagcaaggcagaggggatcccatttatttggg 307

Qy     198 cctgaatggactcaatctctgcctgatgtgtgctaaagtcggggaccagcccacactgca 257
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Db     308 aatccagaatccagaaatgtgtttgtattgtgagaaggttggagaacagcccacattgca 367

Qy     258 gctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttct 317
           ||| || ||  || | || ||||||  ||||   |||||||||||| |||||  |||| ||
Db     368 gctaaaagagcagaagatcatggatctgtatggccaacccgagcccgtgaaacccttcct 427

Qy     318 cttctaccacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctg 377
            |||||||    | ||| ||| |||| ||||||| | |||||||||| |||||  | |||
Db     428 tttctaccgtgccaagactggtaggacctccacccttgagtctgtggccttcccggactg 487

Qy     378 gttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaa 437
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Db     488 gttcat---tgcctcctccaagagagaccagcccatcattctgacttcagaacttgggaa 544

Qy     438 agccaacactactgactttgggttaactat 467
             |  |||  |||| |||||  |||| |||
Db     545 gtcatacaacactgcctttgaattaaatat 574
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RESULT 12
AAX86458
ID AAX86458 standard; DNA; 1291 BP.
XX
AC AAX86458;
XX
DT 30-SEP-1999 (first entry)
XX
DE cDNA encoding a human SPOIL-I protein (also known as hTANGO 080-I).
XX
KW SPOIL-I; interleukin-1 receptor antagonist; IL-1ra; modulating agent;
KW bone metabolism disorder; proinflammatory disorder; immune disorder;
KW inflammatory disease; septic shock; stroke; diabetes; arthritis;
KW intercolitis; pneumonitis; epithelial cell; skin disease;
KW proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;
KW epithelial cancer; squamous cell carcinoma; bone resorption disorder;
KW osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;
KW osteogenesis imperfecta; fibrous displasia; hypophosphatasia;
KW bone sarcoma; myeloma bone disorder; osteolytic bone lesion;
KW hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;
KW bone fracture; hTANGO 80-I; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 124..633
FT /*tag= a
FT /product= SPOIL-1
XX
PN WO9937662-A1.
XX
PD 29-JUL-1999.
XX
PF 26-JAN-1999; 99WO-US01575.
XX
PR 27-JAN-1998; 98US-0013810.
XX
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI Busfield SJ;
XX
DR WPI; 1999-458675/38.
DR P-PSDB; AAY24043.
XX
PT New isolated SPOIL proteins, used to develop products for treating,
PT e.g. inflammatory and immune disorders
XX
PS Example 1; Fig 4A-B; 126pp; English.
XX
CC The present sequence encodes a SPOIL-I protein. The SPOIL proteins have
CC homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.
CC The SPOIL proteins are used as modulating agents in regulating a variety
CC of cellular processes. The products can be used for treating disorders
CC characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone
CC metabolism disorder, a proinflammatory disorder or an immune disorder.
CC They can be used for treating e.g. inflammatory diseases and disorders
CC e.g. inflammation, septic shock, stroke, diabetes, arthritis,
CC intercolitis and pneumonitis, epithelial cell and/or skin diseases and
CC disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma
CC and Kaposi's sarcoma and other epithelial cancers including squamous cell
CC carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and
CC bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's
CC disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,
CC fibrous displasia, hypophosphatasia, bone sarcoma, myeloma bone disorder
CC (e.g. osteolytic bone lesions) and hypercalcemia. SPOIL molecules and
CC SPOIL modulators are useful for regulation of bone mass (e.g. increase in
CC bone mass and/or inhibit bone loss), management of bone fragility (e.g.
CC decrease bone fragility); and prevention and/or treatment of bone pain,
CC bone deformities and/or bone fractures. The products can also be used for
CC detection, diagnosis and screening assays.
XX
SQ Sequence 1291 BP; 375 A; 271 C; 291 G; 354 T; 0 other;

Query Match 42.3%; Score 202; DB 20; Length 1291;
Best Local Similarity 67.1%; Pred. No. 3.4e-52;
Matches 302; Conservative 0; Mismatches 145; Indels 3; Gaps 1;

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           |||    | ||||      ||||  ||| | ||| | ||||| |  ||||||   |||||
Db     177 aatgtgtaaacctattactgggactattaatgatttgaatcagcaagtgtggacccttca 236

Qy      78 ggaccagacgctcatagcagtcccgaggaaggaccgtatgtctccagtcactattgcctt 137
           ||  ||||  ||  | ||||| ||  | |  ||| || || | |||||||| ||||  |
Db     237 gggtcagaaccttgtggcagttccacgaagtgacagtgtgaccccagtcactgttgctgt 296

Qy     138 aatctcatgccgacatgtggagacccttgagaaagacagagggaacccccatctacctggg 197
            ||| |||||    ||   ||| | |||||| ||| ||||||| | ||||| ||  ||||
Db     297 tatcacatgcaagtatccagaggctcttgagcaaggcagaggggatcccatttatttggg 356

Qy     198 cctgaatggactcaatctctgcctgatgtgtgctaaagtcggggaccagcccacactgca 257
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Db     357 aatccagaatccagaaatgtgtttgtattgtgagaaggttggagaacagcccacattgca 416

Qy     258 gctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtccttttct 317
           ||| || ||  || | || |||||| ||||   ||||||||||| |||||  |||| ||
Db     417 gctaaaagagcagaagatcatggatctgtatggccaacccgagcccgtgaaacccttcct 476

Qy     318 cttctaccacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctg 377
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Qy     378 gttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaa 437
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Qy     438 agccaacactactgactttgggttaactat 467
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Db     594 gtcatacaacactgcctttgaattaaatat 623


RESULT  13
AAS26915
ID   AAS26915 standard; cDNA; 673 BP.
XX
AC   AAS26915;
XX
DT   07-NOV-2001  (first entry)
XX
DE   Human cDNA encoding a novel secreted protein, SEQ ID 107.
XX
KW   Human; immunosuppressive; antiarthritic; ss; antirheumatic;
KW   cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;
KW   neuroprotective; antibacterial; virucide; fungicide; opthalmalogical;
KW   vulnerary; secreted protein; rheumatoid arthritis;
KW   hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
KW   cerebrovascular disorder; cerebral ischaemia; angiogenesis;
KW   nervous system disorder; Alzheimer's disease; infection; ocular disorder;
KW   corneal infection; wound healing; epithelial cell proliferation;
KW   skin ageing; food additive; preservative; antiproliferative.
XX
OS   Homo sapiens.
XX
PN   WO200155441-A2.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US01320.
XX
PR   31-JAN-2000; 2000US-0179065.
PR   04-FEB-2000; 2000US-0180628.
PR   24-FEB-2000; 2000US-0184664.
PR   02-MAR-2000; 2000US-0186350.
PR   16-MAR-2000; 2000US-0189874.
PR   17-MAR-2000; 2000US-0190076.
PR   18-APR-2000; 2000US-0198123.
PR   19-MAY-2000; 2000US-0205515.
PR   07-JUN-2000; 2000US-0209467.
PR   28-JUN-2000; 2000US-0214886.
PR   30-JUN-2000; 2000US-0215135.
PR   07-JUL-2000; 2000US-0216647.
PR   07-JUL-2000; 2000US-0216880.
PR   11-JUL-2000; 2000US-0217487.
PR   11-JUL-2000; 2000US-0217496.
PR   14-JUL-2000; 2000US-0218290.
PR   26-JUL-2000; 2000US-0220963.
PR   26-JUL-2000; 2000US-0220964.
PR   14-AUG-2000; 2000US-0224518.
PR   14-AUG-2000; 2000US-0224519.
PR   14-AUG-2000; 2000US-0225213.
PR   14-AUG-2000; 2000US-0225214.
PR   14-AUG-2000; 2000US-0225266.
PR   14-AUG-2000; 2000US-0225267.
PR   14-AUG-2000; 2000US-0225268.
PR   14-AUG-2000; 2000US-0225270.
PR   14-AUG-2000; 2000US-0225447.
PR   14-AUG-2000; 2000US-0225757.
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PR   14-AUG-2000; 2000US-0225759.
PR   18-AUG-2000; 2000US-0226279.
PR   22-AUG-2000; 2000US-0226681.
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PR   30-AUG-2000; 2000US-0228924.
PR   01-SEP-2000; 2000US-0229287.
PR   01-SEP-2000; 2000US-0229343.
PR   01-SEP-2000; 2000US-0229344.
PR   01-SEP-2000; 2000US-0229345.
PR   05-SEP-2000; 2000US-0229509.
PR   05-SEP-2000; 2000US-0229513.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-476222/51.
DR P-PSDB; AAU17010.
XX
PT Novel polypeptides and polynucleotides useful as diagnostic reagents to
PT diagnose diseases or disorders associated with aberrant expression or
PT activity of polypeptides, for treating blood clotting disorder,
PT haemophilia -
XX
PS Claim 1; SEQ ID No 107; 601pp; English.
XX
CC The invention relates to isolated nucleic acid molecules and their
CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They
CC are also used in diagnosing a pathological condition or susceptibility
CC to a pathological condition. Antibodies to the proteins can also
CC be used in alleviating symptoms associated with the disorders and in
CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked
CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated
CC include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi
CC and ocular disorders e.g. corneal infection, and many other
CC disorders listed in the specification. The polypeptides can also
CC be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present

Query Match 42.3%; Score 201.6; DB 22; Length 673;
Best Local Similarity 66.9%; Pred. No. 3.4e-52;
Matches 301; Conservative 1; Mismatches 145; Indels 3; Gaps 1;

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AC AAD16762;
XX
DT 22-NOV-2001 (first entry)
XX
DE Human novel protein-encoding gene 13 cDNA clone HAICQ62, SEQ ID NO:23.
XX
KW Human; cytostatic; gene therapy; inflammatory disorder; neural disorder;
KW Parkinson's disease; Alzheimer's disease; immune system disorder; AIDS;
KW autoimmune disease; rheumatoid arthritis; muscular disorder; ischaemia;
KW reproductive disorder; Crohn's disease; pulmonary disorder; cancer;
KW myocardial infarction; glomerulonephritis; nephrotic syndrome; tumour;
KW haematopoietic disorder; rhinitis; asthma; diabetes; atherosclerosis;
KW anti-sense therapy; endocrine disorder; leukaemia; ss.
XX
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XX
FH Key Location/Qualifiers
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FT /product= "Human novel protein"
FT /transl_except= (pos:634..636, aa:Xaa)
FT /note= "CDS does not include start and stop codon; Xaa
FT is an unknown amino acid"
FT /partial
XX
PN WO200155202-A1.
XX
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XX

PF 17-JAN-2001; 2001WO-US01325.
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PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-451925/48.
DR P-PSDB; AAE09702.
XX

PT Isolated polypeptide for treating, preventing and/ or prognosing
PT medical disorders and also for testing and detection e.g. diagnosis and
PT screening for agonists -
XX
PS Claim 1; SEQ ID No 23; 469pp; English.
XX
CC AAD16750-AAD16775 represent cDNAs corresponding to novel human protein
CC genes, and AAE09690-AAE09715 represent the proteins they encode. AAD16777
CC -AAD16780 represent novel human genomic DNA fragments. The novel proteins
CC and their DNAs are useful for diagnosing, treating, preventing and/or
CC prognosing inflammatory disorders (bursitis or tendonitis); neural
CC disorders (e.g. Parkinson's disease, Alzheimer's disease); immune system
CC disorders; AIDS; autoimmune diseases (e.g., rheumatoid arthritis);
CC muscular disorders; reproductive disorders; gastrointestinal disorders
CC (malabsorption syndrome, Crohn's disease); pulmonary disorders;
CC cardiovascular disorders (myocardial infarction, ischaemia, arrhythmias);
CC renal disorders (glomerulonephritis, nephrotic syndrome); cancerous
CC disease and conditions (breast cancer); hyperproliferative disorders
CC (leukaemia, hyperplasia); tumours; foetal and developmental
CC abnormalities; haematopoietic disorders; respiratory disorders (rhinitis,
CC asthma); angiogenic disorders; diabetes; atherosclerosis; endocrine
CC disorders; pregnancy-related disorders and infections. The novel protein
CC DNA is useful in gene therapy and anti-sense therapy. The proteins can

Query Match 42.3%; Score 201.6; DB 22; Length 673;
Best Local Similarity 66.9%; Pred. No. 3.4e-52;
Matches 301; Conservative 1; Mismatches 145; Indels 3; Gaps 1;

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Qy     318 cttctaccacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctg 377
            |||||||    | ||| ||| |||| ||||||| | |||||||||| ||||| | |||
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RESULT 15
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XX
AC AAX86459;
XX
DT 30-SEP-1999 (first entry)
XX
DE cDNA encoding a human SPOIL-II protein (also known as hTANGO 080-II).
XX
KW SPOIL-II; interleukin-1 receptor antagonist; IL-1ra; modulating agent;
KW bone metabolism disorder; proinflammatory disorder; immune disorder;
KW inflammatory disease; septic shock; stroke; diabetes; arthritis;
KW intercolitis; pneumonitis; epithelial cell; skin disease;
KW proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;
KW epithelial cancer; squamous cell carcinoma; bone resorption disorder;
KW osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;
KW osteogenesis imperfecta; fibrous displasia; hypophosphatasia;
KW bone sarcoma; myeloma bone disorder; osteolytic bone lesion;
KW hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;
KW bone fracture; hTANGO 80-I; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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FT /*tag= a
FT /product= SPOIL-II
XX
PN WO9937662-A1.
XX
PD 29-JUL-1999.
XX
PF 26-JAN-1999; 99WO-US01575.
XX
PR 27-JAN-1998; 98US-0013810.
XX
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI Busfield SJ;
XX
DR WPI; 1999-458675/38.
DR P-PSDB; AAY24044.
XX
PT New isolated SPOIL proteins, used to develop products for treating,
PT e.g. inflammatory and immune disorders
XX
PS Claim 1; Fig 5; 126pp; English.
XX
CC The present sequence encodes a SPOIL-II protein. The SPOIL proteins have
CC homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.
CC The SPOIL proteins are used as modulating agents in regulating a variety
CC of cellular processes. The products can be used for treating disorders
CC characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone
CC metabolism disorder, a proinflammatory disorder or an immune disorder.
CC They can be used for treating e.g. inflammatory diseases and disorders
CC e.g. inflammation, septic shock, stroke, diabetes, arthritis,
CC intercolitis and pneumonitis, epithelial cell and/or skin diseases and
CC disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma
CC and Kaposi's sarcoma and other epithelial cancers including squamous cell
CC carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and
CC bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's
CC disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,
CC fibrous displasia, hypophosphatasia, bone sarcoma, myeloma bone disorder
CC (e.g. osteolytic bone lesions) and hypercalcemia. SPOIL molecules and
CC SPOIL modulators are useful for regulation of bone mass (e.g. increase in
CC bone mass and/or inhibit bone loss), management of bone fragility (e.g.
CC decrease bone fragility); and prevention and/or treatment of bone pain,
CC bone deformities and/or bone fractures. The products can also be used for
CC detection, diagnosis and screening assays.
XX
SQ Sequence 1377 BP; 377 A; 304 C; 316 G; 380 T; 0 other;

Query Match 42.2%; Score 201.4; DB 20; Length 1377;
Best Local Similarity 67.5%; Pred. No. 5.4e-52;
Matches 299; Conservative 0; Mismatches 141; Indels 3; Gaps 1;

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Db     275 aaacctattactgggactattaatgatttgaatcagcaagtgtggacccttcagggtcag 334

Qy      85 acgctcatagcagtcccgaggaaggaccgtatgtctccagtcactattgccttaatctca 144
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Db     335 aaccttgtggcagttccacgaagtgacagtgtgaccccagtcactgttgctgttatcaca 394
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Qy    145 tgccgacatgtggagacccttgagaaagacagagggaaccccatctacctgggcctgaat 204
          |||    ||   ||| | |||||| ||| ||||||| | ||||| ||  |||| | |
Db    395 tgcaagtatccagaggctcttgagcaaggcagaggggatcccatttatttgggaatccag 454

Qy    205 ggactcaatctctgcctgatgtgtgctaaagtcggggaccagcccacactgcagctgaag 264
             |  | | ||  ||   |||| || || || || ||||||||| ||||||| ||
Db    455 aatccagaaatgtgtttgtattgtgagaaggttggagaacagcccacattgcagctaaaa 514

Qy    265 gaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctac 324
          ||  || | || |||||| ||||   |||||||||||| |||||  |||| || ||||||
Db    515 gagcagaagatcatggatctgtatggccaacccgagcccgtgaaacccttcctttttctac 574

Qy    325 cacagccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatc 384
          |    | ||| ||| |||| ||||||| | |||||||||||| ||||| | |||||||||
Db    575 cgtgccaagactggtaggacctccacccttgagtctgtggccttcccggactggttcat- 633

Qy    385 gctgtcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaac 444
            || |  |||  |  ||| |   ||  |||| || ||   |||||| |||||  |  ||
Db    634 --tgcctcctccaagagagaccagcccatcattctgacttcagaacttgggaagtcatac 691

Qy    445 actactgactttgggttaactat 467
          |  |||| |||||  |||| |||
Db    692 aacactgcctttgaattaaatat 714
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Search completed: June 21, 2002, 12:03:00
Job time: 14923 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: June 21, 2002, 11:09:01 ; Search time 2828.95 Seconds
(without alignments)
2275.773 Million cell updates/sec

Title: US-09-763-498-12
Perfect score: 477
Sequence: 1 atggaaaaagcattgaaaat.....ggttaactatgctgttttaa 477

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	238.6	50.0	883	11	AK004061	AK004061 Mus muscu
	2	129.2	27.1	479	9	AA030324	AA030324 mi08c10.r
c	3	124.4	26.1	612	10	BM386666	BM386666 UI-R-CN1-
c	4	122	25.6	539	9	AW368430	AW368430 CM3-HT019
	5	122	25.6	555	9	AW361172	AW361172 RC1-CT025
c	6	122	25.6	557	9	AW368437	AW368437 CM3-HT019
c	7	122	25.6	559	9	AW578451	AW578451 RC1-CT025
c	8	121	25.4	555	10	BE695960	BE695960 RC1-CT025
c	9	120.4	25.2	436	9	AW361164	AW361164 RC1-CT025
	10	120.4	25.2	536	9	AW853610	AW853610 RC1-CT025
	11	120	25.2	1219	11	AK009787	AK009787 Mus muscu
	12	113.2	23.7	870	10	BF244205	BF244205 601863146
c	13	111	23.3	434	9	AW753217	AW753217 RC1-CT025
	14	97.4	20.4	560	9	AW361245	AW361245 RC1-CT025
	15	74.8	15.7	1020	10	BG245180	BG245180 602357579
	16	72	15.1	997	9	AL554778	AL554778 AL554778
	17	71.8	15.1	594	10	BI961215	BI961215 MONO1_7_E
	18	71.6	15.0	626	9	BB612586	BB612586 BB612586
	19	71.4	15.0	435	10	W78043	W78043 zd72d01.r1
	20	70.8	14.8	635	9	AW262191	AW262191 xq62f01.x
	21	70.8	14.8	889	9	AL540334	AL540334 AL540334
	22	70.8	14.8	910	9	AL549965	AL549965 AL549965
	23	70.8	14.8	938	10	BE563703	BE563703 601335323
	24	70.8	14.8	955	10	BM009048	BM009048 603618892
	25	69.2	14.5	640	10	BG288796	BG288796 602388126
	26	69.2	14.5	864	10	BI489807	BI489807 603031536
c	27	67.6	14.2	371	10	BI020838	BI020838 CM4-MT021
	28	67.6	14.2	549	10	BE706905	BE706905 QV0-HT036
	29	65.6	13.8	508	9	AW464284	AW464284 BP230015A
	30	65	13.6	531	9	AW951593	AW951593 EST363663
	31	62.6	13.1	393	9	AV011778	AV011778 AV011778
	32	62	13.0	832	10	BI517352	BI517352 603041588
	33	61.4	12.9	900	11	AY026753	AY026753 Homo sapi
c	34	61.2	12.8	350	10	BI020732	BI020732 CM4-MT021
	35	61.2	12.8	1051	11	AK009741	AK009741 Mus muscu
	36	61.2	12.8	1199	11	AK008977	AK008977 Mus muscu
	37	60.8	12.7	726	10	BI089828	BI089828 602855071
	38	60.8	12.7	858	10	BI090567	BI090567 602855674
	39	60.8	12.7	932	9	AL545100	AL545100 AL545100
	40	60.4	12.7	726	10	BI766516	BI766516 603052319
	41	56.8	11.9	824	10	BI762103	BI762103 603049281
	42	56.2	11.8	690	10	BI912302	BI912302 603069864
	43	56	11.7	281	10	R50241	R50241 yj58a03.r1
	44	55.8	11.7	260	10	R46871	R46871 yj54f05.r1
	45	54.4	11.4	2843	11	AK014576	AK014576 Mus muscu

ALIGNMENTS

RESULT 1
AK004061
LOCUS AK004061 883 bp mRNA linear HTC 19-JAN-2002
DEFINITION Mus musculus 18 days embryo whole body cDNA, RIKEN full-length enriched library, clone:1110033G16:interleukin 1 family, member 6 (epsilon), full insert sequence.
ACCESSION AK004061
VERSION AK004061.1 GI:12835089
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (strain:C57BL/6J) 18 days embryo cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:1110033G16.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2 (sites)
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3 (sites)
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913
PUBMED 11076861
REFERENCE 4 (sites)
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5 (bases 1 to 883)
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0. Second strand cDNA was prepared with the primer adapter of sequence[5' GAGAGAGAGAAGGATCCAAGAGCTCAATTAATTTAATTAAACCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.

FEATURES Location/Qualifiers
source 1. .883
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="MGD:MGI:1900693"
/db_xref="taxon:10090"
/clone="1110033G16"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="18 days embryo"
gene 162. .644
/gene="Il1f6"
CDS 162. .644
/gene="Il1f6"
/note="data source:MGD, source key:MGI:1859324, evidence:ISS
interleukin 1 family, member 6 (epsilon)
putative"
/codon_start=1
/protein_id="BAB23147.1"
/db_xref="GI:12835090"
/translation="MNKEKELRAASPSLRHVQDLSSRVWILQNNILTAVPRKEQTVPV TITLLPCQYLDTLETNRGDPTYMGVQRPMSCLFCTKDGEQPVLQLGEGNIMEMYNKKE PVKASLFYHKKSGTTSTFESAAFPGWFIAVCSKGSCPLILTQELGEIFITDFEMIVVH "
polyA_signal 860. .865
/note="putative"
polyA_site 883
/note="putative"

BASE COUNT 255 a 193 c 200 g 235 t
ORIGIN

Query Match 50.0%; Score 238.6; DB 11; Length 883;
Best Local Similarity 68.8%; Pred. No. 1.1e-60;
Matches 328; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

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Qy      1 atggaaaaagcattgaaaattgacacacctcagcgggggagcattcaggatatcaatcat 60
          | ||| |||| | | | |   |  |||||  ||   |     |||||||| | | | |
Db    168 AAGGAGAAAGAACTAAGAGCAGCATCACCTTCGCTTAGACATGTTCAGGATCTTAGTAGT 227

Qy     61 cgggtgtgggttcttcaggaccagacgctcatagcagtcccgaggaaggaccgtatgtct 120
          || |||||| | || ||| || | |  |||| ||||||||  ||||| || |  |    |
Db    228 CGTGTGTGGATCCTGCAGAACAATATCCTCACTGCAGTCCCAAGGAAAGAGCAAACAGTT 287

Qy    121 ccagtcactattgccttaatctcatgccgacatgtggagacccttgagaaagacagaggg 180
          |||||||||||| ||||  || ||||||  | || |||| || ||||||||   |||| |||
Db    288 CCAGTCACTATTACCTTGCTCCCATGCCAATATCTGGACACTCTTGAGACGAACAGGGGG 347

Qy    181 aaccccatctacctgggcctgaatggactcaatctctgcctgatgtgtgctaaagtcggg 240
          | ||||  ||| ||||  || |  | |  |    ||||||| | ||  | || | |||
Db    348 GATCCCACGTACATGGGAGTGCAAAGGCCGATGAGCTGCCTGTTCTGCACAAAGGATGGG 407

Qy    241 gaccagcccacactgcagctgaaggaaaaggatataatggatttgtacaaccaacccgag 300
          || |||||    || |||||   ||||  | | ||||||||  ||||||||  ||   ||
Db    408 GAGCAGCCTGTGCTACAGCTTGGGGAAGGGAACATAATGGAAATGTACAACAAAAAGGAA 467

Qy    301 cctgtgaagtcctttctcttctaccacagccagagtggcaggaactccaccttcgagtct 360
          |||||  ||  ||| |||||||||  ||||   |||||||  |  | ||| || || ||||||
Db    468 CCTGTAAAAGCCTCTCTCTTCTATCACAAGAAGAGTGGTACAACCTCTACATTTGAGTCT 527

Qy    361 gtggctttccctggctggttcatcgctgtcagctctgaaggaggctgtcctctcatcctt 420
          |  || |||||||| |||||||||||||||| |||||  ||||  ||||  || |||||  ||
Db    528 GCAGCCTTCCCTGGTTGGTTCATCGCTGTCTGCTCTAAAGGGAGCTGCCCACTCATTCTG 587

Qy    421 acccaagaactggggaaagccaacactactgactttgggttaactatgctgttttaa 477
          |||||||||||||||  ||  |  ||  |||||||| | | | | | || |   ||||
Db    588 ACCCAAGAACTGGGGGAAATCTTCATCACTGACTTCGAGATGATTGTGGTACATTAA 644
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RESULT 2
AA030324
LOCUS AA030324 479 bp mRNA linear EST 21-JAN-1997
DEFINITION mi08c10.r1 Soares mouse placenta 4NbMP13.5 14.5 Mus musculus cDNA clone IMAGE:459858 5', mRNA sequence.
ACCESSION AA030324
VERSION AA030324.1 GI:1497479
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 479)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:276746
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 467.

```
FEATURES             Location/Qualifiers
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                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:459858"
                     /clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
                     /sex="unknown"
                     /tissue_type="placenta"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
                     with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Not I - oligo(dT) primer
                     [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGGAAATTTTTTTTTTTTTTTTTTTTTTT
                     T 3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      148 a    108 c    102 g    121 t
ORIGIN


  Query Match           27.1%;  Score 129.2;  DB 9;  Length 479;
  Best Local Similarity  73.9%;  Pred. No. 5.9e-28;
  Matches  164;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy    256 cagctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtccttt 315
          |||  |  |||||  | | ||||||||  ||||||||  ||   ||  |||||  ||  |||  |
Db    195 CAGTTCCAGGAAGGGAACATAATGGAAATGTACAACAAAAAGGAACCTGTAAAAGCCTCT 254

Qy    316 ctcttctaccacagccagagtggcaggaactccaccttcgagtctgtggctttccctggc 375
          ||||||||  ||||   |||||||  |  | |||  ||  ||  |||||||   ||  ||||||||
Db    255 CTCTTCTATCACAAGAAGAGTGGTACAACCTCTACATTTGAGTCTGCAGCCTTCCCTGGT 314

Qy    376 tggttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaagaactgggg 435
          ||||||||||||||||  |||||  ||||   ||||  ||  |||||  ||  ||||||||||||||||
Db    315 TGGTTCATCGCTGTCTGCTCTAAAGGGAGCTGCCCACTCATTCTGACCCAAGAACTGGGG 374

Qy    436 aaagccaacactactgactttgggttaactatgctgttttaa 477
          ||   |  ||  ||||||||  |  |  |  |  |  ||  |   ||||
Db    375 GAAATCTTCATCACTGACTTCGAGATGATTGTGGTACATTAA 416


RESULT   3
BM386666/c
LOCUS       BM386666                 612 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  UI-R-CN1-cjg-1-09-0-UI.s1 UI-R-CN1 Rattus norvegicus cDNA clone
            UI-R-CN1-cjg-1-09-0-UI 3', mRNA sequence.
ACCESSION   BM386666
VERSION     BM386666.1  GI:18186719
KEYWORDS    EST.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 612)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to identify it as a clone from the
            normalized fundus library cDNA Library Preparation: M.B. Soares Lab
            Clone distribution: clones will be available through Research
            Genetics (www.resgen.com)
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .612
                     /organism="Rattus norvegicus"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-CN1-cjg-1-09-0-UI"
                     /clone_lib="UI-R-CN1"
                     /dev_stage="adult"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CN1
                     library is a subtracted library derived from the following
                     pool of seven normalized rat libraries: normalized rat
                     seminal vesicles, normalized rat penis, normalized rat
                     bladder, normalized rat cervix, normalized rat brown
                     adipose, normalized rat fundus, and normalized rat
                     salivary gland.  It was constructed according to the
                     procedure described by Bonaldo, Lennon & Soares (Genome
                     Research Genome 6:  791-806, 1996).  For construction of
                     the CN1 library, plasmid DNA from the pool of normalized
                     libraries was electroporated into competent bacteria for
                     the production of single-stranded circular DNA.  This was
                     then used as a tracer in a subtractive hybridization with
                     a driver (PCR amplified inserts from a plamid DNA template
                     preparation) comprising: a) a pool of about 34,000 clones
                     from the Rat Unigene Set corresponding to plates R-5-AA-NN
                     excluding plates R-5-MM and MN.  This pool represented 40%
                     of the final driver population.  b) a pool of about 29,000
                     clones from subtracted libraries CA0 and CA1 corresponding
                     to plates R-CA0-AWV through R-CA0-AXS, R-CA0-AZX through
                     R-CA0-BAZ, R-CA0-BFE through R-CA0-BHY, R-CA0-BJS,
                     R-CA0-BKE, R-CA0-BKG-H, R-CA0-BKJ-K, R-CA0-BKP through
                     R-CA0-BKS, R-CA0-BKU-V, R-CA0-BLY through R-CA0-BMA,
                     R-CA0-BMC through R-CA0-BME, R-CA0-BNS, R-CA0-BOB through
                     R-CA0-BOJ, R-CA0-BPA through R-CA0-BPG, R-CA1-BBA through
                     R-CA1-BDA, R-CA1-BHZ through R-CA1-BJF, R-CA1-BJR,
                     R-CA1-BJT through R-CA1-BKB, R-CA1-BKD, R-CA1-BKF,
                     R-CA1-BKI, R-CA1-BKT, R-CA1-BLF, R-CA1-BLH through
                     R-CA1-BLN, R-CA1-BLS, R-CA1-BLU-V, R-CA1-BNR, and
                     R-CA1-BLE.  The resulting pool represented 20% of the
                     final driver population.  c) a pool of about 15,000 clones
                     from non-normalized libraries CS0s, CT0s, CU0s, CW0s, CX0s
                     and normalized libaries CS0, CT0, CU0, CW0, and CX0
                     corresponding to plates R-CS0s-CBD through R-CS0s-CBO,
                     R-CT0s-CAM through R-CT0s-CAX, R-CU0s-CBP through
                     R-CU0s-CCA, R-CW0s-CCB through R-CW0s-CCM, R-CX0s-CCN
                     through R-CX0s-CCX, R-CS0-BSD, R-CS0-BTD through R-CS0-BTV
                     , R-CS0-BVM, R-CT0-BTW through R-CT0-BUP, R-CT0-BVN,
                     R-CU0-BUQ through R-CU0-BVL, R-CW0-BVV through R-CW0-BWP,
                     R-CW0-BXN through R-CW0-BXO, R-CX0-BWQ through R-CX0-BXM.
                     The resulting pool represented 5% of the final driver
                     population.  d) a pool of about 5,000 clones (1,000 from
                     non-normalized eye library CV0 and 4,000 from normalized
                     eye library CV1) corresponding to plates R-CV0-BRH through
                     R-CV0-BRR, R-CV1-BRS through R-CV1-BSC, R-CV1-BSE through
                     R-CV1-BTC, and R-CV1-BV0 through R-CV1-BVU. This pool
                     represented about 5% of the final driver population.  e) A
                     pool of about 10,000 clones from subtracted library BS2,
                     BV0 and BV0p (7-9.5 kb cDNA library fraction from rat
                     whole embryo), and BX0 (0.5-7kb cDNA library fraction from
                     rat whole embryo) corresponding to plates R-BS2-BDB
                     through R-BS2-BFB, R-BV0-ANK through R-BV0-ANR, R-BV0p-AOI
                     through R-BV0p-AOX, and R-BX0-AQY through R-BX0-ASH.  The
                     resulting pool represented 5% of the final driver
```

population. f) a pool of about 7,000 clones from the seven non-normalized libraries that make up the tracer including CY0, CZ0, DA0, DB0, DC0, DD0, and DE0 corresponding to plates R-CY0-BXP through R-CY0-BXZ, R-CZ0-BYA through R-CZ0-BYI, R-CZ0-BZB-C, R-DA0-BYJ through R-DA0-BYP, R-DA0-BZD through R-DA0-BZH, R-DB0-BYQ through R-DB0-BZA, R-DC0-BZI through R-DC0-BZQ, R-DC0-CAY through R-DC0-CBA, R-DD0-BZR through R-DD0-CAA, R-DD0-CBB-C, and R-DE0-CAB through R-DE0-CAL. The resulting pool represented about 10% of the final driver population. g) a pool of about 2,000 clones from the pool of normalized libraries, CN0, that makes up the tracer. The corresponding plates are R-CN0-BKW through R-CN0-BLD, R-CN0-BLG, R-CN0-BLP through R-CNO-BLR, R-CN0-BLT, R-CN0-BLW-X, R-CN0-BMB, and R-CN0-BMF through R-CN0-BML. This pool represented 5% of the final driver population. h) a pool of the 28 most abundant clones in the CN0 pool corresponding to the following addresses: bkw-a-09-0-UI, bkw-b-09-0-UI, bkw-b-11-0-UI, bkx-b-10-0-UI, bkx-d-01-0-UI , bkx-d-06-0-UI, bkx-g-08-0-UI, bkx-h-12-0-UI, bky-a-05-0-UI, bkz-a-06-0-UI, bkz-a-11-0-UI, bkz-c-06-0-UI , bkz-c-09-0-UI, bkz-d-10-0-UI, bla-a-01-0-UI, bla-a-02-0-UI, bla-f-04-0-UI, bla-g-07-0-UI, bla-g-12-0-UI , blb-a-12-0-UI, blb-f-02-0-UI, blc-a-11-0-UI, blc-e-95-0-UI, bld-1-08-0-UI, bld-f-02-0-UI, blq-h-04-0-UI , blr-a-05-0-UI, blt-f-08-0-UI. This pool represented 5% of the final driver population. i) One abundant CN0 clone (corresponding to the address bkz-a-11-0-UI) was digested with Not I and Eco RI and the resulting insert was gel purified. This purified insert was added directly to the driver so that it represented 5% of the final driver population.
TAG_LIB=UI-R-CN1
TAG_TISSUE=fundus
TAG_SEQ=TTCGG"

BASE COUNT 160 a 130 c 124 g 198 t
ORIGIN

Query Match 26.1%; Score 124.4; DB 10; Length 612;
Best Local Similarity 58.3%; Pred. No. 1.9e-26;
Matches 218; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

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Qy      89 tcatagcagtcccgaggaaggaccgtatgtctccagtcactattgccttaatctcatgcc 148
           | | ||| || ||    |   || | |     | |||| | ||  ||| ||  ||||
Db     579 TGACAGCGGTTCCTGCTAGCAACAGCGTCAAATCTGTCATTCTTAGCTTGATAGCATGTA 520

Qy     149 gacatgtggagacccttgagaaagacagagggaaccccatctacctgggcctgaatggac 208
           || |  ||||   ||  ||  || | |  || || |   | | ||||||  | || ||
Db     519 GAGACATGGAATTCCAAGATGAAAAGAAGGGTAATCTAGTTTTCCTGGGAATCAAAGGCA 460

Qy     209 tcaatctctgcctgatgtgtgctaaagtcggggaccagcccacactgcagctgaaggaaa 268
           | |||||||||  | ||||||  |  ||| || | | || ||  |||||||  |||||
Db     459 GAAGTCTCTGCCTCTTCTGTGCTGAGATCGAGGGCAAACCGACTTTGCAGCTTAAGGATG 400

Qy     269 aggatataatggatttgtacaaccaacccgagcctgtgaagtcctttctcttctaccaca 328
           || || ||||||||||||||  |     |  |   |||  ||||||||||||||||
Db     399 TAGACATCATGGATTTGTACAATGAGAAAAAAGCACAGAAAGCCTTTCTCTTCTACCATG 340

Qy     329 gccagagtggcaggaactccaccttcgagtctgtggctttccctggctggttcatcgctg 388
           ||      ||    | ||   |||  |||| ||    |  ||||||||||| || ||
Db     339 GCATAGAGGGATCTACTTCTGTCTTTCAGTCAGTCTTGTATCCTGGCTGGTTTATAGCCA 280

Qy     389 tcagctctgaaggaggctgtcctctcatccttacccaagaactggggaaagccaacacta 448
           |   ||   || | |     |  |||| ||||| || ||   |||  |||| || |  |
Db     279 CCTCTTCCACAGCAAGACAAACAATCATTCTTACACAGGAGAGGGGTGAAGCTAATAACA 220

Qy     449 ctgactttgggtta 462
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Db     219 CTAACTTCTACTTA 206
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RESULT 4

AW368430/c
LOCUS AW368430 539 bp mRNA linear EST 04-FEB-2000
DEFINITION CM3-HT0192-071099-022-e12 HT0192 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW368430
VERSION AW368430.1 GI:6873080
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 539)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM3&t2=CM3-HT0192-071099-022-e12&t3=1999-10-07&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 21
High quality sequence stop: 539.

FEATURES Location/Qualifiers
source 1. .539
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0192"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 145 a 131 c 123 g 140 t
ORIGIN

Query Match 25.6%; Score 122; DB 9; Length 539;
Best Local Similarity 71.9%; Pred. No. 9.1e-26;
Matches 174; Conservative 0; Mismatches 65; Indels 3; Gaps 1;

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Qy     226 tgtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggatataatggatttg 285
           ||||  || || || || ||||||||| |||||| || ||  || | || |||||| ||
Db     536 TGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCTG 477

Qy     286 tacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcaggaac 345
           ||   |||||||||||| |||||  |||| || |||||||    | ||| ||| |||| |
Db     476 TATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACC 417

Qy     346 tccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaaggaggc 405
           |||||| | |||||||||| ||||| | |||||||||   || |  ||| |  ||| |
Db     416 TCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT---TGCCTCCTCCAAGAGAGAC 360

Qy     406 tgtcctctcatccttacccaagaactggggaaagccaacactactgactttgggttaact 465
             ||  |||| || ||   |||||| |||||  |  |||  |||| |||||  |||| |
Db     359 CAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGAATTAAAT 300

Qy     466 at 467
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Db     299 AT 298
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RESULT 5
AW361172

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LOCUS       AW361172                555 bp    mRNA    linear   EST 04-FEB-2000
DEFINITION  RC1-CT0251-141099-012-h04 CT0251 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW361172
VERSION     AW361172.1  GI:6865822
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 555)
  AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
  TITLE     The FAPESP/LICR Human Cancer Genome Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC1&t2=RC1-CT0251-
            141099-012-h04&t3=1999-10-14&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 555.
FEATURES             Location/Qualifiers
     source          1. .555
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="CT0251"
                     /dev_stage="Adult"
                     /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT      148 a    129 c    130 g    147 t      1 others
ORIGIN
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  Query Match             25.6%;  Score 122;  DB 9;  Length 555;
  Best Local Similarity   71.9%;  Pred. No. 9.3e-26;
  Matches  174;  Conservative    0;  Mismatches   65;  Indels    3;  Gaps    1;

Qy     226 tgtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggatataatggatttg 285
           ||||  || || || || |||||||| ||||||| || ||  || | || ||||||  ||
Db       4 TGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCTG 63

Qy     286 tacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcaggaac 345
           ||   ||||||||||||| |||||  |||| || |||||||    | ||| ||| |||| |
Db      64 TATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACC 123

Qy     346 tccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaaggaggc 405
           |||||| | |||||||||||| ||||| | |||||||||   || |  |||  |  ||| |
Db     124 TCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT---TGCCTCCTCCAAGAGAGAC 180

Qy     406 tgtcctctcatccttacccaagaactggggaaagccaacactactgactttgggttaact 465
             ||  |||| || ||   |||||| |||||  |  |||  |||| |||||  |||| |
Db     181 CAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGAATTAAAT 240

Qy     466 at 467
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Db     241 AT 242
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RESULT   6
AW368437/c
LOCUS       AW368437                557 bp    mRNA    linear   EST 04-FEB-2000
DEFINITION  CM3-HT0192-071099-022-h06 HT0192 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW368437
VERSION     AW368437.1  GI:6873087
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 557)
  AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
  TITLE     The FAPESP/LICR Human Cancer Genome Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM3&t2=CM3-HT0192-
            071099-022-h06&t3=1999-10-07&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 43
            High quality sequence stop: 557.
FEATURES             Location/Qualifiers
     source          1. .557
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="HT0192"
                     /dev_stage="Adult"
                     /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT      149 a    130 c    130 g    147 t      1 others
ORIGIN
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  Query Match             25.6%;  Score 122;  DB 9;  Length 557;
  Best Local Similarity   71.9%;  Pred. No. 9.3e-26;
  Matches  174;  Conservative    0;  Mismatches   65;  Indels    3;  Gaps    1;

Qy     226 tgtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggatataatggatttg 285
           ||||  || || || || |||||||| ||||||| || ||  || | || ||||||  ||
Db     554 TGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCTG 495

Qy     286 tacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcaggaac 345
           ||   ||||||||||||| |||||  |||| || |||||||    | ||| ||| |||| |
Db     494 TATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACC 435

Qy     346 tccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaaggaggc 405
           |||||| | |||||||||||| ||||| | |||||||||   || |  |||  |  ||| |
Db     434 TCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT---TGCCTCCTCCAAGAGAGAC 378

Qy     406 tgtcctctcatccttacccaagaactggggaaagccaacactactgactttgggttaact 465
             ||  |||| || ||   |||||| |||||  |  |||  |||| |||||  |||| |
Db     377 CAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGAATTAAAT 318

Qy     466 at 467
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Db     317 AT 316
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RESULT   7
AW578451/c
LOCUS       AW578451                559 bp    mRNA    linear   EST 16-MAR-2000
DEFINITION  RC1-CT0252-030100-023-b06 CT0252 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW578451
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VERSION     AW578451.1  GI:7253500
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 559)
  AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
  TITLE     The FAPESP/LICR Human Cancer Genome Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-CT0252-
            030100-023-b06&t3=2000-01-03&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 37
            High quality sequence stop: 559.
FEATURES             Location/Qualifiers
     source          1. .559
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="CT0252"
                     /dev_stage="Adult"
                     /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT      148 a    130 c    132 g    149 t
ORIGIN


  Query Match             25.6%;  Score 122;  DB 9;  Length 559;
  Best Local Similarity   71.9%;  Pred. No. 9.3e-26;
  Matches  174;  Conservative    0;  Mismatches   65;  Indels    3;  Gaps    1;

Qy     226 tgtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggatataatggatttg 285
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Db     556 TGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCTG 497

Qy     286 tacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcaggaac 345
           ||   |||||||||||| |||||  |||| || |||||||    | ||| ||| |||| |
Db     496 TATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACC 437

Qy     346 tccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaaggaggc 405
           |||||| | |||||||||| |||| | |||||||||   || |  |||  |  ||| |
Db     436 TCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT---TGCCTCCTCCAAGAGAGAC 380

Qy     406 tgtcctctcatccttacccaagaactggggaaagccaacactactgactttgggttaact 465
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Db     379 CAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGACTTAAAT 320

Qy     466 at 467
           ||
Db     319 AT 318


RESULT   8
BE695960/c
LOCUS       BE695960                 555 bp    mRNA    linear   EST 11-SEP-2000
DEFINITION  RC1-CT0252-150600-028-h05 CT0252 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE695960
VERSION     BE695960.1  GI:10083120
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 555)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC1-CT0252-150
            600-028-h05&t3=2000-06-15&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 9
            High quality sequence stop: 555.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone_lib="CT0252"
                     /dev_stage="Adult"
                     /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT      147 a    131 c    129 g    148 t
ORIGIN


  Query Match             25.4%;  Score 121;  DB 10;  Length 555;
  Best Local Similarity   71.8%;  Pred. No. 1.9e-25;
  Matches  173;  Conservative    0;  Mismatches   65;  Indels    3;  Gaps    1;

Qy     227 gtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggatataatggatttgt 286
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Db     555 GTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCTGT 496

Qy     287 acaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcaggaact 346
           |   |||||||||||| |||||  |||| || |||||||    | ||| ||| |||| ||
Db     495 ATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACCT 436

Qy     347 ccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaaggaggct 406
           ||||| | |||||||||| ||||| | |||||||||   || |  |||  |  ||| |
Db     435 CCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT---TGCCTCCTCCAAGAGAGACC 379

Qy     407 gtcctctcatccttacccaagaactggggaaagccaacactactgactttgggttaacta 466
             ||  |||| || ||   |||||| ||||| |  |||  |||| |||||  |||| ||
Db     378 AGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGAATTAAATA 319

Qy     467 t 467
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Db     318 T 318
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RESULT   9
AW361164/c
LOCUS       AW361164                436 bp    mRNA    linear   EST 04-FEB-2000
DEFINITION  RC1-CT0251-141099-012-c02 CT0251 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW361164
VERSION     AW361164.1  GI:6865814
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 436)
  AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
  TITLE     The FAPESP/LICR Human Cancer Genome Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC1&t2=RC1-CT0251-
            141099-012-c02&t3=1999-10-14&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 35
            High quality sequence stop: 436.
FEATURES             Location/Qualifiers
     source          1. .436
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="CT0251"
                     /dev_stage="Adult"
                     /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT      123 a     96 c    103 g    114 t
ORIGIN


  Query Match           25.2%;  Score 120.4;  DB 9;  Length 436;
  Best Local Similarity  71.5%;  Pred. No. 2.5e-25;
  Matches  173;  Conservative    0;  Mismatches   66;  Indels    3;  Gaps    1;

Qy     226 tgtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggatataatggatttg 285
           ||||  || || || || |||||||||| ||||||| || ||  || | || |||||| ||
Db     433 TGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCTG 374

Qy     286 tacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcaggaac 345
           ||   |||||||||||| |||||  |||| || |||||||    | ||| ||| |||| |
Db     373 TATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACC 314

Qy     346 tccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaaggaggc 405
           |||||| | |||||||||| ||||| | |||||||||   || |  |||  |  ||| |
Db     313 TCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT---TGCCTCCTCCAAGAGAGAC 257

Qy     406 tgtcctctcatccttacccaagaactggggaaagccaacactactgactttgggttaact 465
             ||  |||| || ||   |||||| |||||  |  |||  |||| |||||   ||| |
Db     256 CAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGCAGTAAAT 197

Qy     466 at 467
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Db     196 AT 195


RESULT  10
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AW853610
LOCUS       AW853610                536 bp    mRNA    linear   EST 19-MAY-2000
DEFINITION  RC1-CT0252-170200-025-c06 CT0252 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW853610
VERSION     AW853610.1  GI:7949212
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 536)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=RC1-CT0252-170
            200-025-c06&t3=2000-02-17&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 15
            High quality sequence stop: 535.
FEATURES             Location/Qualifiers
     source          1. .536
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="CT0252"
                     /dev_stage="Adult"
                     /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT      140 a    123 c    129 g    144 t
ORIGIN


  Query Match           25.2%;  Score 120.4;  DB 9;  Length 536;
  Best Local Similarity  71.5%;  Pred. No. 2.8e-25;
  Matches  173;  Conservative    0;  Mismatches   66;  Indels    3;  Gaps    1;

Qy     226 tgtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggatataatggatttg 285
           ||||  || || || || |||||||||| ||||||| || ||  || | || |||||| ||
Db       4 TGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCTG 63

Qy     286 tacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcaggaac 345
           ||   |||||||||||| |||||  |||| || |||||||    | ||| ||| |||| |
Db      64 TATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACC 123

Qy     346 tccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaaggaggc 405
           |||||| | |||||||||| ||||| | |||||||||   || |  | |  |  ||| |
Db     124 TCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT---TGCCTCCACCAAGAGAGAC 180

Qy     406 tgtcctctcatccttacccaagaactggggaaagccaacactactgactttgggttaact 465
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Db     181 CAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGACTTAAAT 240
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Qy     466 at 467
           ||
Db     241 AT 242


RESULT  11
AK009787
LOCUS       AK009787               1219 bp    mRNA    linear   HTC 19-JAN-2002
DEFINITION  Mus musculus adult male tongue cDNA, RIKEN full-length enriched
            library, clone:2310043N20:homolog to FIL1 ETA, full insert
            sequence.
ACCESSION   AK009787
VERSION     AK009787.1  GI:12844799
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA,
            clone_lib:RIKEN full-length enriched mouse cDNA library
            clone:2310043N20.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (sites)
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2  (sites)
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3  (sites)
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4  (sites)
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5  (bases 1 to 1219)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
            Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
            Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
            Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
            Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
            Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,
            Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
            Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Gemomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
  COMMENT   Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. cDNA went
            through one round of normalization to Rot = 5.0 and subtraction to
            Rot = 25.0. Second strand cDNA was prepared with the primer adapter
            of sequence [5'
            GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA was cleaved
            with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
            Host: SOLR.
  FEATURES             Location/Qualifiers
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                       /strain="C57BL/6J"
                       /db_xref="MGD:MGI:1901829"
                       /db_xref="taxon:10090"
                       /clone="2310043N20"
                       /sex="male"
                       /tissue_type="tongue"
                       /clone_lib="RIKEN full-length enriched mouse cDNA library"
                       /dev_stage="adult"
       CDS             78. .629
                       /note="data source:SPTR, source key:Q9UHA5, evidence:ISS
                       homolog to FIL1 ETA
                       putative"
                       /codon_start=1
                       /protein_id="BAB26505.1"
                       /db_xref="GI:12844800"
                       /translation="MMAFPPQSCVHVLPPKSIQMWEPNHNTMHGSSQSPRNYRVHDSQ
                       QMVWVLTGNTLTAVPASNNVKPVILSLIACRDTEFQDVKKGNLVFLGIKNRNLCFCCV
                       EMEGKPTLQLKEVDIMNLYKERKAQKAFLFYHGIEGSTSVFQSVLYPGWFIATSSIER
                       QTIILTHQRGKLVNTNFYIESEK"
       polyA_signal    1199. .1204
                       /note="putative"
       polyA_site      1219
                       /note="putative"
  BASE COUNT      380 a    272 c    217 g    350 t
  ORIGIN


    Query Match           25.2%;  Score 120;  DB 11;  Length 1219;
    Best Local Similarity   55.5%;  Pred. No. 5.5e-25;
    Matches  231;  Conservative    0;  Mismatches  185;  Indels    0;  Gaps    0;

  Qy      40 agcattcaggatatcaatcatcgggtgtgggttcttcaggaccagacgctcatagcagtc 99
             ||  |||| ||     | ||   ||| ||||| ||    |   | ||  | | ||||||
  Db     192 AGGGTTCATGACTCACAACAGATGGTATGGGTCCTGACTGGAAATACTTTAACAGCAGTT 251

  Qy     100 ccgaggaaggaccgtatgtctccagtcactattgccttaatctcatgccgacatgtggag 159
             ||    |   ||  | |    || |||| | ||  ||| ||  ||||  || |   |||
  Db     252 CCTGCTAGCAACAATGTCAAGCCTGTCATTCTTAGCTTGATAGCATGTAGAGACACGGAA 311

  Qy     160 accttgagaaagacagagggaaccccatctacctgggcctgaatggactcaatctctgc 219
               ||  ||   | | | ||| || |   | | ||||||  | ||       |||||||||
  Db     312 TTCCAAGATGTAAAGAAAGGTAATCTAGTTTTCCTGGGAATCAAGAACAGAAATCTCTGC 371

  Qy     220 ctgatgtgtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggatataatg 279
               |  |||| | |  | | || | | || ||  |||||||  |||||   || || |||
  Db     372 TTCTGCTGTGTTGAGATGGAGGGCAAACCAACTTTGCAGCTTAAGGAAGTAGACATCATG 431

  Qy     280 gatttgtacaaccaacccgagcctgtgaagtccttttctcttctaccacagccagagtggc 339
             ||||||||||  |     |  |    ||  |||||||  |||||  ||  ||      |||
  Db     432 AATTTGTACAAAGAGAGAAAAGCACAAAAAGCCTTTCTGTTCTATCATGGCATAGAGGGC 491

  Qy     340 aggaactccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaa 399
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Db    492 TCCACTTCTGTCTTTCAGTCAGTCCTCTATCCTGGCTGGTTTATAGCCACCTCTTCCATA 551

Qy    400 ggaggctgtcctctcatccttacccaagaactggggaaagccaacactactgacttt 455
Db    552 GAAAGACAGACAATCATCCTCACACATCAGCGGGGTAAATTGGTTAACACTAACTT 607
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RESULT 12
BF244205
LOCUS BF244205 870 bp mRNA linear EST 14-NOV-2000
DEFINITION 601863146F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4080899 5', mRNA sequence.
ACCESSION BF244205
VERSION BF244205.1 GI:11158135
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 870)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM941 row: k column: 12
High quality sequence stop: 582.
FEATURES Location/Qualifiers
source 1. .870
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4080899"
/clone_lib="NIH_MGC_57"
/tissue_type="glioblastoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
BASE COUNT 256 a 216 c 171 g 227 t
ORIGIN

Query Match 23.7%; Score 113.2; DB 10; Length 870;
Best Local Similarity 58.2%; Pred. No. 5.1e-23;
Matches 199; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

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Qy    136 ttaatctcatgccgacatgtggagacccttgagaaagacagagggaaccccatctacctg 195
Db      5 TTAATAGCCTGTAGAGACACAGAATTCAGTGACAAGGAAAAGGGTAATATGGTTTACCTG 64

Qy    196 ggcctgaatggactcaatctctgcctgatgtgtgctaaagtcggggaccagcccacactg 255
Db     65 GGAATCAAGGGAAAAGATCTCTGTCTCTTCTGTGCAGAAATTCAGGGCAAGCCTACTTTG 124

Qy    256 cagctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtgaagtccttt 315
Db    125 CAGCTTAAGGAAAAAAATATCATGGACCTGTATGTGGAGAAGAAAGCACAGAAGCCCTTT 184

Qy    316 ctcttctaccacagccagagtggcaggaactccaccttcgagtctgtggctttccctggc 375
Db    185 CTCTTTTTCCACAATAAAGAAGGCTCCACTTCTGTCTTTCAGTCAGTCTCTTACCCTGGC 244

Qy    376 tggttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaagaactgggg 435
Db    245 TGGTTCATAGCCACCTCCACCACATCAGGACAGCCCATCTTTCTCACCAAGGAGAGAGGC 304

Qy    436 aaagccaacactactgactttgggttaactatgctgttttaa 477
Db    305 ATAACTAATAACACTAACTTCTACTTAGATTCTGTGGAATAA 346
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RESULT 13
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LOCUS AW753217 434 bp mRNA linear EST 28-APR-2000
DEFINITION RC1-CT0251-081099-011-a04 CT0251 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW753217
VERSION AW753217.1 GI:7668149
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 434)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC1&t2=RC1-CT0251-081099-011-a04&t3=1999-10-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 42
High quality sequence stop: 67.
FEATURES Location/Qualifiers
source 1. .434
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0251"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 125 a 94 c 101 g 114 t
ORIGIN

Query Match 23.3%; Score 111; DB 9; Length 434;
Best Local Similarity 71.6%; Pred. No. 1.6e-22;
Matches 174; Conservative 0; Mismatches 65; Indels 4; Gaps 2;

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Qy    226 tgtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggata-taatggattt 284
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Db     431 TGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATTCATGGATCT 372

Qy     285 gtacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcaggaa 344
           |||   ||||||||||||  |||||  ||||  ||  |||||||     |  |||  |||  ||||
Db     371 GTATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGAC 312

Qy     345 ctccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaaggagg 404
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Db     311 CTCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCAT---TGCCTCCTCCAAGAGAGA 255

Qy     405 ctgtcctctcatccttacccaagaactggggaaagccaacactactgactttgggttaac 464
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Db     254 CCAGCCCATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGAATTAAA 195

Qy     465 tat 467
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Db     194 TAT 192
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RESULT 14
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LOCUS AW361245 560 bp mRNA linear EST 04-FEB-2000
DEFINITION RC1-CT0252-181299-022-e08 CT0252 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW361245
VERSION AW361245.1 GI:6865895
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 560)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC1&t2=RC1-CT0252-
181299-022-e08&t3=1999-12-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 13
High quality sequence stop: 551.
FEATURES Location/Qualifiers
source 1. .560
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0252"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 143 a 131 c 141 g 145 t
ORIGIN

Query Match 20.4%; Score 97.4; DB 9; Length 560;
Best Local Similarity 65.4%; Pred. No. 2.3e-18;
Matches 159; Conservative 0; Mismatches 81; Indels 3; Gaps 1;

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Qy     225 gtgtgctaaagtcggggaccagcccacactgcagctgaaggaaaaggatataatggattt 284
           ||  ||  | |    ||  | |   |    |||||||  |  ||  ||   || ||||||  |
```

```
Db      21 GTATGTGAGAAGGTGGAGCAAAGGCCATATGCAGCTCAGAGAGCAGACGATCATGGATCT 80

Qy     285 gtacaaccaacccgagcctgtgaagtcctttctcttctaccacagccagagtggcaggaa 344
           |||   |  | |||||||  |||||  ||||  ||  ||||||     |  |||  |||  ||||
Db      81 GTATGGCACAACCGAGCCCGTGAAACCCTTCCTTGTCTACCGGGCCAAGACTGGTAGGAC 140

Qy     345 ctccaccttcgagtctgtggctttccctggctggttcatcgctgtcagctctgaaggagg 404
           |||||||  |  ||||||||||  |||||  |  ||||||||||    |  |||  |  |||
Db     141 CTCCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCATCGC---CTCCTCCAAGAGAGA 197

Qy     405 ctgtcctctcatccttacccaagaactggggaaagccaacactactgactttgggttaac 464
           |   ||  ||||  ||  ||   ||||||  |||||  |  |||  ||||  |||||  ||||
Db     198 CCAGCCCATCATTCTGACTTCAGAACTCGGGAAGTCATACAACACTGCCTTTGAATTAAA 257

Qy     465 tat 467
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Db     258 TAT 260
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RESULT 15
BG245180
LOCUS BG245180 1020 bp mRNA linear EST 13-FEB-2001
DEFINITION 602357579F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4486098 5',
mRNA sequence.
ACCESSION BG245180
VERSION BG245180.1 GI:12754995
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1020)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10328 row: n column: 19
High quality sequence start: 4
High quality sequence stop: 653.
FEATURES Location/Qualifiers
source 1. .1020
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4486098"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 282 a 269 c 268 g 201 t
ORIGIN

Query Match 15.7%; Score 74.8; DB 10; Length 1020;
Best Local Similarity 55.9%; Pred. No. 1.9e-11;
Matches 142; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

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Qy     188 tctacctgggcctgaatggactcaatctctgcctgatgtgtgctaaagtcggggaccagc 247
           | | | |||||  |  | ||   |||  ||  ||||||   |||||  ||    ||  ||  |
Db     288 TGTTCTTGGGCATCCACGGGGGCAAGCTGTGCCTGTCTTGTGCCAAGTCTGGAGATGATA 347
```

```
Qy     248 ccacactgcagctgaaggaaaaggatataatggatttgtacaaccaacccgagcctgtga 307
           ||  || |||||| |||||    | || |  ||| ||  |||  |    ||    |  |
Db     348 TCAAGCTCCAGCTGGAGGAAGTTAACATCACTGATCTGAGCAAGAACAAAGAAGAAGACA 407

Qy     308 agtcctttctcttctaccacagccagagtggcaggaactccaccttcgagtctgtggctt 367
           ||  ||||  ||||  || |    |||  |||   | | ||| ||| ||||| |  || |
Db     408 AGCGCTTTACCTTCATCCGCTCTGAGAAAGGCCCCACCACCAGCTTTGAGTCAGCTGCCT 467

Qy     368 tccctggctggttcatcgctgtcagctctgaaggaggctgtcctctcatccttacccaag 427
             || || |||||| ||      |     || |  | | ||||| | | ||| ||| |
Db     468 GTCCAGGATGGTTCCTCTGCACAACACTAGAGGCTGACCGTCCTGTGAGCCTCACCAACA 527

Qy     428 aactggggaaagcc 441
           || ||   |  ||
Db     528 CACCGGAAGAGCCC 541


Search completed: June 21, 2002, 11:09:02
Job time: 17650 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 20, 2002, 15:03:08 ; Search time 73.84 Seconds
(without alignments)
237.671 Million cell updates/sec

Title: US-09-763-498-13
Perfect score: 830
Sequence: 1 MEKALKIDTPQRGSIQDINH.....ILTQELGKANTTDFGLTMLF 158

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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22: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	830	100.0	158	21	AAY70218	Human Interleukin-
2	826	99.5	158	21	AAY70217	Human Interleukin-
3	806	97.1	273	22	AAE03417	Human interleukin-
4	646	77.8	130	22	AAB85001	Human interleukin-
5	466.5	56.2	169	19	AAW63136	Interleukin-1 rece
6	466.5	56.2	169	20	AAY24043	A human SPOIL-I pr
7	466.5	56.2	169	20	AAY24395	Human interleukin-
8	466.5	56.2	169	22	AAE06656	Human interleukin-
9	466.5	56.2	169	22	AAB83008	Human IL-1ra prote
10	466.5	56.2	173	22	AAU16937	Human novel secret
11	466.5	56.2	208	20	AAY24044	A human SPOIL-II p
12	463	55.8	157	22	AAE06662	Mouse interleukin-
13	463	55.8	160	19	AAW86286	Rodent interleukin
14	463	55.8	160	20	AAY24049	Amino acid sequenc
15	459.5	55.4	172	22	AAU17010	Human novel secret
16	459.5	55.4	172	22	AAE09702	Human gene 13 enco
17	389	46.9	170	22	AAB85000	Human interleukin-
18	384	46.3	157	22	AAE04299	Human Interleukin-
19	384	46.3	157	22	AAB50444	Human IL-1 eta. H
20	371	44.7	70	21	AAY70216	Partial human Inte
21	367.5	44.3	134	21	AAB18924	A novel polypeptid
22	367.5	44.3	134	21	AAY96935	Human IL-1 recepto
23	244.5	29.5	98	20	AAY24040	Amino acid sequenc
24	239	28.8	72	19	AAW86285	Rodent interleukin
25	214	25.8	218	21	AAY71084	Human zilla4-E200D
26	211	25.4	176	22	AAB48081	Human extracellula
27	210	25.3	163	21	AAY97069	Human IL-1 recepto
28	210	25.3	167	21	AAY96932	Human IL-1 recepto
29	210	25.3	192	21	AAY95297	Human interleukin-
30	210	25.3	193	21	AAY96934	Processed human IL
31	210	25.3	193	22	AAB87596	Human PRO3435. Ho
32	210	25.3	197	21	AAY95300	Human interleukin-
33	210	25.3	198	22	AAB85138	Interleukin-1 homo
34	210	25.3	203	21	AAY96933	Human IL-1R1a fuse
35	210	25.3	207	21	AAY96938	Human IL-1 recepto
36	210	25.3	218	21	AAB28266	Human interleukin-
37	210	25.3	218	21	AAY96940	Human IL-1 recepto
38	210	25.3	218	21	AAY70927	Human zilla4 prote
39	210	25.3	218	21	AAY95299	Human interleukin-
40	210	25.3	218	21	AAY91885	Primate interleuki
41	210	25.3	218	22	AAG68116	Human interleukin
42	210	25.3	218	22	AAB85136	Interleukin-1 homo
43	210	25.3	218	22	AAB47186	IL-1 related polyp
44	208	25.1	218	21	AAY70933	Human zilla4-E200K
45	205	24.7	218	21	AAY91884	Primate interleuki

ALIGNMENTS

RESULT 1
AAY70218
ID AAY70218 standard; Protein; 158 AA.
XX
AC AAY70218;
XX
DT 06-JUN-2000 (first entry)
XX
DE Human Interleukin-1 epsilon polymorphic variant.
XX
KW Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;
KW gene mapping; immune system; treatment; inflammatory disease;
KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
KW psoriasis; polymorphic variant; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 12
FT /note= "Wild type Gln replaced with Arg"
XX
PN WO200011174-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US18771.
XX
PR 21-AUG-1998; 98US-0097413.
PR 31-AUG-1998; 98US-0098595.
PR 11-SEP-1998; 98US-0099974.
XX
PA (IMMV) IMMUNEX CORP.
XX

PI Sims JE, Smith DE;
XX
DR WPI; 2000-237653/20.
DR N-PSDB; AAZ51248.
XX
PT Nucleotide sequences encoding human interleukin -1 epsilon, useful to
PT treat inflammatory and immune system-related diseases such as
PT rheumatoid arthritis and inflammatory bowel disease -
XX
PS Claim 1b; Fig 2; 76pp; English.
XX
CC The present protein sequence is that of human Interleukin-1 (IL-1)
CC epsilon polymorphic variant. IL-1 epsilon gene is mapped to chromosome 2q
CC and is mainly expressed in spleen, lymph node, thymus, tonsil and
CC leucocyte tissues. IL-1 epsilon is a cytokine, with antiinflammatory,
CC immunosuppressant, antirheumatic, antiarthritic and antipsoriatic
CC activity. It can be used in the treatment of inflammatory or autoimmune
CC diseases such as rheumatoid arthritis, inflammatory bowel disease and
CC psoriasis. The DNA sequence can be used in chromosome identification,
CC gene mapping and study of immune system.
XX
SQ Sequence 158 AA;

Query Match 100.0%; Score 830; DB 21; Length 158;
Best Local Similarity 100.0%; Pred. No. 5.2e-81;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 MEKALKIDTPQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRG 60
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Db       1 mekalkidtpqrgsiqdinhrvwvlqdqtliavprkdrmspvtialiscrhvetlekdrg 60

Qy      61 NPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFES 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 npiylglnglnlclmcakvgdqptlqlkekdimdlynqpepvksflfyhsqsgrnstfes 120

Qy     121 VAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTMLF 158
           ||||||||||||||||||||||||||||||||||||||
Db     121 vafpgwfiavsseggcpliltqelgkanttdfgltmlf 158
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RESULT 2
AAY70217
ID AAY70217 standard; Protein; 158 AA.
XX
AC AAY70217;
XX
DT 06-JUN-2000 (first entry)
XX
DE Human Interleukin-1 epsilon protein.
XX
KW Interleukin-1 epsilon; IL-1; chromosome 2q; cytokine; antiinflammatory;
KW immunosuppressant; antirheumatic; antiarthritic; antipsoriatic;
KW gene mapping; immune system; treatment; inflammatory disease;
KW autoimmune disease; rheumatoid arthritis; inflammatory bowel disease;
KW psoriasis; human.
XX
OS Homo sapiens.
XX
PN WO200011174-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US18771.
XX
PR 21-AUG-1998; 98US-0097413.
PR 31-AUG-1998; 98US-0098595.
PR 11-SEP-1998; 98US-0099974.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Sims JE, Smith DE;
XX

DR WPI; 2000-237653/20.
DR N-PSDB; AAZ51247.
XX
PT Nucleotide sequences encoding human interleukin -1 epsilon, useful to
PT treat inflammatory and immune system-related diseases such as
PT rheumatoid arthritis and inflammatory bowel disease -
XX
PS Claim 1b; Fig 2; 76pp; English.
XX
CC The present sequence is that of human Interleukin-1 (IL-1) epsilon
CC protein. IL-1 epsilon gene is mapped to chromosome 2q and is mainly
CC expressed in spleen, lymph node, thymus, tonsil and leucocyte
CC tissues. IL-1 epsilon is a cytokine, with antiinflammatory,
CC immunosuppressant, antirheumatic, antiarthritic and antipsoriatic
CC activity. It can be used in the treatment of inflammatory or autoimmune
CC diseases such as rheumatoid arthritis, inflammatory bowel disease and
CC psoriasis. The DNA sequence can be used in chromosome identification,
CC gene mapping and study of immune system.
XX
SQ Sequence 158 AA;

Query Match 99.5%; Score 826; DB 21; Length 158;
Best Local Similarity 99.4%; Pred. No. 1.4e-80;
Matches 157; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 MEKALKIDTPQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRG 60
           ||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mekalkidtpqqgsiqdinhrvwvlqdqtliavprkdrmspvtialiscrhvetlekdrg 60

Qy      61 NPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFES 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 npiylglnglnlclmcakvgdqptlqlkekdimdlynqpepvksflfyhsqsgrnstfes 120

Qy     121 VAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTMLF 158
           ||||||||||||||||||||||||||||||||||||||
Db     121 vafpgwfiavsseggcpliltqelgkanttdfgltmlf 158
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RESULT 3
AAE03417
ID AAE03417 standard; Protein; 273 AA.
XX
AC AAE03417;
XX
DT 03-AUG-2001 (first entry)
XX
DE Human interleukin-1 receptor antagonist-like (IL-1ra-L).
XX
KW Human; interleukin-1 receptor antagonist-like protein; IL-1ra-L; therapy;
KW rheumatoid arthritis; psoriatic arthritis; inflammatory arthritis; lupus;
KW joint disease; autoimmune disease; multiple sclerosis; diabetes; obesity;
KW transplant rejection; graft versus host disease; strain; sprain; leprosy;
KW cartilage damage; hepatitis; human immunodeficiency virus; HIV; anorexia;
KW clostridium-associated diarrhoea; pulmonary tuberculosis; septic shock;
KW myopathy; Alzheimer's disease; Parkinson's disease; memory disorder;
KW acute respiratory disease syndrome; cystic fibrosis; asthma; psoriasis;
KW eczema; glomerulonephritis; osteoporosis; Paget's disease; lymphoma;
KW hypercalcaemia; haemorrhage; ischaemia; atherosclerosis; leukaemia;
KW infertility; endometriosis; retinal neuropathy; acute pancreatitis;
KW Kawasaki's disease; cancer.
XX
OS Homo sapiens.
XX
PN WO200141792-A1.
XX
PD 14-JUN-2001.
XX
PF 04-DEC-2000; 2000WO-US32891.
XX
PR 10-DEC-1999; 99US-0170105.
PR 28-NOV-2000; 2000US-0724859.
XX

PA (AMGE-) AMGEN INC.
XX
PI Calzone FJ, Luethy R, Boedigheimer MJ, Zhu J, Chung Y, Jing S;
XX
DR WPI; 2001-381495/40.
DR N-PSDB; AAD06911.
XX
PT Novel Interleukin-1 Receptor Antagonist-Like nucleic acid molecule, the
PT polypeptide encoded by the nucleic acid is useful diagnosis, treatment,
PT and prevention of diseases such as arthritis, diabetes, transplant
PT rejection -
XX
PS Claim 13; Fig 1A; 127pp; English.
XX
CC The present sequence is human interleukin-1 receptor antagonist-like
CC (IL-1ra-L) protein. IL-1ra-L is useful for treating, preventing or
CC ameliorating IL-1ra-L polypeptide-related disease, condition or disorder
CC which include rheumatoid arthritis, psoriatic arthritis, inflammatory
CC arthritis, osteoarthritis, autoimmune disease, multiple sclerosis,
CC lupus, diabetes, transplant rejection, inflammatory joint disease, graft
CC versus host disease and inflammatory conditions resulting from strain,
CC sprain, cartilage damage, trauma, orthopaedic surgery, hepatitis, human
CC immunodeficiency virus (HIV) infection, clostridium-associated
CC diarrhoea, leprosy, pulmonary tuberculosis, septic shock, obesity,
CC anorexia, myopathies, Alzheimer's disease, Parkinson's disease, memory
CC disorders, acute respiratory disease syndrome, cystic fibrosis, asthma,
CC psoriasis, eczema, acute and chronic glomerulonephritis, osteoporosis,
CC Paget's disease, hypercalcaemia, haemorrhage, ischaemia, atherosclerosis,
CC lymphomas, lung and breast cancer, leukaemias, infertility,
CC endometriosis, retinal degeneration, retinal neuropathy, acute
CC pancreatitis and Kawasaki's disease.
XX
SQ Sequence 273 AA;

Query Match 97.1%; Score 806; DB 22; Length 273;
Best Local Similarity 99.4%; Pred. No. 3.9e-78;
Matches 153; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy       5 LKIDTPQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIY 64
          ||||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db     120 lkidtpqrgsiqdinhrvwvlqdqtliavprkdrmspvtialiscrhvetlekdrgdpiy 179

Qy      65 LGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFP 124
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     180 lglnglnlclmcakvgdqptlqlkekdimdlynqpepvksflfyhsqsgrnstfesvafp 239

Qy     125 GWFIAVSSEGGCPLILTQELGKANTTDFGLTMLF 158
          ||||||||||||||||||||||||||||||||
Db     240 gwfiavsseggcpliltqelgkanttdfgltmlf 273
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RESULT 4
AAB85001
ID AAB85001 standard; Protein; 130 AA.
XX
AC AAB85001;
XX
DT 06-AUG-2001 (first entry)
XX
DE Human interleukin-1 receptor antagonist (NOVINTRA C) polypeptide.
XX
KW NOVX; transmembrane protein; NOVTRAN; neuromedin peptide; NOVNEUR;
KW gonadotropin-like protein; NOVGON; interleukin-1; NOVINTRA; human;
KW cytostatic; neuroprotective; reproductive; antiinflammatory; cancer;
KW antibacterial; cerebroprotective; antidiabetic; antiarthritic;
KW antiasthmatic; antiallergic.
XX
OS Homo sapiens.
XX
PN WO200140291-A2.
XX
PD 07-JUN-2001.
XX
PF 06-DEC-2000; 2000WO-US33029.
XX
PR 06-DEC-1999; 99US-0169056.
PR 09-DEC-1999; 99US-0169866.
PR 09-DEC-1999; 99US-0169886.
PR 10-DEC-1999; 99US-0170252.
PR 12-JAN-2000; 2000US-0175740.
PR 05-DEC-2000; 2000US-0170252.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Burgess CE, Prayaga SK, Shimkets RA, Rastelli L, Zerhusen BD;
PI Mezes PS;
XX
DR WPI; 2001-374790/39.
DR N-PSDB; AAF83870.
XX
PT Novel isolated human transmembrane, neuromedin peptide
PT gonadotropin-like protein and interleukin-1 receptor antagonist
PT proteins, useful for treating cancer, immune response disorder,
PT metabolic function disorders -
XX
PS Claim 53; Fig 15B; 138pp; English.
XX
CC The invention provides novel polypeptides (NOVX) selected from human
CC transmembrane protein (NOVTRAN), neuromedin peptide (NOVNEUR),
CC gonadotropin-like protein (NOVGON) and two interleukin-1 receptor
CC antagonist proteins (NOVINTRA A and B). The invention also provides
CC methods in which a NOVX polypeptide, polynucleotide and antibody are
CC used in the detection, prevention and treatment of a broad range of
CC pathological states. NOVTRAN can be used to treat is a cell signaling
CC disorder such as cancer, immune response disorder, hematopoietic
CC disorder, neurodegenerative disorder. NOVNEUR can be used to treat
CC endocrine disorder, muscle disorder, neurologic disorder, cancers of
CC central nervous system, breast, colon, ovary, kidney, prostate and
CC thyroid. NOVGON can be used to treat reproductive development disorder,
CC metabolic function disorder and melanoma. NOVINTRA A and B can be used
CC to treat bone metabolism or structure disorder, inflammatory response
CC disorder, immune regulation disorder, septic shock, stroke, diabetes,
CC arthritis and cancer. The present sequence represents the NOVINTRA C
CC polypeptide.
XX
SQ Sequence 130 AA;

Query Match 77.8%; Score 646; DB 22; Length 130;
Best Local Similarity 95.5%; Pred. No. 2.1e-61;
Matches 126; Conservative 1; Mismatches 1; Indels 4; Gaps 2;

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Qy      17 DINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNGLNLCLMC 76
           |||||||||||||||||||  : ||||||||||||||||||||||||||||||||||||
Db       1 dinhrvwvlqdqtliavprk--vfpvtialiscrhvetlekdrgnpiylglnglnlclmc 58

Qy      77 AKVGDQPTLQLK--EKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEG 134
           ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db      59 akvgdqptlqlklqekdimdlynqpepvksflfyhsqsgrnstfesvafpgwfiavsseg 118

Qy     135 GCPLILTQELGK 146
           ||||||||||||
Db     119 gcpliltqelgk 130
```

RESULT 5
AAW63136
ID AAW63136 standard; Protein; 169 AA.
XX
AC AAW63136;
XX
DT 14-OCT-1998 (first entry)
XX
DE Interleukin-1 receptor antagonist beta (IL-1ra-beta).
XX

KW Interleukin-1 receptor antagonist beta; IL-1ra-beta; IL-1 alpha;
KW IL-1 beta; inflammatory response; treatment; inflammation; septicaemia;
KW cancer; anaemia; arthritis; inflammatory bowel disease;
KW graft vs. host rejection; autoimmunity; stroke; cardiac ischaemia;
KW acute respiratory disease syndrome; psoriasis; restenosis;
KW traumatic brain injury; acquired immune deficiency syndrome;
KW cachexia.
XX
OS Homo sapiens.
XX
PN EP855404-A1.
XX
PD 29-JUL-1998.
XX
PF 27-JAN-1998; 98EP-0300572.
XX
PR 28-JAN-1997; 97US-0790032.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Young PR;
XX
DR WPI; 1998-389778/34.
DR N-PSDB; AAV42659.
XX
PT New nucleic acid encoding human interleukin-1 receptor antagonist
PT beta polypeptides - and related expression systems, transformed
PT cells, proteins, antibodies, agonists and antagonists, useful for
PT treatment, prevention and diagnosis of inflammation, septicaemia,
PT cancer etc
XX
PS Claim 13; Fig 2; 20pp; English.
XX
CC The present sequence represents human Interleukin-1 receptor antagonist
CC beta (IL-ra-beta). IL-1 alpha and IL-1 beta play key roles in
CC inflammatory responses, and are produced as zymogens which are cleaved
CC upon secretion to yield mature carboxyl terminal 17 kD fragments.
CC IL-1ra-beta polypeptides and polynucleotides are useful in treatment of
CC chronic and acute inflammation, septicaemia, cancer, anaemia, arthritis,
CC inflammatory bowel disease, graft vs. host rejection, autoimmunity,
CC stroke, cardiac ischaemia, acute respiratory disease syndrome (ARDS),
CC psoriasis, restenosis, traumatic brain injury, acquired immune
CC deficiency syndrome (AIDS) and cachexia. These conditions (or
CC susceptibility to them) may be diagnosed by detecting mutations in the
CC IL-1ra-beta coding sequence analysing a sample for presence or amount
CC of IL-1ra-beta.
XX
SQ Sequence 169 AA;

```
  Query Match             56.2%;  Score 466.5;  DB 19;  Length 169;
  Best Local Similarity   59.9%;  Pred. No. 5.1e-42;
  Matches   88;  Conservative   24;  Mismatches   34;  Indels    1;  Gaps    1;

Qy      10 PQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNG 69
           |  |:| |:| :|| || | |:|||| | ::|||:|:|:|:: | ||: ||:|||||:
Db      22 pitgtindlnqqvwtlqgqnlvavprsdsvtpvtvavitckypealeqgrgdpiylgiqn 81

Qy      70 LNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIA 129
             :|| | |||:||||||||: ||||| |||||| |||| :::|| || |||||| ||||
Db      82 pemclycekvgeqptlqlkeqkimdlygqpepvkpflfyraktgrtstlesvafpdwfia 141

Qy     130 VSSEGGCPLILTQELGKANTTDFGLTM 156
           ||:   |:||| ||||:  | | | :
Db     142 -sskrdqpiiltselgksyntafelni 167
```

RESULT 6
AAY24043
ID AAY24043 standard; Protein; 169 AA.
XX
AC AAY24043;
XX

DT 30-SEP-1999 (first entry)
XX
DE A human SPOIL-I protein (also known as hTANGO 080-I).
XX
KW SPOIL-I; interleukin-1 receptor antagonist; IL-1ra; modulating agent;
KW bone metabolism disorder; proinflammatory disorder; immune disorder;
KW inflammatory disease; septic shock; stroke; diabetes; arthritis;
KW intercolitis; pneumonitis; epithelial cell; skin disease;
KW proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;
KW epithelial cancer; squamous cell carcinoma; bone resorption disorder;
KW osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;
KW osteogenesis imperfecta; fibrous displasia; hypophosphatasia;
KW bone sarcoma; myeloma bone disorder; osteolytic bone lesion;
KW hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;
KW bone fracture; hTANGO 80-I.
XX
OS Homo sapiens.
XX
PN WO9937662-A1.
XX
PD 29-JUL-1999.
XX
PF 26-JAN-1999; 99WO-US01575.
XX
PR 27-JAN-1998; 98US-0013810.
XX
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI Busfield SJ;
XX
DR WPI; 1999-458675/38.
DR N-PSDB; AAX86458.
XX
PT New isolated SPOIL proteins, used to develop products for treating,
PT e.g. inflammatory and immune disorders
XX
PS Example 1; Fig 4A-B; 126pp; English.
XX
CC The present sequence represents a SPOIL-I protein. SPOIL proteins have
CC homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.
CC The SPOIL proteins are used as modulating agents in regulating a variety
CC of cellular processes. The products can be used for treating disorders
CC characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone
CC metabolism disorder, a proinflammatory disorder or an immune disorder.
CC They can be used for treating e.g. inflammatory diseases and disorders
CC e.g. inflammation, septic shock, stroke, diabetes, arthritis,
CC intercolitis and pneumonitis, epithelial cell and/or skin diseases and
CC disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma
CC and Kaposi's sarcoma and other epithelial cancers including squamous cell
CC carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and
CC bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's
CC disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,
CC fibrous displasia, hypophosphatasia, bone sarcoma, myeloma bone disorder
CC (e.g. osteolytic bone lesions) and hypercalcemia. SPOIL molecules and
CC SPOIL modulators are useful for regulation of bone mass (e.g. increase in
CC bone mass and/or inhibit bone loss), management of bone fragility (e.g.
CC decrease bone fragility); and prevention and/or treatment of bone pain,
CC bone deformities and/or bone fractures. The products can also be used for
CC detection, diagnosis and screening assays.
XX
SQ Sequence 169 AA;

```
  Query Match             56.2%;  Score 466.5;  DB 20;  Length 169;
  Best Local Similarity   59.9%;  Pred. No. 5.1e-42;
  Matches   88;  Conservative   24;  Mismatches   34;  Indels    1;  Gaps    1;

Qy      10 PQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNG 69
           |  |:| |:| :|| || | |:|||| | ::|||:|:|:|:: | ||: ||:|||||:
Db      22 pitgtindlnqqvwtlqgqnlvavprsdsvtpvtvavitckypealeqgrgdpiylgiqn 81

Qy      70 LNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIA 129
             :|| | |||:||||||||: ||||| |||||| |||| :::|| || |||||| ||||
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```
Db      82 pemclycekvgeqptlqlkeqkimdlygqpepvkpflfyraktgrtstlesvafpdwfia 141

Qy     130 VSSEGGCPLILTQELGKANTTDFGLTM 156
           ||:   |:||| ||||:  | | | :
Db     142 -sskrdqpiiltselgksyntafelni 167


RESULT   7
AAY24395
ID   AAY24395 standard; Protein; 169 AA.
XX
AC   AAY24395;
XX
DT   20-SEP-1999  (first entry)
XX
DE   Human interleukin-1 receptor antagonist beta.
XX
KW   Human; interleukin-1 receptor antagonist beta; IL-1RA beta; septicemia;
KW   chronic inflammation; acute inflammation; arthritis; autoimmunity;
KW   inflammatory bowel disease; graft vs. host disease; stroke; psoriasis;
KW   cardiac ischaemia; acute respiratory disease syndrome; ARDS; restenosis;
KW   traumatic brain injury; AIDS; cachexia; allergy; parasite infection;
KW   allergic rhinitis; allergic asthma; atopic dermatitis; gene therapy;
KW   allergic inflammatory disease; delayed hypersensitivity; vaccine.
XX
OS   Homo sapiens.
XX
PN   WO9936541-A1.
XX
PD   22-JUL-1999.
XX
PF   14-JAN-1999;   99WO-US00847.
XX
PR   29-APR-1998;   98US-0069619.
PR   14-JAN-1998;   98US-0007464.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Marshall L,  Young PR;
XX
DR   WPI; 1999-430615/36.
DR   N-PSDB; AAX90135.
XX
PT   New interleukin-1 receptor antagonist beta, useful for treating
PT   inflammation and autoimmune diseases
XX
PS   Claim 15; Fig 1; 34pp; English.
XX
CC   The present sequence represents human interleukin-1 receptor antagonist
CC   beta (IL-1RA beta). IL-1RA beta polypeptides and polynucleotides are
CC   useful for diagnosing diseases (or susceptibility to diseases) related
CC   to the expression or activity of IL-1RA beta, by determining mutations
CC   in the IL-1RA beta nucleic acid sequences and/or analysing for the
CC   presence or amount of IL-1RA beta polypeptide. IL-1RA beta polypeptides
CC   are also useful for screening for compounds which affect activity of the
CC   protein. These can be used in treatment to inhibit (antagonist) or
CC   enhance (agonist) IL-1RA beta activity, in addition to direct
CC   administration of IL-1RA beta polypeptides to treat conditions, or
CC   direct administration of antisense sequences to prevent expression.
CC   IL-1RA beta polypeptides (administered directly, in a vector i.e. gene
CC   therapy, and as a vaccine) and antibodies induce an immune response to
CC   immunise and prevent disease. Diseases diagnosed, prevented or treated
CC   include chronic and acute inflammation, septicemia, arthritis,
CC   inflammatory bowel disease, graft vs. host disease, autoimmunity,
CC   stroke, cardiac ischaemia, acute respiratory disease syndrome (ARDS),
CC   psoriasis, restenosis, traumatic brain injury, AIDS, cachexia, allergy,
CC   parasite infection, allergic rhinitis, allergic asthma, atopic
CC   dermatitis, allergic inflammatory diseases and delayed hypersensitivity.
XX
SQ   Sequence   169 AA;

  Query Match          56.2%;  Score 466.5;  DB 20;  Length 169;
  Best Local Similarity   59.9%;  Pred. No. 5.1e-42;
  Matches   88;  Conservative   24;  Mismatches   34;  Indels    1;  Gaps    1;

Qy      10 PQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNG 69
           |  |:| |:| :|| || | |:|||| | ::|||:|:|:|:: | ||: ||:|||||:
Db      22 pitgtindlnqqvwtlqgqnlvavprsdsvtpvtvavitckypealeqgrgdpiylgiqn 81

Qy      70 LNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIA 129
             :|| | |||:||||||||: ||||| |||||| |||| :::|| || |||||| ||||
Db      82 pemclycekvgeqptlqlkeqkimdlygqpepvkpflfyraktgrtstlesvafpdwfia 141

Qy     130 VSSEGGCPLILTQELGKANTTDFGLTM 156
           ||:   |:||| ||||:  | | | :
Db     142 -sskrdqpiiltselgksyntafelni 167


RESULT   8
AAE06656
ID   AAE06656 standard; Protein; 169 AA.
XX
AC   AAE06656;
XX
DT   16-OCT-2001  (first entry)
XX
DE   Human interleukin-1epsilon (IL-1epsilon) protein.
XX
KW   Human; interleukin-1epsilon; IL-1epsilon; virucide; hepatotropic; fever;
KW   immunological disorder; tumour; inflammatory disorder; hypoglycaemia;
KW   autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;
KW   psoriasis; viral infection; allergy; cytokine; HIV; drug screening.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Binding-site    17..20
FT                   /note= "IL-1 receptor beta subunit binding region"
FT   Binding-site    23
FT                   /note= "IL-1 receptor beta subunit binding region"
FT   Region          23..27
FT                   /note= "Beta sheet region"
FT   Binding-site    28
FT                   /note= "IL-1 receptor alpha subunit binding region"
FT   Binding-site    30..32
FT                   /note= "IL-1 receptor alpha subunit binding region"
FT   Region          34..36
FT                   /note= "Beta sheet region"
FT   Binding-site    36..38
FT                   /note= "IL-1 receptor alpha subunit binding region"
FT   Region          42..45
FT                   /note= "Beta sheet region"
FT   Binding-site    43
FT                   /note= "IL-1 receptor alpha subunit binding region"
FT   Binding-site    45..50
FT                   /note= "IL-1 receptor alpha subunit binding region"
FT   Binding-site    52
FT                   /note= "IL-1 receptor alpha subunit binding region"
FT   Region          56..61
FT                   /note= "Beta sheet region"
FT   Binding-site    61
FT                   /note= "IL-1 receptor beta subunit binding region"
FT   Binding-site    63
FT                   /note= "IL-1 receptor beta subunit binding region"
FT   Binding-site    68
FT                   /note= "IL-1 receptor beta subunit binding region"
FT   Binding-site    70..71
FT                   /note= "IL-1 receptor beta subunit binding region"
FT   Binding-site    73
FT                   /note= "IL-1 receptor beta subunit binding region"
FT   Binding-site    73..97
FT                   /note= "IL-1 receptor alpha subunit binding region"
FT   Region          74..79
FT                   /note= "Beta sheet region"
FT   Region          84..89
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FT                   /note= "Beta sheet region"
FT   Region          96..101
FT                   /note= "Beta sheet region"
FT   Binding-site    110..112
FT                   /note= "IL-1 receptor beta subunit binding region"
FT   Region          117..122
FT                   /note= "Beta sheet region"
FT   Binding-site    121
FT                   /note= "IL-1 receptor beta subunit binding region"
FT   Binding-site    123..124
FT                   /note= "IL-1 receptor beta subunit binding region"
FT   Binding-site    126..127
FT                   /note= "IL-1 receptor beta subunit binding region"
FT   Region          129..132
FT                   /note= "Beta sheet region"
FT   Region          138..142
FT                   /note= "Beta sheet region"
FT   Binding-site    144..145
FT                   /note= "IL-1 receptor alpha subunit binding region"
FT   Binding-site    147..148
FT                   /note= "IL-1 receptor alpha subunit binding region"
FT   Region          148..152
FT                   /note= "Beta sheet region"
FT   Region          159..167
FT                   /note= "Beta sheet region"
FT   Binding-site    164
FT                   /note= "IL-1 receptor alpha subunit binding region"
FT   Binding-site    166
FT                   /note= "IL-1 receptor alpha subunit binding region"
FT   Binding-site    167
FT                   /note= "IL-1 receptor beta subunit binding region"
FT   Binding-site    169
FT                   /note= "IL-1 receptor beta subunit binding region"
XX
PN   WO200157219-A2.
XX
PD   09-AUG-2001.
XX
PF   01-FEB-2001; 2001WO-US03285.
XX
PR   02-FEB-2000; 2000US-0179638.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Debets JEMA,  Timans JC,  Bazan JF,  Kastelein RA;
XX
DR   WPI; 2001-488886/53.
DR   N-PSDB; AAD12296.
XX
PT   Novel isolated or recombinant antigenic interleukin-1 delta or epsilon
PT   polypeptide useful for treating conditions exhibiting abnormal
PT   expression of interleukin such as immunological disorders, tumor and
PT   allergy -
XX
PS   Claim 18; Fig 1; 103pp; English.
XX
CC   The invention relates to recombinant antigenic interleukin-1 like
CC   molecules and their corresponding nucleic acid sequences, designated
CC   as interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon).
CC   IL-1delta and IL-1epsilon are useful for treating conditions exhibiting
CC   abnormal expression of the interleukin such as immunological disorders,
CC   tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis,
CC   allergy, autoimmune diseases and infectious diseases (e.g., pulmonary
CC   tuberculosis, leprosy, fulminant hepatitis, and viral infections such as
CC   HIV). The invention also relates to methods of using the composition
CC   containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic
CC   utilities. IL-1delta is used as an immunogen for the production of
CC   antisera or antibodies specific, e.g., capable of distinguishing between
CC   IL-1 family members and an IL-1delta, for the interleukin or its
CC   fragment. The purified interleukin is used as a reagent to detect any
CC   antibodies generated in response to the presence of elevated levels of
CC   expression, or immunological disorders which lead to antibody production
CC   to the endogenous cytokine. The invention also contemplates the use of
CC   competitive drug screening assays. The present sequence is human
CC   interleukin-1epsilon (IL-1epsilon) protein.
XX
SQ   Sequence   169 AA;


  Query Match             56.2%;  Score 466.5;  DB 22;  Length 169;
  Best Local Similarity   59.9%;  Pred. No. 5.1e-42;
  Matches   88;  Conservative   24;  Mismatches   34;  Indels    1;  Gaps    1;

Qy      10 PQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNG 69
           |  |:| |:| :|| || | |:|||| | ::|||:|:|:|:: | ||: ||:|||||:
Db      22 pitgtindlnqqvwtlqgqnlvavprsdsvtpvtvavitckypealeqgrgdpiylgiqn 81

Qy      70 LNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIA 129
             :|| | |||:||||||||: ||||| |||||| |||| :::|| || |||||| ||||
Db      82 pemclycekvgeqptlqlkeqkimdlygqpepvkpflfyraktgrtstlesvafpdwfia 141

Qy     130 VSSEGGCPLILTQELGKANTTDFGLTM 156
           ||:   |:||| ||||:  | | | :
Db     142 -sskrdqpiiltselgksyntafelni 167


RESULT   9
AAB83008
ID   AAB83008 standard; protein; 169 AA.
XX
AC   AAB83008;
XX
DT   21-JUN-2001  (first entry)
XX
DE   Human IL-1ra protein.
XX
KW   Human; IL-1ra; interleukin-1 receptor antagonist; antibacterial;
KW   immunosuppressive; antiinflammatory; antiarthritic; nephrotropic;
KW   hepatotropic; virucide; cardiant; vasotropic; antidiabetic; cancer;
KW   neuroprotective; osteopathic; cytostatic; immunomodulator; nootropic;
KW   cerebroprotective; antidepressant; antiarteriosclerotic; infection;
KW   immune disease; autoimmune disease; bone disease; neuronal disease;
KW   cardiovascular disease.
XX
OS   Homo sapiens.
XX
PN   WO200119390-A1.
XX
PD   22-MAR-2001.
XX
PF   28-AUG-2000; 2000WO-IB01192.
XX
PR   14-SEP-1999;   99US-0154010.
XX
PA   (PFIZ ) PFIZER PROD INC.
XX
PI   Littman BH,  Woodworth TLG,  Dombroski MA;
XX
DR   WPI; 2001-327986/34.
XX
PT   Synergistic treatment of interleukin (IL)-mediated diseases, useful for
PT   e.g. septic shock, comprises adjunctively administering IL-1 receptor
PT   antagonist polypeptide and non-steroidal IL-1 processing and release
PT   inhibiting agent -
XX
PS   Disclosure; Page 91; 112pp; English.
XX
CC   The present sequence is a human interleukin-1 receptor antagonist
CC   (IL-1ra). The present sequence or its variant may be administered
CC   in combination with a non-steroidal IL-1 processing and release
CC   inhibiting agent for the treatment or prevention of IL-mediated disease
CC   states. The composition is useful for treating inappropriate host
CC   responses to infectious diseases where active infection exists at any
CC   body site, e.g. septic shock, disseminated intravascular coagulation,
CC   and/or adult respiratory distress syndrome; acute or chronic
CC   inflammation due to antigen, antibody and/or complement deposition;
```

CC inflammatory conditions including arthritis, cholangitis, colitis,
CC encephalitis, endocarditis, glomerulonephritis, hepatitis, myocarditis,
CC pancreatitis, pericarditis, and reperfusion injury vasculitis. It is
CC also useful for treating immune-based diseases including conditions
CC involving T cells and/or macrophages e.g. acute and delayed
CC hypersensitivity, graft rejection, graft-versus-host disease;
CC autoimmune diseases including Type 1 diabetes mellitus and multiple
CC sclerosis. The composition may be used for treating bone and cartilage
CC resorption as well as diseases resulting in excess deposition of
CC extracellular matrix. Such diseases include osteoporosis, periodontal
CC diseases, interstitial pulmonary fibrosis, cirrhosis, systemic sclerosis
CC and keloid formation. It is also useful for treating tumours which
CC produce IL-1 as an autocrine growth factor and for preventing the
CC cachexia associated with certain tumours. It may be used for
CC treating neuronal diseases with an inflammatory component e.g.
CC Alzheimer's disease, stroke, depression and percussion injury and for
CC cardiovascular diseases in which recruitment of monocytes into the
CC subendothelial space plays a role, e.g. the development of
CC atherosclerotic plaques.
XX
SQ Sequence 169 AA;

Query Match 56.2%; Score 466.5; DB 22; Length 169;
Best Local Similarity 59.9%; Pred. No. 5.1e-42;
Matches 88; Conservative 24; Mismatches 34; Indels 1; Gaps 1;

```
Qy      10 PQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNG 69
           |  |:| |:| :|| || | |:|||| | ::|||:|:|:|:: | ||: ||:||||||:
Db      22 pitgtindlnqqvwtlqgqnlvavprsdsvtpvtvavitckypealeqgrgdpiylgiqn 81

Qy      70 LNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIA 129
             :|| | |||:||||||||: ||||| |||||| |||| :::|| || |||||| ||||
Db      82 pemclycekvgeqptlqlkeqkimdlygqpepvkpflfyraktgrtstlesvafpdwfia 141

Qy     130 VSSEGGCPLILTQELGKANTTDFGLTM 156
             ||:   |:||| ||||:  | | | :
Db     142 -sskrdqpiiltselgksyntafelni 167
```

RESULT 10
AAU16937
ID AAU16937 standard; Protein; 173 AA.
XX
AC AAU16937;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human novel secreted protein, SEQ ID 178.
XX
KW Human; immunosuppressive; antiarthritic; antirheumatic;
KW cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;
KW neuroprotective; antibacterial; virucide; fungicide; opthalmalogical;
KW vulnerary; secreted protein; rheumatoid arthritis;
KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;
KW corneal infection; wound healing; epithelial cell proliferation;
KW skin ageing; food additive; preservative; antiproliferative.
XX
OS Homo sapiens.
XX
PN WO200155441-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01320.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.

PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-476222/51.
DR N-PSDB; AAS26842.
XX
PT Novel polypeptides and polynucleotides useful as diagnostic reagents to
PT diagnose diseases or disorders associated with aberrant expression or
PT activity of polypeptides, for treating blood clotting disorder,
PT haemophilia -
XX
PS Claim 11; SEQ ID No 178; 601pp; English.
XX

CC The invention relates to isolated nucleic acid molecules and their
CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They
CC are also used in diagnosing a pathological condition or susceptibility
CC to a pathological condition. Antibodies to the proteins can also
CC be used in alleviating symptoms associated with the disorders and in
CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked
CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated
CC include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi
CC and ocular disorders e.g. corneal infection, and many other
CC disorders listed in the specification. The polypeptides can also
CC be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present

Query Match 56.2%; Score 466.5; DB 22; Length 173;
Best Local Similarity 59.9%; Pred. No. 5.3e-42;
Matches 88; Conservative 24; Mismatches 34; Indels 1; Gaps 1;

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Qy      10 PQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNG 69
           |  |:| |:| :|| || | |:|||| | ::|||:|:|:|:: | ||: ||:|||||:
Db      26 pitgtindlnqqvwtlqgqnlvavprsdsvtpvtvavitckypealeqgrgdpiylgiqn 85

Qy      70 LNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIA 129
             :|| | |||:|||||||: ||||| |||||| |||| :::|| || ||||||  ||||
Db      86 pemclycekvgeqptlqlkeqkimdlygqpepvkpflfyraktgrtstlesvafpdwfia 145

Qy     130 VSSEGGCPLILTQELGKANTTDFGLTM 156
             ||:   |:||| ||||:  | | | :
Db     146 -sskrdqpiiltselgksyntafelni 171
```

RESULT 11
AAY24044
ID AAY24044 standard; Protein; 208 AA.
XX
AC AAY24044;
XX
DT 30-SEP-1999 (first entry)
XX
DE A human SPOIL-II protein (also known as hTANGO 080-II).
XX
KW SPOIL-II; interleukin-1 receptor antagonist; IL-1ra; modulating agent;
KW bone metabolism disorder; proinflammatory disorder; immune disorder;
KW inflammatory disease; septic shock; stroke; diabetes; arthritis;
KW intercolitis; pneumonitis; epithelial cell; skin disease;
KW proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;
KW epithelial cancer; squamous cell carcinoma; bone resorption disorder;
KW osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;
KW osteogenesis imperfecta; fibrous displasia; hypophosphatasia;
KW bone sarcoma; myeloma bone disorder; osteolytic bone lesion;
KW hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;
KW bone fracture; hTANGO 80-I.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 98..724
FT /*tag= a
FT /product= SPOIL-II
XX
PN WO9937662-A1.
XX
PD 29-JUL-1999.

XX
PF 26-JAN-1999; 99WO-US01575.
XX
PR 27-JAN-1998; 98US-0013810.
XX
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI Busfield SJ;
XX
DR WPI; 1999-458675/38.
DR N-PSDB; AAX86459.
XX
PT New isolated SPOIL proteins, used to develop products for treating,
PT e.g. inflammatory and immune disorders
XX
PS Claim 8; Fig 5; 126pp; English.
XX
CC The present sequence represents a SPOIL-II protein. SPOIL proteins have
CC homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.
CC The SPOIL proteins are used as modulating agents in regulating a variety
CC of cellular processes. The products can be used for treating disorders
CC characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone
CC metabolism disorder, a proinflammatory disorder or an immune disorder.
CC They can be used for treating e.g. inflammatory diseases and disorders
CC e.g. inflammation, septic shock, stroke, diabetes, arthritis,
CC intercolitis and pneumonitis, epithelial cell and/or skin diseases and
CC disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma
CC and Kaposi's sarcoma and other epithelial cancers including squamous cell
CC carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and
CC bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's
CC disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,
CC fibrous displasia, hypophosphatasia, bone sarcoma, myeloma bone disorder
CC (e.g. osteolytic bone lesions) and hypercalcemia. SPOIL molecules and
CC SPOIL modulators are useful for regulation of bone mass (e.g. increase in
CC bone mass and/or inhibit bone loss), management of bone fragility (e.g.
CC decrease bone fragility); and prevention and/or treatment of bone pain,
CC bone deformities and/or bone fractures. The products can also be used for
CC detection, diagnosis and screening assays.
XX
SQ Sequence 208 AA;

Query Match 56.2%; Score 466.5; DB 20; Length 208;
Best Local Similarity 59.9%; Pred. No. 6.7e-42;
Matches 88; Conservative 24; Mismatches 34; Indels 1; Gaps 1;

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Qy      10 PQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNG 69
           |  |:| |:| :|| || | |:|||| | ::|||:|:|:|:: | ||: ||:|||||:
Db      61 pitgtindlnqqvwtlqgqnlvavprsdsvtpvtvavitckypealeqgrgdpiylgiqn 120

Qy      70 LNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIA 129
             :|| | |||:||||||||: ||||| |||||| |||| :::|| || |||||| ||||
Db     121 pemclycekvgeqptlqlkeqkimdlygqpepvkpflfyraktgrtstlesvafpdwfia 180

Qy     130 VSSEGGCPLILTQELGKANTTDFGLTM 156
           ||:   |:||| ||||:  | | | :
Db     181 -sskrdqpiiltselgksyntafelni 206
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RESULT 12
AAE06662
ID AAE06662 standard; Protein; 157 AA.
XX
AC AAE06662;
XX
DT 16-OCT-2001 (first entry)
XX
DE Mouse interleukin-1epsilon (IL-1epsilon) protein.
XX
KW Mouse; interleukin-1epsilon; IL-1epsilon; virucide; hepatotropic; fever;
KW immunological disorder; tumour; inflammatory disorder; hypoglycaemia;
KW autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;
KW psoriasis; viral infection; allergy; cytokine; HIV; drug screening.
XX
OS Mus sp.
XX
PN WO200157219-A2.
XX
PD 09-AUG-2001.
XX
PF 01-FEB-2001; 2001WO-US03285.
XX
PR 02-FEB-2000; 2000US-0179638.
XX
PA (SCHE) SCHERING CORP.
XX
PI Debets JEMA, Timans JC, Bazan JF, Kastelein RA;
XX
DR WPI; 2001-488886/53.
XX
PT Novel isolated or recombinant antigenic interleukin-1 delta or epsilon
PT polypeptide useful for treating conditions exhibiting abnormal
PT expression of interleukin such as immunological disorders, tumor and
PT allergy -
XX
PS Disclosure; Fig 1; 103pp; English.
XX
CC The invention relates to recombinant antigenic interleukin-1 like
CC molecules and their corresponding nucleic acid sequences, designated
CC as interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon).
CC IL-1delta and IL-1epsilon are useful for treating conditions exhibiting
CC abnormal expression of the interleukin such as immunological disorders,
CC tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis,
CC allergy, autoimmune diseases and infectious diseases (e.g., pulmonary
CC tuberculosis, leprosy, fulminant hepatitis, and viral infections such as
CC HIV). The invention also relates to methods of using the composition
CC containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic
CC utilities. IL-1delta is used as an immunogen for the production of
CC antisera or antibodies specific, e.g., capable of distinguishing between
CC IL-1 family members and an IL-1delta, for the interleukin or its
CC fragment. The purified interleukin is used as a reagent to detect any
CC antibodies generated in response to the presence of elevated levels of
CC expression, or immunological disorders which lead to antibody production
CC to the endogenous cytokine. The invention also contemplates the use of
CC competitive drug screening assays. The present sequence is mouse
CC interleukin-1epsilon (IL-1epsilon) protein related to the invention.
XX
SQ Sequence 157 AA;

Query Match 55.8%; Score 463; DB 22; Length 157;
Best Local Similarity 54.5%; Pred. No. 1.1e-41;
Matches 85; Conservative 30; Mismatches 41; Indels 0; Gaps 0;

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Qy       2 EKALKIDTPQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGN 61
             || |:  :|    :||:: |||:||:  | |||||::  |||| |: |::::||| :||:
Db       1 ekelraaspslrhvqdlssrvwilqnniltavprkeqtvpvtitllpcqyldtletnrgd 60

Qy      62 PIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESV 121
             | |:|:     || | | |:|| ||| | :||::||: |||||: |||| :||  |||||
Db      61 ptymgvqrpmsclfctkdgeqpvlqlgegnimemynkkepvkaslfyhkksgttstfesa 120

Qy     122 AFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
           |||||||| |:| ||||||||||:   ||| : ::
Db     121 afpgwfiavcskgscpliltqelgeifitdfemivv 156
```

RESULT 13
AAW86286
ID AAW86286 standard; Protein; 160 AA.
XX
AC AAW86286;
XX
DT 19-FEB-1999 (first entry)
XX
DE Rodent interleukin (IL)-1 epsilon polypeptide.

```
XX
KW   Interleukin; IL-1 delta; polyclonal antibody; IL-1 epsilon; cytokine;
KW   inflammatory response; immune system; diagnosis; agonist; antagonist;
KW   chemokine.
XX
OS   Mus sp.
XX
PN   WO9847921-A1.
XX
PD   29-OCT-1998.
XX
PF   17-APR-1998;   98WO-US06879.
XX
PR   06-AUG-1997;   97US-0055111.
PR   21-APR-1997;   97US-0837627.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Bazan JF,  Hedrick JA,  Kastelein RA,  Sana TR;
XX
DR   WPI; 1998-609976/51.
DR   N-PSDB; AAV71960.
XX
PT   Mammalian interleukin 1-delta and 1-epsilon - useful for, e.g.
PT   regulating the immune system and inflammatory responses
XX
PS   Claim 1; Pages 92-93; 113pp; English.
XX
CC   This represents a rodent interleukin (IL)-1 epsilon polypeptide. The
CC   invention relates to a recombinant polypeptide that specifically binds
CC   polyclonal antibodies (Abs) generated against a 12 consecutive amino acid
CC   segment of IL-1 delta or IL-1 epsilon. Agonists or antagonists of these
CC   IL polypeptides are used to regulate a cell involved in an inflammatory
CC   response. The IL-1 delta or IL-1 epsilon polypeptides and peptides are
CC   used to produce Abs and antigen-Ab complexes. The polypeptides, Abs and
CC   the corresponding nucleic acids regulate development and/or the immune
CC   system, and can be used to diagnose and treat conditions associated with
CC   abnormal expression of IL. Agonists or antagonists of IL-1 delta or IL-1
CC   epsilon polypeptides are used with agonists or antagonists of IL-1 alpha,
CC   IL-1RA, IL-1 beta, IL-1 gamma, IL-2 and/or IL-12. The IL-1 delta or IL-1
CC   epsilon polypeptides may be used as a soluble polypeptide or as a fusion
CC   protein with another cytokine or chemokine.
XX
SQ   Sequence   160 AA;
```

```
  Query Match             55.8%;  Score 463;  DB 19;  Length 160;
  Best Local Similarity   54.5%;  Pred. No. 1.1e-41;
  Matches   85;  Conservative   30;  Mismatches   41;  Indels    0;  Gaps    0;

Qy       2 EKALKIDTPQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGN 61
           || |:  :|    :||:: |||:||:  | |||||::  |||| |: |:::::||| :||:
Db       4 ekelraaspslrhvqdlssrvwilqnniltavprkeqtvpvtitllpcqyldtletnrgd 63

Qy      62 PIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESV 121
           | |:|:     || | | |:|| ||| | :||::||: |||||: |||| :||  |||||
Db      64 ptymgvqrpmsclfctkdgeqpvlqlgegnimemynkkepvkaslfyhkksgttstfesa 123

Qy     122 AFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
           ||||||||| |:| |||||||||:   ||| : ::
Db     124 afpgwfiavcskgscpliltqelgeifitdfemivv 159
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```
RESULT  14
AAY24049
ID   AAY24049 standard; Protein; 160 AA.
XX
AC   AAY24049;
XX
DT   30-SEP-1999  (first entry)
XX
DE   Amino acid sequence of a murine SPOIL-II protein.
XX
```

```
KW   SPOIL-II; interleukin-1 receptor antagonist; IL-1ra; modulating agent;
KW   bone metabolism disorder; proinflammatory disorder; immune disorder;
KW   inflammatory disease; septic shock; stroke; diabetes; arthritis;
KW   intercolitis; pneumonitis; epithelial cell; skin disease;
KW   proliferative disorder; skin cancer; melanoma; Kaposi's sarcoma;
KW   epithelial cancer; squamous cell carcinoma; bone resorption disorder;
KW   osteoporosis; Paget's disease; osteoarthritis; degenerative arthritis;
KW   osteogenesis imperfecta; fibrous displasia; hypophosphatasia;
KW   bone sarcoma; myeloma bone disorder; osteolytic bone lesion;
KW   hypercalcemia; bone mass; bone fragility; bone pain; bone deformity;
KW   bone fracture.
XX
OS   Mus sp.
XX
PN   WO9937662-A1.
XX
PD   29-JUL-1999.
XX
PF   26-JAN-1999;   99WO-US01575.
XX
PR   27-JAN-1998;   98US-0013810.
XX
PA   (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI   Busfield SJ;
XX
DR   WPI; 1999-458675/38.
DR   N-PSDB; AAX86460.
XX
PT   New isolated SPOIL proteins, used to develop products for treating,
PT   e.g. inflammatory and immune disorders
XX
PS   Claim 8; Fig 6; 126pp; English.
XX
CC   The present sequence represents a SPOIL-II protein. SPOIL proteins have
CC   homology to interleukin-1 (IL-1) receptor antagonist (IL-1ra) molecules.
CC   The SPOIL proteins are used as modulating agents in regulating a variety
CC   of cellular processes. The products can be used for treating disorders
CC   characterized by aberrant SPOIL and/or IL-1 expression, e.g. a bone
CC   metabolism disorder, a proinflammatory disorder or an immune disorder.
CC   They can be used for treating e.g. inflammatory diseases and disorders
CC   e.g. inflammation, septic shock, stroke, diabetes, arthritis,
CC   intercolitis and pneumonitis, epithelial cell and/or skin diseases and
CC   disorders, e.g. proliferative disorders (e.g. skin cancers e.g. melanoma
CC   and Kaposi's sarcoma and other epithelial cancers including squamous cell
CC   carcinoma, oesophageal cancer and cancer of the mouth and/or throat); and
CC   bone-related and/or bone resorption disorders e.g. osteoporosis, Paget's
CC   disease, osteoarthritis, degenerative arthritis, osteogenesis imperfecta,
CC   fibrous displasia, hypophosphatasia, bone sarcoma, myeloma bone disorder
CC   (e.g. osteolytic bone lesions) and hypercalcemia. SPOIL molecules and
CC   SPOIL modulators are useful for regulation of bone mass (e.g. increase in
CC   bone mass and/or inhibit bone loss), management of bone fragility (e.g.
CC   decrease bone fragility); and prevention and/or treatment of bone pain,
CC   bone deformities and/or bone fractures. The products can also be used for
CC   detection, diagnosis and screening assays.
XX
SQ   Sequence   160 AA;
```

```
  Query Match             55.8%;  Score 463;  DB 20;  Length 160;
  Best Local Similarity   54.5%;  Pred. No. 1.1e-41;
  Matches   85;  Conservative   30;  Mismatches   41;  Indels    0;  Gaps    0;

Qy       2 EKALKIDTPQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGN 61
           || |:  :|    :||:: |||:||:  | |||||::  |||| |: |:::::||| :||:
Db       4 ekelraaspslrhvqdlssrvwilqnniltavprkeqtvpvtitllpcqyldtletnrgd 63

Qy      62 PIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESV 121
           | |:|:     || | | |:|| ||| | :||::||: |||||: |||| :||  |||||
Db      64 ptymgvqrpmsclfctkdgeqpvlqlgegnimemynkkepvkaslfyhkksgttstfesa 123

Qy     122 AFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
           ||||||||| |:| |||||||||:   ||| : ::
```

Db 124 afpgwfiavcskgscpliltqelgeifitdfemivv 159

RESULT 15
AAU17010
ID AAU17010 standard; Protein; 172 AA.
XX
AC AAU17010;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human novel secreted protein, SEQ ID 251.
XX
KW Human; immunosuppressive; antiarthritic; antirheumatic;
KW cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;
KW neuroprotective; antibacterial; virucide; fungicide; opthalmalogical;
KW vulnerary; secreted protein; rheumatoid arthritis;
KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;
KW corneal infection; wound healing; epithelial cell proliferation;
KW skin ageing; food additive; preservative; antiproliferative.
XX
OS Homo sapiens.
XX
PN WO200155441-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01320.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
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PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
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PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
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PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
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PR 08-NOV-2000; 2000US-0246528.
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PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
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PR 17-NOV-2000; 2000US-0249207.
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PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.

PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
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PR 17-NOV-2000; 2000US-0249297.
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PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-476222/51.
DR N-PSDB; AAS26915.
XX
PT Novel polypeptides and polynucleotides useful as diagnostic reagents to
PT diagnose diseases or disorders associated with aberrant expression or
PT activity of polypeptides, for treating blood clotting disorder,
PT haemophilia -
XX
PS Claim 11; SEQ ID No 251; 601pp; English.
XX
CC The invention relates to isolated nucleic acid molecules and their
CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They
CC are also used in diagnosing a pathological condition or susceptibility
CC to a pathological condition. Antibodies to the proteins can also
CC be used in alleviating symptoms associated with the disorders and in
CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked
CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated
CC include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi
CC and ocular disorders e.g. corneal infection, and many other
CC disorders listed in the specification. The polypeptides can also
CC be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present

Query Match 55.4%; Score 459.5; DB 22; Length 172;
Best Local Similarity 59.2%; Pred. No. 3e-41;
Matches 87; Conservative 24; Mismatches 35; Indels 1; Gaps 1;

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Qy      10 PQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNG 69
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Db      26 pitgtindlnqqvwtlqgqnlvavprsdsvtpvtvavitckypealeqgrgdpiylgiqn 85

Qy      70 LNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIA 129
             :|| | |||:||||||||: ||||| |||||| |||| :::|| || |||||| ||||
Db      86 pemclycekvgeqptlqlkeqkimdlygqpepvkpflfyraktgrtstlesvafpdwfia 145

Qy     130 VSSEGGCPLILTQELGKANTTDFGLTM 156
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Db 146 -sskrdqpiiltselxksyntafelni 171

Search completed: June 20, 2002, 15:03:08
Job time: 119 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 20, 2002, 15:03:52 ; Search time 36.86 Seconds
(without alignments)
411.886 Million cell updates/sec

Title: US-09-763-498-13
Perfect score: 830
Sequence: 1 MEKALKIDTPQRGSIQDINH.....ILTQELGKANTTDFGLTMLF 158

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	195.5	23.6	178	2	A44610	interleukin-1 rece
2	190.5	23.0	178	2	C40956	interleukin-1 rece
3	185.5	22.3	155	2	JC7104	interleukin-1 rece
4	183.5	22.1	177	2	A30368	interleukin-1 rece
5	183.5	22.1	180	2	A39386	interleukin-1 rece
6	173.5	20.9	266	1	S23010	interleukin-1 beta
7	170.5	20.5	177	2	A54377	interleukin-1 rece
8	169.5	20.4	266	1	ICBO1B	interleukin-1 beta
9	159.5	19.2	267	2	S38373	interleukin-1 beta
10	155	18.7	267	1	JN0724	interleukin-1 beta
11	143.5	17.3	269	1	ICHU1B	interleukin-1 beta
12	141.5	17.0	268	1	A30584	interleukin-1 beta
13	137.5	16.6	214	2	JC5646	interleukin-1 beta
14	121	14.6	269	1	I55969	interleukin-1 beta
15	81	9.8	256	2	F86463	hypothetical prote
16	78	9.4	407	2	T22554	hypothetical prote
17	78	9.4	501	2	AG0939	glycerol kinase [i
18	77	9.3	268	1	ICBO1A	interleukin-1 alph
19	77	9.3	268	1	A61246	interleukin-1 alph
20	76	9.2	502	1	KIECGL	glycerol kinase (E
21	76	9.2	502	2	C91235	glycerol kinase [i
22	76	9.2	509	2	C86082	glycerol kinase [i
23	75.5	9.1	270	1	S10532	interleukin-1 alph
24	74	8.9	15281	2	S41309	cyclosporin synthe
25	73.5	8.9	1320	2	H64090	phosphoribosylform
26	73	8.8	403	2	AC2271	precorrin-6y-depen
27	73	8.8	837	2	T48407	hypothetical prote
28	72.5	8.7	325	2	E87125	ribonucleotide red
29	72	8.7	1132	2	T43483	translation initia
30	71.5	8.6	325	2	S48698	3-dehydroquinate d
31	71.5	8.6	421	2	A47713	chitin deacetylase
32	71	8.6	1426	2	T30817	homeotic protein C
33	70.5	8.5	270	2	I46620	interleukin-1 alph
34	70.5	8.5	460	2	AG2262	hypothetical prote
35	70.5	8.5	556	2	A44441	B-cell antigen CD1
36	70.5	8.5	944	2	G86720	translation initia
37	70.5	8.5	1077	2	T01474	hypothetical prote
38	70.5	8.5	1093	2	T51503	valine--tRNA ligas
39	70	8.4	447	2	H97146	siderophore/Surfac
40	70	8.4	516	2	H84424	probable MAP kinas
41	70	8.4	1057	2	T46193	hypothetical prote
42	69.5	8.4	454	2	G70476	conserved hypothet
43	69	8.3	327	1	OWPSY	ornithine carbamoy
44	69	8.3	501	1	VGBEMA	glycoprotein A pre
45	69	8.3	501	1	A60005	glycoprotein A pre

ALIGNMENTS

RESULT 1
A44610
interleukin-1 receptor antagonist precursor - mouse
N;Alternate names: IL-1Ra
C;Species: Mus musculus (house mouse)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 16-Jul-1999
C;Accession: A44610; B40956; A49031; I56106; I52970
R;Matsushime, H.; Roussel, M.F.; Matsushima, K.; Hishinuma, A.; Sherr, C.J.
Blood 78, 616-623, 1991
A;Title: Cloning and expression of murine interleukin-1 receptor antagonist in macrop
A;Reference number: A44610; MUID:91316273
A;Accession: A44610
A;Molecule type: mRNA
A;Residues: 1-178 <MAT>
A;Cross-references: GB:M64404; NID:g198296; PIDN:AAA39277.1; PID:g198297
R;Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thomps
Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A;Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene fami
A;Reference number: A40956; MUID:91271363
A;Accession: B40956
A;Molecule type: DNA
A;Residues: 7-178 <EIS>
A;Cross-references: GB:M63100; NID:g198389; PIDN:AAA39310.1; PID:g198390
R;Shuck, M.E.; Eessalu, T.E.; Tracey, D.E.; Bienkowski, M.J.
Eur. J. Immunol. 21, 2775-2780, 1991
A;Title: Cloning, heterologous expression and characterization of murine interleukin
A;Reference number: A49031; MUID:92037824
A;Accession: A49031
A;Molecule type: mRNA
A;Residues: 23-178 <SHU>
A;Cross-references: GB:S64082; NID:g238584; PIDN:AAB20265.1; PID:g238585
A;Experimental source: peritoneal macrophages, ICR strain
A;Note: sequence extracted from NCBI backbone (NCBIN:64082, NCBIP:64085)
R;Zahedi, K.; Seldin, M.F.; Rits, M.; Ezekowitz, R.B.; Whitehead, A.S.
J. Immunol. 146, 4228-4233, 1991
A;Title: Mouse IL-1 receptor antagonist protein: Molecular characterization, gene map
A;Reference number: I56106; MUID:91250712
A;Accession: I56106
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-178 <RES>
A;Cross-references: GB:M74294; NID:g198387; PIDN:AAA39309.1; PID:g198388
R;Zahedi, K.A.; Uhlar, C.M.; Rits, M.; Prada, A.E.; Whitehead, A.S.
Cytokine 6, 1-9, 1994
A;Title: The mouse interleukin 1 receptor antagonist protein: gene structure and regu
A;Reference number: I52970; MUID:94271931
A;Accession: I52970
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-178 <RE2>
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A;Gene: IL-1rn
A;Introns: 40/2; 70/1; 107/3
C;Superfamily: interleukin-1
C;Keywords: cytokine receptor
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-178/Product: interleukin-1 receptor antagonist #status predicted <MA2>

Query Match 23.6%; Score 195.5; DB 2; Length 178;
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Matches 47; Conservative 21; Mismatches 45; Indels 21; Gaps 2;

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Qy      15 IQDINHRVWVLQDQTLIA-------VPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGL 67
Db      41 IWDTNQKTFYLRNNQLIAGYLQGPNIKLEEKIDMVPIDLHS-------------VFLGI 86

Qy      68 NGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWF 127
Db      87 HGGKLCLSCAKSGDDIKLQLEEVNITDLSKNKEEDKRFTFIRSEKGPTTSFESAACPGWF 146

Qy     128 IAVSSEGGCPLILT 141
Db     147 LCTTLEADRPVSLT 160
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RESULT 2
C40956
interleukin-1 receptor antagonist precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 16-Jul-1999
C;Accession: C40956
R;Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson,
Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A;Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family
A;Reference number: A40956; MUID:91271363
A;Accession: C40956
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-178 <EIS>
A;Cross-references: GB:M63101; NID:g204928; PIDN:AAA41434.1; PID:g204929
C;Superfamily: interleukin-1
C;Keywords: cytokine receptor

Query Match 23.0%; Score 190.5; DB 2; Length 178;
Best Local Similarity 35.1%; Pred. No. 1.5e-11;
Matches 46; Conservative 20; Mismatches 50; Indels 15; Gaps 2;

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Db      41 IWDTNQKTFYLRNNQLIAGYLQGPNTKLEEKIDMVPIDFRNV----------FLGIHGG 89

Qy      71 NLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAV 130
Db      90 KLCLSCVKSGDDTKLQLEEVNITDLNKNKEEDKRFTFIRSETGPTTSFESLACPGWFLCT 149

Qy     131 SSEGGCPLILT 141
Db     150 TLEADHPVSLT 160
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RESULT 3
JC7104
interleukin-1 receptor antagonist - human
C;Species: Homo sapiens (man)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C;Accession: JC7104
R;Mulero, J.J.; Pace, A.M.; Nelken, S.T.; Loeb, D.B.; Correa, T.R.; Drmanac, R.; Ford, J
Biochem. Biophys. Res. Commun. 263, 702-706, 1999
A;Title: IL1HY1: A novel interleukin-1 receptor antagonist gene.
A;Reference number: JC7104; MUID:99443727
A;Accession: JC7104
A;Molecule type: mRNA
A;Residues: 1-155 <MUL>
A;Cross-references: GB:AF186094; NID:g6049804; PIDN:AAF02757.1; PID:g6049805
C;Genetics:
A;Gene: il1hy1
A;Map position: 2q14
C;Keywords: macrophage

Query Match 22.3%; Score 185.5; DB 2; Length 155;
Best Local Similarity 44.8%; Pred. No. 4e-11;
Matches 43; Conservative 13; Mismatches 35; Indels 5; Gaps 3;

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Qy      61 NPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFES 120
Db      55 SPVILGVQGGSQCLSCG-VGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFES 113

Qy     121 VAFPGWFIAVSSEGGCPLILTQ--ELG--KANTTDF 152
Db     114 AAYPGWFLCTVPEADQPVRLTQLPENGGWNAPITDF 149
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RESULT 4
A30368
interleukin-1 receptor antagonist secreted form precursor - human
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-May-2000
C;Accession: A40956; I37894; A30368; S08160; S08159; A37822
R;Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thomps
Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A;Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene fami
A;Reference number: A40956; MUID:91271363
A;Accession: A40956
A;Molecule type: DNA
A;Residues: 1-177 <EIS>
A;Cross-references: GB:M63099; NID:g186385; PIDN:AAB41943.1; PID:g186386
R;Lennard, A.; Gorman, P.; Carrier, M.; Griffiths, S.; Scotney, H.; Sheer, D.; Solari
Cytokine 4, 83-89, 1992
A;Title: Cloning and chromosome mapping of the human interleukin-1 receptor antagonis
A;Reference number: I37894; MUID:92338323
A;Accession: I37894
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-177 <LEN>
A;Cross-references: EMBL:X64532; NID:g33798; PIDN:CAA45832.1; PID:g33799
R;Carter, D.B.; Deibel Jr., M.R.; Dunn, C.J.; Tomich, C.S.C.; Laborde, A.L.; Slightom
J.G.; Sieu, L.C.; Hardee, M.M.; Zurcher-Neely, H.A.; Reardon, I.M.; Heinrikson, R.L.;
Nature 344, 633-638, 1990
A;Title: Purification, cloning, expression and biological characterization of an inte
A;Reference number: A30368; MUID:90220867
A;Accession: A30368
A;Molecule type: mRNA
A;Residues: 1-177 <CAR>
A;Cross-references: GB:X53296; NID:g32578; PIDN:CAA37386.1; PID:g32579
A;Note: parts of this sequence, including the amino end of the mature protein, were c
R;Eisenberg, S.P.; Evans, R.J.; Arend, W.P.; Verderber, E.; Brewer, M.T.; Hannum, C.H
Nature 343, 341-346, 1990
A;Title: Primary structure and functional expression from complementary DNA of a huma
A;Reference number: S08160; MUID:90136921
A;Accession: S08160
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-177 <EI2>
A;Cross-references: GB:X52015; NID:g32576; PIDN:CAA36262.1; PID:g32577
R;Hannum, C.H.; Wilcox, C.J.; Arend, W.P.; Joslin, F.G.; Dripps, D.J.; Heimdal, P.L.;
Nature 343, 336-340, 1990
A;Title: Interleukin-1 receptor antagonist activity of a human interleukin-1 inhibito
A;Reference number: S08159; MUID:90136920
A;Accession: S08159
A;Molecule type: protein
A;Residues: 26-75;97-108;110-116;120-131;163-176 <HAN>
R;Bienkowski, M.J.; Eessalu, T.E.; Berger, A.E.; Truesdell, S.E.; Shelly, J.A.; Labor
J. Biol. Chem. 265, 14505-14511, 1990
A;Title: Purification and characterization of interleukin 1 receptor level antagonist

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A;Reference number: A37822; MUID:90354444
A;Accession: A37822
A;Molecule type: protein
A;Residues: 26-52;70-77;122-127;170-175 <BIE>
A;Experimental source: culture medium, PMA-stimulated THP-1 cells
C;Comment: For an alternative splice form, see PIR:A39386
C;Genetics:
A;Gene: GDB:IL1RN
A;Cross-references: GDB:125897; OMIM:147679
A;Map position: 2q14.2-2q14.2
A;Introns: 39/2; 69/1; 106/3
C;Superfamily: interleukin-1
C;Keywords: alternative splicing; cytokine receptor; extracellular protein; glycoprotein
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F;26-177/Product: interleukin-1 receptor antagonist #status experimental <MAT>
F;109/Binding site: carbohydrate (Asn) (covalent) #status experimental
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Query Match 22.1%; Score 183.5; DB 2; Length 177;
Best Local Similarity 30.6%; Pred. No. 7.5e-11;
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Qy      68 NGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWF 127
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Db      86 HGGKMCLSCVKSGDETRLQLEAVNITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWF 145

Qy     128 IAVSSEGGCPLILTQELGKANTTDFGL 154
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Db     146 LCTAMEADQPVSLT------NMPDEGV 166
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RESULT   5
A39386
interleukin-1 receptor antagonist, long intracellular splice form - human
N;Contains: interleukin-1 receptor antagonist, short intracellular splice form
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1992 #sequence_revision 11-Apr-1997 #text_change 26-May-2000
C;Accession: I37893; A39386
R;Muzio, M.; Polentarutti, N.; Sironi, M.; Poli, G.; De Gioia, L.; Introna, M.; Mantovan
J. Exp. Med. 182, 623-628, 1995
A;Title: Cloning and characterization of a new isoform of the interleukin 1 receptor ant
A;Reference number: I37893; MUID:95355865
A;Accession: I37893
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-180 <RES>
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R;Haskill, S.; Martin, G.; Van Le, L.; Morris, J.; Peace, A.; Bigler, C.F.; Jaffe, G.J.;
Proc. Natl. Acad. Sci. U.S.A. 88, 3681-3685, 1991
A;Title: cDNA cloning of an intracellular form of the human interleukin 1 receptor antag
A;Reference number: A39386; MUID:91219436
A;Accession: A39386
A;Molecule type: mRNA
A;Residues: 1-3,25-180 <HAS>
A;Cross-references: GB:M55646; NID:g186291; PIDN:AAA59138.1; PID:g186292
C;Comment: For an alternative splice form, see PIR:A30368
C;Genetics:
A;Gene: GDB:IL1RN
A;Cross-references: GDB:125897; OMIM:147679
A;Map position: 2q14.2-2q14.2
C;Superfamily: interleukin-1
C;Keywords: alternative splicing; cytokine receptor
F;1-180/Product: interleukin-1 receptor antagonist, long intracellular splice form #stat
F;1-3,25-180/Product: interleukin-1 receptor antagonist, short intracellular splice form
```

Query Match 22.1%; Score 183.5; DB 2; Length 180;
Best Local Similarity 30.6%; Pred. No. 7.6e-11;
Matches 45; Conservative 26; Mismatches 49; Indels 27; Gaps 3;

```
Qy      15 IQDINHRVWVLQDQTLIA-------VPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGL 67
           | |:| : : |::  |:|       |  ::::  | |               : ::||:
Db      43 IWDVNQKTFYLRNNQLVAGYLQGPNVNLEEKIDVVPI-------------EPHALFLGI 88

Qy      68 NGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWF 127
           :|  :|| | | ||:  |||:  :| ||    :  | | |  | ||  ::||| | ||||
Db      89 HGGKMCLSCVKSGDETRLQLEAVNITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWF 148

Qy     128 IAVSSEGGCPLILTQELGKANTTDFGL 154
           :  : |   |: ||      |  | |:
Db     149 LCTAMEADQPVSLT------NMPDEGV 169
```

```
RESULT   6
S23010
interleukin-1 beta precursor - sheep
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 08-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 15-Oct-1999
C;Accession: S23010; S43047; S13092; B61246
R;Seow, H.F.; Rothel, J.S.; David, M.J.; Wood, P.R.
DNA Seq. 1, 423-426, 1991
A;Title: Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.
A;Reference number: S23010; MUID:92119335
A;Accession: S23010
A;Molecule type: mRNA
A;Residues: 1-266 <SEO>
A;Cross-references: EMBL:X56972; NID:g1808; PIDN:CAA40293.1; PID:g1809
A;Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in having an a
R;Sargan, D.R.
submitted to the EMBL Data Library, May 1992
A;Reference number: S43047
A;Accession: S43047
A;Molecule type: mRNA
A;Residues: 1-13,'C',15-54,'K',56-63,'A',65-144,'L',146-266 <SAR>
A;Cross-references: EMBL:X54796; NID:g1273; PIDN:CAA38566.1; PID:g1274
R;Fiskerstrand, C.; Sargan, D.
Nucleic Acids Res. 18, 7165, 1990
A;Title: Nucleotide sequence of ovine interleukin-1 beta.
A;Reference number: S13092; MUID:91088326
A;Accession: S13092
A;Molecule type: mRNA
A;Residues: 1-13,'C',15-54,'K',56-61,'S',63,'A',65-144,'L',146-266 <FIS>
A;Cross-references: EMBL:X54796
A;Note: the authors translated the codon AGT for residue 62 as Arg
R;Andrews, A.E.; Barcham, G.J.; Brandon, M.R.; Nash, A.D.
Immunology 74, 453-460, 1991
A;Title: Molecular cloning and characterization of ovine IL-1alpha and IL-1beta.
A;Reference number: A61246; MUID:92120716
A;Accession: B61246
A;Molecule type: mRNA
A;Residues: 1-144,'L',146-266 <AND>
C;Comment: This protein lacks a conventional signal sequence for protein export. Clea
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin
C;Genetics:
A;Gene: IL-1-beta
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;114-266/Product: interleukin-1 beta #status predicted <MAT>
```

Query Match 20.9%; Score 173.5; DB 1; Length 266;
Best Local Similarity 30.8%; Pred. No. 1.2e-09;
Matches 48; Conservative 27; Mismatches 62; Indels 19; Gaps 4;

```
Qy       2 EKALKIDTPQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGN 61
           :|:| :|:|             ||:    : :| ::    |   :     |:  |:|
Db     128 QKSLVLDSP-----------CVLK---ALHLPSQEMSREVVFCM---SFVQGEERDNKI 169

Qy      62 PIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESV 121
           |: ||:   || | | | || |||||:| |   :| :    | |:|| ::      ||||
```

```
Db    170 PVALGIRDKNLYLSCVKKGDTPTLQLEEVD-PKVYPKRNMEKRFVFYKTEIKNTVEFESV 228

Qy    122 AFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
          :| |:|: |     |: | :  |  : ||| :  |
Db    229 LYPNWYISTSQIEEKPVFLGRFRGGQDITDFRMETL 264


RESULT   7
A54377
interleukin-1 receptor antagonist secreted form precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C;Accession: A54377; I46729
R;Cominelli, F.; Bortolami, M.; Pizarro, T.T.; Monsacchi, L.; Ferretti, M.; Brewer, M.T.
J. Biol. Chem. 269, 6962-6971, 1994
A;Title: Rabbit interleukin-1 receptor antagonist. Cloning, expression, functional chara
A;Reference number: A54377; MUID:94165101
A;Accession: A54377
A;Molecule type: mRNA
A;Residues: 1-177 <COM>
A;Cross-references: GB:S68977; NID:g545740; PIDN:AAB30093.1; PID:g545741
A;Experimental source: colon tissue
A;Note: sequence extracted from NCBI backbone (NCBIN:144168, NCBIP:144169)
R;Goto, F.; Goto, K.; Miyata, T.; Ohkawara, S.; Takao, T.; Mori, S.; Furukawa, S.; Maeda
Immunology 77, 235-244, 1992
A;Title: Interleukin-1 recetor antagonist in inflammatory exudate cells of rabbits. Prod
A;Reference number: I46729; MUID:93052512
A;Accession: I46729
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-177 <GOT>
A;Cross-references: GB:D21832; NID:g425787; PIDN:BAA04860.1; PID:g452205
C;Superfamily: interleukin-1
C;Keywords: cytokine receptor; extracellular protein; glycoprotein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;109/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match             20.5%;  Score 170.5;  DB 2;  Length 177;
  Best Local Similarity   30.6%;  Pred. No. 1.5e-09;
  Matches   44;  Conservative   21;  Mismatches   52;  Indels   27;  Gaps    3;

Qy     15 IQDINHRVWVLQDQTLIA-------VPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGL 67
          | |:| : : |::  |:|          ::|:  | :                  ::||:
Db     40 IWDVNQKTFYLRNNQLVAGYLQGPNAKLEERIDVVPL-------------EPQLLFLGI 85

Qy     68 NGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWF 127
             ||| | | ||:  | |:  :| ||    |  | | |  | ||  :|||| : ||||
Db     86 QRGKLCLSCVKSGDKMKLHLEAVNITDLGKNKEQDKRFTFIRSNSGPTTTFESASCPGWF 145

Qy    128 IAVSSEGGCPLILTQELGKANTTD 151
          :  : |   |: ||      || |
Db    146 LCTALEADQPVSLT------NTPD 163


RESULT   8
ICBO1B
interleukin-1 beta precursor - bovine
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
C;Accession: JL0010; S01380
R;Maliszewski, C.R.; Baker, P.E.; Schoenborn, M.A.; Davis, B.S.; Cosman, D.; Gillis, S.;
Mol. Immunol. 25, 429-437, 1988
A;Title: Cloning, sequence and expression of bovine interleukin 1-alpha and interleukin
A;Reference number: A94695; MUID:88318652
A;Accession: JL0010
A;Molecule type: mRNA
A;Residues: 1-266 <MAL>
A;Cross-references: GB:M37211; NID:g163200; PIDN:AAA30584.1; PID:g163201
R;Leong, S.R.; Flaggs, G.M.; Lawman, M.; Gray, P.W.
Nucleic Acids Res. 16, 9054, 1988
A;Title: The nucleotide sequence for the cDNA of bovine interleukin-1 beta.
A;Reference number: S01380; MUID:89016591
A;Accession: S01380
A;Molecule type: mRNA
A;Residues: 1-251,'A',253-266 <LEO>
A;Cross-references: EMBL:X12498; NID:g448; PIDN:CAA31018.1; PID:g449
C;Comment: This protein is a cytokine that mediates a variety of immunoregulatory and
C;Comment: This protein lacks a conventional signal sequence for protein export. Clea
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;114-266/Product: interleukin-1 beta #status predicted <MAT>


  Query Match             20.4%;  Score 169.5;  DB 1;  Length 266;
  Best Local Similarity   37.7%;  Pred. No. 3e-09;
  Matches   40;  Conservative   16;  Mismatches   49;  Indels    1;  Gaps    1;

Qy     52 VETLEKDRGNPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQ 111
          |:  |:|   |: ||:   || | | | || |||||:| |   :| :    | |:|| ::
Db    160 VQGEERDNKIPVALGIKDKNLYLSCVKKGDTPTLQLEEVD-PKVYPKRNMEKRFVFYKTE 218

Qy    112 SGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
                ||||  :| |:|: |     |: |    |  : ||| :  |
Db    219 IKNTVEFESVLYPNWYISTSQIEERPVFLGHFRGGQDITDFRMETL 264


RESULT   9
S38373
interleukin-1 beta precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 20-May-1994 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999
C;Accession: S38373
R;Vandenbroeck, K.; Fiten, P.; Beuken, E.; Martens, E.; Janssen, A.; van Damme, J.; O
Eur. J. Biochem. 217, 45-52, 1993
A;Title: Gene sequence, cDNA construction, expression in Escherichia coli and genetic
A;Reference number: S38373; MUID:94039070
A;Accession: S38373
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-267 <VAN>
A;Cross-references: EMBL:X74568; NID:g407899; PIDN:CAA52660.1; PID:g407900
C;Genetics:
A;Introns: 16/2; 33/3; 99/1; 154/1; 197/3
C;Superfamily: interleukin-1


  Query Match             19.2%;  Score 159.5;  DB 2;  Length 267;
  Best Local Similarity   34.3%;  Pred. No. 3e-08;
  Matches   35;  Conservative   18;  Mismatches   48;  Indels    1;  Gaps    1;

Qy     56 EKDRGNPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRN 115
          : |   |: ||: | || | |    | |||||:: |    | : :  | |:|| ::
Db    165 DSDDKIPVTLGIKGKNLYLSCVMKDDTPTLQLEDVDPKS-YPKRDMEKRFVFYKTEIKNR 223

Qy    116 STFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
            |||  :| |:|: |     |: |    |: : ||| : :|
Db    224 VEFESALYPNWYISTSQAEQKPVFLGNSKGRQDITDFTMEVL 265


RESULT  10
JN0724
interleukin-1 beta precursor - pig
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 14-Jul-1994 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999
C;Accession: JN0724
R;Huether, M.J.; Lin, G.; Smith, D.M.; Murtaugh, M.P.; Molitor, T.W.
Gene 129, 285-289, 1993
A;Title: Cloning, sequencing and regulation of an mRNA encoding porcine interleukin-1
A;Reference number: JN0724; MUID:93314975
A;Accession: JN0724
A;Molecule type: mRNA
```

```
A;Residues: 1-267 <HUE>
A;Cross-references: GB:M86725; NID:g164607; PIDN:AAA02584.1; PID:g164608
A;Experimental source: alveolar macrophage
C;Comment: This protein is a pleiotropic cytokine that mediates a variety of processes i
C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavag
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophag
F;115-267/Product: interleukin-1 beta #status predicted <IL1>
F;77/Binding site: myristate (Lys) (covalent) #status predicted


  Query Match             18.7%;  Score 155;  DB 1;  Length 267;
  Best Local Similarity   22.8%;  Pred. No. 8.3e-08;
  Matches   52;  Conservative   34;  Mismatches   66;  Indels   76;  Gaps    7;

Qy       5 LKIDTPQRGSIQ-DINHRVW---VLQDQTLIAVPRKDRMSPVT----------------- 43
           | : : : ||||  |:|::|   : |  ::|    |   :| :
Db      39 LDLGSLRNGSIQLQISHQLWNKSIRQMVSVIVAVEKPMKNPSSQAFCDDDQKSIFSFIFE 98

Qy      44 ---IALISCR-------HVETLE----------------------------------- 56
              | | :|        :|:::|
Db      99 EEPIILETCNDDFVCDANVQSMECKLQDKDHKSLVLAGPHMLKALHLLTGDLKREVVFCM 158

Qy      57 -----KDRGN--PIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYH 109
                 |  |  |: ||: | || | |    : |||||:: |    | : :  | |:||
Db     159 SFVQGDDSNNKIPVTLGIKGKNLYLSCVMKDNTPTLQLEDID-PKRYPKRDMEKRFVFYK 217

Qy     110 SQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
           ::      |||  :| |:|: |     |: |    |: : ||| : :|
Db     218 TEIKNRVEFESALYPNWYISTSQAEQKPVFLGNSKGRQDITDFTMEVL 265


RESULT  11
ICHU1B
interleukin-1 beta precursor [validated] - human
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1986 #sequence_revision 15-May-1998 #text_change 15-Sep-2000
C;Accession: A25542; A29019; A94023; A93361; I51852; I65200; I38132; B27616; A01848; S19
R;Clark, B.D.; Collins, K.L.; Gandy, M.S.; Webb, A.C.; Auron, P.E.
Nucleic Acids Res. 14, 7897-7914, 1986
A;Title: Genomic sequence for human prointerleukin 1 beta: possible evolution from a rev
A;Reference number: A25542; MUID:87040762
A;Accession: A25542
A;Molecule type: DNA; mRNA
A;Residues: 1-5,'K',7-269 <CLA>
A;Cross-references: GB:X04500; NID:g33788
A;Note: the mRNA sequence had codon AAG for 6-Lys, the DNA sequence had GAG for 6-Glu
R;Bensi, G.; Raugei, G.; Palla, E.; Carinci, V.; Buonamassa, D.T.; Melli, M.
Gene 52, 95-101, 1987
A;Title: Human interleukin-1 beta gene.
A;Reference number: A29019; MUID:87248099
A;Accession: A29019
A;Molecule type: DNA
A;Residues: 1-269 <BEN>
A;Cross-references: GB:M15840; NID:g186281; PIDN:AAA74137.1; PID:g386816
R;Auron, P.E.; Webb, A.C.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Dinare
Proc. Natl. Acad. Sci. U.S.A. 81, 7907-7911, 1984
A;Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
A;Reference number: A94023; MUID:85088517
A;Accession: A94023
A;Molecule type: mRNA
A;Residues: 1-5,'K',7-269 <AUR>
A;Cross-references: GB:K02770; NID:g186268; PIDN:AAA36106.1; PID:g307043
R;March, C.J.; Mosley, B.; Larsen, A.; Cerretti, D.P.; Braedt, G.; Price, V.; Gillis, S.
Nature 315, 641-647, 1985
A;Title: Cloning, sequence and expression of two distinct human interleukin-1 complement
A;Reference number: A93361; MUID:85240547
A;Accession: A93361
A;Molecule type: mRNA
A;Residues: 1-269 <MAR>
A;Cross-references: GB:X02532; NID:g33789; PIDN:CAA26372.1; PID:g33790
A;Note: parts of this sequence, including the amino end of the mature form, were conf
R;Webb, A.C.; Dinarello, C.A.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.;
Adv. Gene Technol. 22, 339-340, 1985
A;Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
A;Reference number: I51852
A;Accession: I51852
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-5,'K',7-19,'H',21-110,'Q',112-176,'A',178-213,'P',215-269 <WEB>
A;Cross-references: GB:M54933; NID:g186287; PIDN:AAA59136.1; PID:g186288
R;Nishida, T.; Nishino, N.; Takano, M.; Kawai, K.; Bando, K.; Masui, Y.; Nakai, S.; H
Biochem. Biophys. Res. Commun. 143, 345-352, 1987
A;Title: cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell line.
A;Reference number: I52217; MUID:87156769
A;Accession: I65200
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-269 <NIS>
A;Cross-references: GB:M15330; NID:g186283; PIDN:AAA59135.1; PID:g307045
R;Kotenko, S.V.; Bulenkov, M.T.; Veiko, V.P.; Epishin, S.M.; Lomakin, I.B.; Emel'yano
ii, S.A.; Vinetskii, Y.P.
Dokl. Akad. Nauk SSSR 309, 1005-1008, 1989
A;Title: [Cloning of the cDNA coding for human prointerleukin-1 alpha and prointerleu
A;Reference number: I38131; MUID:90249285
A;Accession: I38132
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-269 <KOT>
A;Cross-references: EMBL:X56087; NID:g35662; PIDN:CAA39567.1; PID:g35663
R;Zsebo, K.M.; Wypych, J.; Yuschenkoff, V.N.; Lu, H.; Hunt, P.; Dukes, P.P.; Langley,
Blood 71, 962-968, 1988
A;Title: Effects of hematopoietin-1 and interleukin 1 activities on early hematopoiet
A;Reference number: A90732; MUID:88184226
A;Accession: B27616
A;Molecule type: protein
A;Residues: 117-123,'X',125-126,'X',128 <ZSE>
R;Stevenson, F.T.; Bursten, S.L.; Fanton, C.; Locksley, R.M.; Lovett, D.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 7245-7249, 1993
A;Title: The 31-kDa precursor of interleukin 1alpha is myristoylated on specific lysi
A;Reference number: A48293; MUID:93348250
A;Contents: annotation; myristylation of lysines
R;Nanduri, V.B.; Hulmes, J.D.; Pan, Y.C.E.; Kilian, P.L.; Stern, A.S.
Biochim. Biophys. Acta 1118, 25-35, 1991
A;Title: The role of arginine residues in interleukin 1 receptor binding.
A;Reference number: S19608; MUID:92110334
A;Contents: annotation; type 1 IL-1 receptor interaction site
A;Note: modification of Arg-120 by phenylglyoxal blocks receptor binding
R;Clore, G.M.; Gronenborn, A.M.
submitted to the Brookhaven Protein Data Bank, January 1991
A;Reference number: A50049; PDB:6I1B
A;Contents: annotation; conformation by (13)C- and (1)H-NMR, residues 117-269
R;Clore, G.M.; Wingfield, P.T.; Gronenborn, A.M.
Biochemistry 30, 2315-2323, 1991
A;Title: High-resolution three-dimensional structure of interleukin 1beta in solution
A;Reference number: A44675; MUID:91159409
A;Contents: annotation; (1)H-NMR structural determination
R;Hazuda, D.J.; Strickler, J.; Simon, P.; Young, P.R.
J. Biol. Chem. 266, 7081-7086, 1991
A;Title: Structure-function mapping of interleukin 1 precursors. Cleavage leads to a
A;Reference number: A39774; MUID:91201363
A;Contents: annotation
R;Finzel, B.C.; Watenpaugh, K.D.; Einspahr, H.M.
submitted to the Brookhaven Protein Data Bank, December 1989
A;Reference number: A50016; PDB:1I1B
A;Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 119-269
R;Finzel, B.C.; Clancy, L.L.; Holland, D.R.; Muchmore, S.W.; Watenpaugh, K.D.; Einspa
J. Mol. Biol. 209, 779-791, 1989
A;Title: Crystal structure of recombinant human interleukin-1beta at 2.0 angstrom res
A;Reference number: A44666; MUID:90064532
A;Contents: annotation; X-ray crystallography, 2.0 angstroms
C;Comment: This protein lacks a conventional signal sequence for protein export. Clea
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
```

```
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a
C;Genetics:
A;Gene: GDB:IL1B
A;Cross-references: GDB:120094; OMIM:147720
A;Map position: 2q13-2q21
A;Introns: 16/2; 33/3; 101/1; 156/1; 199/3
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophag
F;117-269/Product: interleukin-1 beta #status experimental <IL1>
F;76/Binding site: myristate (Lys) (covalent) (partial) #status experimental
F;123/Binding site: carbohydrate (Asn) (covalent) #status absent


  Query Match             17.3%;  Score 143.5;  DB 1;  Length 269;
  Best Local Similarity   34.5%;  Pred. No. 1.2e-06;
  Matches   39;  Conservative   15;  Mismatches   56;  Indels    3;  Gaps    2;

Qy      46 LISCRHVETLEKDRGNPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSF 105
           : |   |:  | :   |: |||   || | |    |:|||||:  |  : | : :  | |
Db     157 VFSMSFVQGEESNDKIPVALGLKEKNLYLSCVLKDDKPTLQLESVDPKN-YPKKKMEKRF 215

Qy     106 LFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTMLF 158
           :|   :      |||  || |:|: |     |: |    |  : |||  || |
Db     216 VFNKIEINNKLEFESAQFPNWYISTSQAENMPVFLGGTKGGQDITDF--TMQF 266


RESULT  12
A30584
interleukin-1 beta precursor - rabbit
N;Alternate names: hematopoietin-1; IL-1 beta; lymphocyte proliferation potentiating fac
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 25-May-1989 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999
C;Accession: A27714; A30584; JU0082; A32166
R;Mori, S.; Goto, F.; Goto, K.; Ohkawara, S.; Maeda, S.; Shimada, K.; Yoshinaga, M.
Biochem. Biophys. Res. Commun. 150, 1237-1243, 1988
A;Title: Cloning and sequence analysis of a cDNA for lymphocyte proliferation potentiati
A;Reference number: A27714; MUID:88134238
A;Accession: A27714
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-268 <MOR>
R;Cannon, J.G.; Clark, B.D.; Wingfield, P.; Schmeissner, U.; Losberger, C.; Dinarello, C
J. Immunol. 142, 2299-2306, 1989
A;Title: Rabbit IL-1. Cloning, expression, biologic properties, and transcription during
A;Reference number: A30584; MUID:89176242
A;Accession: A30584
A;Molecule type: mRNA
A;Residues: 1-268 <CAN>
A;Cross-references: GB:M26295; NID:g516632; PIDN:AAA31373.1; PID:g516633
R;Young, P.R.; Sylvester, D.
Protein Eng. 2, 545-551, 1989
A;Title: Cloning of rabbit interleukin-1 beta: differential evolution of IL-1 alpha and
A;Reference number: A94230; MUID:89315718
A;Accession: JU0082
A;Molecule type: mRNA
A;Residues: 1-268 <YOU>
C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavag
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;117-268/Product: interleukin-1 beta #status predicted <ILB>


  Query Match             17.0%;  Score 141.5;  DB 1;  Length 268;
  Best Local Similarity   33.0%;  Pred. No. 1.8e-06;
  Matches   36;  Conservative   16;  Mismatches   56;  Indels    1;  Gaps    1;

Qy      46 LISCRHVETLEKDRGNPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSF 105
           : |   |:  | :   |: ||| | || | |    |:|||||:  |  : | : :  | |
Db     156 VFSMSFVQGEESNDKIPVALGLRGKNLYLSCVMKDDKPTLQLESVD-PNRYPKKKMEKRF 214

Qy     106 LFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGL 154
           :|   :      |||  || |:|: |     |: |    |  : |||
Db     215 VFNKIEIKDKLEFESAQFPNWYISTSQTEYMPVFLGNNSGGQDLIDFSM 263


RESULT  13
JC5646
interleukin-1 beta - horse
C;Species: Equus caballus (domestic horse)
C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 20-Jun-2000
C;Accession: JC5646
R;Kato, H.; Youn, H.Y.; Ohashi, T.; Watari, T.; Goitsuka, R.; Tsujimoto, H.; Hasegawa
Gene 177, 11-16, 1996
A;Title: Identification of an alternatively spliced transcript of equine interleukin-
A;Reference number: JC5646; MUID:97080493
A;Accession: JC5646
A;Molecule type: mRNA
A;Residues: 1-214 <KAT>
A;Cross-references: DDBJ:D42165; NID:g2463549; PIDN:BAA22528.1; PID:g2463550
C;Comment: This protein mediates a variety of physiological response to infections an
synthesis by hepatocytes, and stimulation of chondrocytes and synovial cells to produ
C;Superfamily: interleukin-1


  Query Match             16.6%;  Score 137.5;  DB 2;  Length 214;
  Best Local Similarity   28.8%;  Pred. No. 3.5e-06;
  Matches   44;  Conservative   21;  Mismatches   71;  Indels   17;  Gaps    3;

Qy       1 MEKALKIDTPQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISC-RHVETLEKDR 59
           :||  ||  |   : || : |                 | :   :: |   |:  |:
Db      71 VEKLKKIPVPCSQAFQDDDLR--------------SLFSVIFEEVVFCMSFVQGEEETD 115

Qy      60 GNPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFE 119
             |: |||   || | |     :|||||:  |  : | : :  | |:|   :   |  ||
Db     116 KIPVALGLKEKNLYLSCGMKDGKPTLQLETVD-PNTYPKRKMEKRFVFNKMEIKGNVEFE 174

Qy     120 SVAFPGWFIAVSSEGGCPLILTQELGKANTTDF 152
           |  :| |:|: |     |: |    |  : |||
Db     175 SAMYPNWYISTSQAEKSPVFLGNTRGGRDITDF 207


RESULT  14
I55969
interleukin-1 beta precursor - mouse
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999
C;Accession: I55969; A24719; S13029
R;Gray, P.W.; Glaister, D.; Chen, E.; Goeddel, D.V.; Pennica, D.
J. Immunol. 137, 3644-3648, 1986
A;Title: Two interleukin 1 genes in the mouse: Cloning and expression of the cDNA for
A;Reference number: I55969; MUID:87058957
A;Accession: I55969
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-269 <RES>
A;Cross-references: GB:M15131; NID:g198293; PIDN:AAA39276.1; PID:g309398
R;Telford, J.L.; Macchia, G.; Massone, A.; Carinci, V.; Palla, E.; Melli, M.
Nucleic Acids Res. 14, 9955-9963, 1986
A;Title: The murine interleukin 1-beta gene: structure and evolution.
A;Reference number: A24719; MUID:87117546
A;Accession: A24719
A;Molecule type: mRNA
A;Residues: 1-269 <TEL>
A;Cross-references: GB:X04964; NID:g52666; PIDN:CAA28637.1; PID:g52667
R;Daumy, G.O.; Wilder, C.L.; Merenda, J.M.; McColl, A.S.; Geoghegan, K.F.; Otterness,
FEBS Lett. 278, 98-102, 1991
A;Title: Reduction of biological activity of murine recombinant interleukin-1beta by
A;Reference number: S13029; MUID:91130610
A;Accession: S13029
A;Status: preliminary
A;Molecule type: protein
A;Residues: 118-269 <DAU>
C;Comment: This protein lacks a conventional signal sequence for protein export. Clea
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ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a
C;Genetics:
A;Gene: IL-1-beta
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;118-269/Product: interleukin-1 beta #status experimental <IL1>

Query Match 14.6%; Score 121; DB 1; Length 269;
Best Local Similarity 35.2%; Pred. No. 0.0002;
Matches 32; Conservative 11; Mismatches 46; Indels 2; Gaps 2;

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Qy      62 PIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESV 121
           |: ||| | || | |      |||||:  |    | : :  | |:|   :      |||
Db     174 PVALGLKGKNLYLSCVMKDGTPTLQLESVDPKQ-YPKKKMEKRFVFNKIEVKSKVEFESA 232

Qy     122 AFPGWFIAVSSEGGCPLILTQELGKANTTDF 152
            || |:|: |     |: |    |: :  ||
Db     233 EFPNWYISTSQAEHKPVFLGNNSGQ-DIIDF 262
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RESULT 15
F86463
hypothetical protein F12G12.19 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C;Accession: F86463
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: F86463
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-256 <STO>
A;Cross-references: GB:AE005172; NID:g10086476; PIDN:AAG12536.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1

Query Match 9.8%; Score 81; DB 2; Length 256;
Best Local Similarity 25.2%; Pred. No. 1.8;
Matches 32; Conservative 18; Mismatches 45; Indels 32; Gaps 6;

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Qy      30 LIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNGLNLCLMCAKVGDQPTLQLKE 89
           ::|   :  :||||: |  |                  | |:          ||:
Db      22 MVASLEESGLSPVTVDLTGC------------------GFNM----TDTNTVSTLEEYS 58

Qy      90 KDIMDLY-NQPEPVKSFLFYHSQSGRNSTFESVAFP-----GWFIAVS--SEGGCPL-IL 140
           | ::||  | ||  |  |  ||  | : ::    ||       |:  :  |:|  |  :
Db      59 KPLIDLLENLPEEEKVILVGHSTGGASISYALERFPEKISKAIFVCATMVSDGQRPFDVF 118

Qy     141 TQELGKA 147
           ::||| |
Db     119 SEELGSA 125
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Search completed: June 20, 2002, 15:03:52
Job time: 162 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 20, 2002, 15:11:20 ; Search time 19.43 Seconds
(without alignments)
314.858 Million cell updates/sec

Title: US-09-763-498-13
Perfect score: 830
Sequence: 1 MEKALKIDTPQRGSIQDINH.....ILTQELGKANTTDFGLTMLF 158

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	195.5	23.6	178	1	IL1X_MOUSE	P25085 mus musculu
2	190.5	23.0	178	1	IL1X_RAT	P25086 rattus norv
3	186.5	22.5	177	1	IL1X_HORSE	O18999 equus cabal
4	183.5	22.1	177	1	IL1X_HUMAN	P18510 homo sapien
5	178.5	21.5	177	1	IL1X_PIG	Q29056 sus scrofa
6	173.5	20.9	266	1	IL1B_SHEEP	P21621 ovis aries
7	172.5	20.8	174	1	IL1X_BOVIN	O77482 bos taurus
8	170.5	20.5	177	1	IL1X_RABIT	P26890 oryctolagus
9	167	20.1	266	1	IL1B_CEREL	P51745 cervus elap
10	163.5	19.7	266	1	IL1B_BOVIN	P09428 bos taurus
11	162.5	19.6	266	1	IL1B_CAPHI	P79162 capra hircu
12	155	18.7	267	1	IL1B_PIG	P26889 sus scrofa
13	145.5	17.5	268	1	IL1B_MACFA	P79182 macaca fasc
14	145.5	17.5	269	1	IL1B_MACMU	P48090 macaca mula
15	143.5	17.3	269	1	IL1B_HUMAN	P01584 homo sapien
16	143.5	17.3	269	1	IL1B_MACNE	P51493 macaca neme
17	142.5	17.2	266	1	IL1B_CAVPO	Q9wvg1 cavia porce
18	141.5	17.0	268	1	IL1B_RABIT	P14628 oryctolagus
19	137.5	16.6	269	1	IL1B_CERTO	P46648 cercocebus
20	133.5	16.1	268	1	IL1B_HORSE	Q28386 equus cabal
21	128	15.4	268	1	IL1B_RAT	Q63264 rattus norv
22	126.5	15.2	267	1	IL1B_FELCA	P41687 felis silve
23	121	14.6	269	1	IL1B_MOUSE	P10749 mus musculu
24	118.5	14.3	269	1	IL1B_TRIVU	Q9xs77 trichosurus
25	82	9.9	270	1	IL1A_HORSE	Q28385 equus cabal
26	79	9.5	268	1	IL1A_CAPHI	P79161 capra hircu
27	79	9.5	270	1	IL1A_FELCA	O46613 felis silve
28	77	9.3	268	1	IL1A_BOVIN	P08831 bos taurus
29	76	9.2	501	1	GLPK_ECOLI	P08859 escherichia
30	75.5	9.1	270	1	IL1A_PIG	P18430 sus scrofa
31	75	9.0	1505	1	CUT2_HUMAN	O14529 homo sapien
32	74	8.9	268	1	IL1A_SHEEP	Q28579 ovis aries
33	73.5	8.9	1297	1	PUR4_HAEIN	P43847 haemophilus
34	72.5	8.7	325	1	RIR2_MYCLE	Q9cbq2 mycobacteri
35	72.5	8.7	950	1	IF2_LACLC	Q9x764 lactococcus
36	72	8.7	1220	1	IF2P_HUMAN	O60841 homo sapien
37	72	8.7	1955	1	PC15_HUMAN	Q96qu1 homo sapien
38	71.5	8.6	421	1	CHDE_MUCRO	P50325 mucor rouxi
39	71	8.6	872	1	MGR2_HUMAN	Q14416 homo sapien
40	71	8.6	1426	1	CUT2_MOUSE	P70298 mus musculu
41	71	8.6	1943	1	PC15_MOUSE	Q99pj1 mus musculu
42	70.5	8.5	271	1	IL1A_MACFA	P79340 macaca fasc
43	70.5	8.5	556	1	CD19_HUMAN	P15391 homo sapien
44	70.5	8.5	944	1	IF2_LACLA	P58002 lactococcus
45	70	8.4	265	1	IL1A_CANFA	O46612 canis famil

ALIGNMENTS

RESULT 1
IL1X_MOUSE
ID IL1X_MOUSE STANDARD; PRT; 178 AA.
AC P25085; O70207;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE (IRAP).
GN IL1RN OR IL-1RA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=91250712; PubMed=1828262;
RA Zahedi K., Seldin M.F., Rits M., Ezekowitz R.A., Whitehead A.S.;
RT "Mouse IL-1 receptor antagonist protein. Molecular characterization,
RT gene mapping, and expression of mRNA in vitro and in vivo.";
RL J. Immunol. 146:4228-4233(1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=91316273; PubMed=1830498;
RA Matsushime H., Roussel M.F., Matsushima K., Hishinuma A., Sherr C.J.;
RT "Cloning and expression of murine interleukin-1 receptor antagonist
RT in macrophages stimulated by colony-stimulating factor 1.";
RL Blood 78:616-623(1991).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=SWISS;
RX MEDLINE=94271931; PubMed=8003626;
RA Zahedi K.A., Uhlar C.M., Rits M., Prada A.E., Whitehead A.S.;
RT "The mouse interleukin 1 receptor antagonist protein: gene structure
RT and regulation in vitro.";
RL Cytokine 6:1-9(1994).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=FVBXDBA/1 LACJ;
RX MEDLINE=98209757; PubMed=9550387;
RA Gabay C., Porter B., Fantuzzi G., Arend W.P.;
RT "Mouse IL-1 receptor antagonist isoforms: complementary DNA cloning
RT and protein expression of intracellular isoform and tissue
RT distribution of secreted and intracellular IL-1 receptor antagonist in
RT vivo.";
RL J. Immunol. 159:5905-5913(1997).
RN [5]
RP SEQUENCE OF 7-178 FROM N.A.
RX MEDLINE=91271363; PubMed=1828896;
RA Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
RA Brandhuber B.J., Thompson R.C.;
RT "Interleukin 1 receptor antagonist is a member of the interleukin 1
RT gene family: evolution of a cytokine control mechanism.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
RN [6]
RP SEQUENCE OF 23-178 FROM N.A.

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RX   MEDLINE=92037824; PubMed=1834470;
RA   Shuck M.E., Eessalu T.E., Tracey D.E., Bienkowski M.J.;
RT   "Cloning, heterologous expression and characterization of murine
RT   interleukin 1 receptor antagonist protein.";
RL   Eur. J. Immunol. 21:2775-2780(1991).
CC   -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC       RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC   -!- SUBCELLULAR LOCATION: SECRETED (ISOFORM 1) OR INTRACELLULAR
CC       (ISOFORM 2).
CC   -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC       produced by alternative splicing.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M74294; AAA39309.1; -.
DR   EMBL; M64404; AAA39277.1; -.
DR   EMBL; L32838; AAA20576.1; -.
DR   EMBL; AF001795; AAC15251.1; -.
DR   EMBL; M57525; AAA39278.1; -.
DR   EMBL; M63100; AAA39310.1; -.
DR   EMBL; S64082; AAB20265.1; -.
DR   PIR; B40956; B40956.
DR   PIR; A44610; A44610.
DR   HSSP; P18510; 1IRA.
DR   MGD; MGI:96547; Il1rn.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Glycoprotein; Signal; Alternative splicing.
FT   SIGNAL        1     26       BY SIMILARITY.
FT   CHAIN        27    178       INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT                                 PROTEIN.
FT   DISULFID     92    142       BY SIMILARITY.
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC      1     21       MEICWGPYSHLISLLLLILLFH -> MA (IN ISOFORM
FT                                 2).
SQ   SEQUENCE   178 AA;  20274 MW;  84AA002A3119C024 CRC64;
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  Query Match             23.6%;  Score 195.5;  DB 1;  Length 178;
  Best Local Similarity   35.1%;  Pred. No. 2.3e-13;
  Matches   47;  Conservative   21;  Mismatches   45;  Indels   21;  Gaps    2;

Qy      15 IQDINHRVWVLQDQTLIA-------VPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGL 67
           | | | : : |::  |||       :  ::::  | | | |              ::|||:
Db      41 IWDTNQKTFYLRNNQLIAGYLQGPNIKLEEKIDMVPIDLHS--------------VFLGI 86

Qy      68 NGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWF 127
           :|  ||| ||| ||   |||:| :| ||    |  | | |  |: |  ::||| | ||||
Db      87 HGGKLCLSCAKSGDDIKLQLEEVNITDLSKNKEEDKRFTFIRSEKGPTTSFESAACPGWF 146

Qy     128 IAVSSEGGCPLILT 141
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Db     147 LCTTLEADRPVSLT 160
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RESULT   2
IL1X_RAT
ID   IL1X_RAT       STANDARD;      PRT;   178 AA.
AC   P25086;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE   (IRAP).
GN   IL1RN OR IL-1RA.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91271363; PubMed=1828896;
RA   Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
RA   Brandhuber B.J., Thompson R.C.;
RT   "Interleukin 1 receptor antagonist is a member of the interleukin 1
RT   gene family: evolution of a cytokine control mechanism.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
CC   -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC       RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M63101; AAA41434.1; -.
DR   PIR; C40956; C40956.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Glycoprotein; Signal.
FT   SIGNAL        1     26       BY SIMILARITY.
FT   CHAIN        27    178       INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT                                 PROTEIN.
FT   DISULFID     92    142       BY SIMILARITY.
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   178 AA;  20282 MW;  F3A5754FB6C51B03 CRC64;
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  Query Match             23.0%;  Score 190.5;  DB 1;  Length 178;
  Best Local Similarity   35.1%;  Pred. No. 7.5e-13;
  Matches   46;  Conservative   20;  Mismatches   50;  Indels   15;  Gaps    2;

Qy      15 IQDINHRVWVLQDQTLIA----VPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNGL 70
           | | | : : |::  |||    |      : :  |  |:|           :||::|
Db      41 IWDTNQKTFYLRNNQLIAGYLQGPNTKLEEKIDMVPIDFRNV----------FLGIHGG 89

Qy      71 NLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAV 130
           |||  | | ||   |||:| :| ||    |  | | |  |::|  ::|||:| ||||:
Db      90 KLCLSCVKSGDDTKLQLEEVNITDLNKNKEEDKRFTFIRSETGPTTSFESLACPGWFLCT 149

Qy     131 SSEGGCPLILT 141
           : |   |: ||
Db     150 TLEADHPVSLT 160
```

```
RESULT   3
IL1X_HORSE
ID   IL1X_HORSE     STANDARD;      PRT;   177 AA.
AC   O18999; O77745;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE   (IRAP).
GN   IL1RN OR IL1RA.
OS   Equus caballus (Horse).
```

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97366446; PubMed=9223227;
RA   Kato H., Ohashi T., Matsushiro H., Watari T., Goitsuka R.,
RA   Tsujimoto H., Hasegawa A.;
RT   "Molecular cloning and functional expression of equine interleukin-1
RT   receptor antagonist.";
RL   Vet. Immunol. Immunopathol. 56:221-231(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98285942; PubMed=9622739;
RA   Howard R.D., McIlwraith C.W., Trotter G.W., Nyborg J.K.;
RT   "Cloning of equine interleukin-1 receptor antagonist and
RT   determination of its full-length cDNA sequence.";
RL   Am. J. Vet. Res. 59:712-716(1998).
CC   -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC       RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D83714; BAA22529.1; -.
DR   EMBL; U92482; AAC39257.1; -.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Glycoprotein; Signal.
FT   SIGNAL        1     25       BY SIMILARITY.
FT   CHAIN        26    177       INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT                                PROTEIN.
FT   DISULFID      91    141      BY SIMILARITY.
FT   CARBOHYD     109    109      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT      19     19      F -> L (IN REF. 2).
SQ   SEQUENCE   177 AA;  20459 MW;  1ABC377F1F1CF80B CRC64;


  Query Match             22.5%;  Score 186.5;  DB 1;  Length 177;
  Best Local Similarity   33.3%;  Pred. No. 2e-12;
  Matches   43;  Conservative   25;  Mismatches   54;  Indels    7;  Gaps    2;

Qy      15 IQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNGLNLCL 74
           | |:| : : :::  |:|   ::  : :   :     |  :| |    ::|||:|  |||
Db   .  40 IWDVNQKTFYMRNNQLVAGYLQESNTKLQEKI----DVVPIEPD---ALFLGLHGRKLCL 92

Qy      75 MCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIAVSSEG 134
             | | ||:   ||:  :| ||    |  | | |  | ||  ::||| | ||||:  : |
Db      93 ACVKSGDEIRFQLEAVNITDLSKNKEENKRFTFIRSNSGPTTSFESAACPGWFLCTAQEA 152

Qy     135 GCPLILTQE 143
             |: || :
Db     153 DRPVSLTNK 161


RESULT   4
IL1X_HUMAN
ID   IL1X_HUMAN     STANDARD;      PRT;   177 AA.
AC   P18510; Q14628; Q9UPC0;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Interleukin-1 receptor antagonist protein precursor (IL-1RA) (ICIL-
DE   1RA) (IRAP) (IL-1RN).
GN   IL1RN OR IL1RA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=90220867; PubMed=2139180;
RA   Carter D.B., Deibel M.R. Jr., Dunn C.J., Tomich C.S.C., Laborde A.L.,
RA   Slightom J.L., Berger A.E., Bienkowski M.J., Sun F.F., McEwan R.N.,
RA   Harris P.K.W., Yem A.W., Waszak G.A., Chosay J.G., Sieu L.C.,
RA   Hardee M.M., Zurcher-Neely H.A., Reardon I.M., Heinrikson R.L.,
RA   Truesdell S.E., Shelly J.A., Eessalu T.E., Taylor B.M., Tracey D.E.;
RT   "Purification, cloning, expression and biological characterization of
RT   an interleukin-1 receptor antagonist protein.";
RL   Nature 344:633-638(1990).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=90136921; PubMed=2137201;
RA   Eisenberg S.P., Evans R.J., Arend W.P., Verderber E., Brewer M.T.,
RA   Hannum C.H., Thompson R.C.;
RT   "Primary structure and functional expression from complementary DNA
RT   of a human interleukin-1 receptor antagonist.";
RL   Nature 343:341-346(1990).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=91271363; PubMed=1828896;
RA   Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
RA   Brandhuber B.J., Thompson R.C.;
RT   "Interleukin 1 receptor antagonist is a member of the interleukin 1
RT   gene family: evolution of a cytokine control mechanism.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=92338323; PubMed=1385987;
RA   Lennard A., Gorman P., Carrier M., Griffiths S., Scotney H.,
RA   Sheer D., Solari R.;
RT   "Cloning and chromosome mapping of the human interleukin-1 receptor
RT   antagonist gene.";
RL   Cytokine 4:83-89(1992).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
RX   MEDLINE=97146044; PubMed=8992991;
RA   Jenkins J.K., Drong R.F., Shuck M.E., Bienkowski M.J., Slightom J.L.,
RA   Arend W.P., Smith M.F. Jr.;
RT   "Intracellular IL-1 receptor antagonist promoter: cell type-specific
RT   and inducible regulatory regions.";
RL   J. Immunol. 158:748-755(1997).
RN   [6]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RX   MEDLINE=91219436; PubMed=1827201;
RA   Haskill S., Martin G., van Le L., Morris J., Peace A., Bigler C.F.,
RA   Jaffe G.J., Hammerberg C., Sporn S.A., Fong S., Arend W.P., Ralph P.;
RT   "cDNA cloning of an intracellular form of the human interleukin 1
RT   receptor antagonist associated with epithelium.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:3681-3685(1991).
RN   [7]
RP   SEQUENCE FROM N.A. (ISOFORM 3).
RX   MEDLINE=95355865; PubMed=7629520;
RA   Muzio M., Polentarutti N., Sironi M., Poli G., De Gioia L.,
RA   Introna M., Mantovani A., Colotta F.;
RT   "Cloning and characterization of a new isoform of the interleukin 1
RT   receptor antagonist.";
RL   J. Exp. Med. 182:623-628(1995).
RN   [8]
RP   SEQUENCE OF 26-45.
RX   MEDLINE=90136920; PubMed=2137200;
RA   Hannum C.H., Wilcox C.J., Arend W.P., Joslin F.G., Dripps D.J.,
RA   Heimdal P.L., Armes L.G., Sommer A., Eisenberg S.P., Thompson R.C.;
RT   "Interleukin-1 receptor antagonist activity of a human interleukin-1
RT   inhibitor.";
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RL   Nature 343:336-340(1990).
RN   [9]
RP   SEQUENCE OF 26-52.
RX   MEDLINE=90354444; PubMed=2143761;
RA   Bienkowski M.J., Eessalu T.E., Berger A.E., Truesdell S.E.,
RA   Shelly J.A., Laborde A.L., Zurcher-Neely H.A., Reardon I.M.,
RA   Heinrikson R.L., Chosay J.G., Tracey D.E.;
RT   "Purification and characterization of interleukin 1 receptor level
RT   antagonist proteins from THP-1 cells.";
RL   J. Biol. Chem. 265:14505-14511(1990).
RN   [10]
RP   SEQUENCE OF 35-177 FROM N.A. (ISOFORM 4).
RX   MEDLINE=98183404; PubMed=9514884;
RA   Weissbach L., Tran K., Colquhoun S.A., Champliaud M.F., Towle C.A.;
RT   "Detection of an interleukin-1 intracellular receptor antagonist mRNA
RT   variant.";
RL   Biochem. Biophys. Res. Commun. 244:91-95(1998).
RN   [11]
RP   STRUCTURE BY NMR.
RX   MEDLINE=92297633; PubMed=1534997;
RA   Stockman B.J., Scahill T.A., Roy M., Ulrich E.L., Strakalaitis N.A.,
RA   Brunner D.P., Yem A.W., Deibel M.R. Jr.;
RT   "Secondary structure and topology of interleukin-1 receptor
RT   antagonist protein determined by heteronuclear three-dimensional NMR
RT   spectroscopy.";
RL   Biochemistry 31:5237-5244(1992).
RN   [12]
RP   STRUCTURE BY NMR.
RX   MEDLINE=94320651; PubMed=8045306;
RA   Stockman B.J., Scahill T.A., Strakalaitis N.A., Brunner D.P.,
RA   Yem A.W., Deibel M.R. Jr.;
RT   "Solution structure of human interleukin-1 receptor antagonist
RT   protein.";
RL   FEBS Lett. 349:79-83(1994).
RN   [13]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=94230368; PubMed=8175703;
RA   Vigers G.P.A., Caffes P., Evans R.J., Thompson R.C., Eisenberg S.P.,
RA   Brandhuber B.J.;
RT   "X-ray structure of interleukin-1 receptor antagonist at 2.0-A
RT   resolution.";
RL   J. Biol. Chem. 269:12874-12879(1994).
RN   [14]
RP   X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX   MEDLINE=95172072; PubMed=7867645;
RA   Schreuder H.A., Rondeau J.-M., Tardif C., Soffientini A., Sarubbi E.,
RA   Akeson A., Bowlin T.L., Yanofsky S., Barrett R.W.;
RT   "Refined crystal structure of the interleukin-1 receptor antagonist.
RT   Presence of a disulfide link and a cis-proline.";
RL   Eur. J. Biochem. 227:838-847(1995).
RN   [15]
RP   X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 32-177 IN COMPLEX WITH IL1R.
RX   MEDLINE=97215904; PubMed=9062194;
RA   Schreuder H., Tardif C., Trump-Kallmeyer S., Soffientini A.,
RA   Sarubbi E., Akeson A., Bowlin T., Yanofsky S., Barrett R.W.;
RT   "A new cytokine-receptor binding mode revealed by the crystal
RT   structure of the IL-1 receptor with an antagonist.";
RL   Nature 386:194-200(1997).
CC   -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC       RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC   -!- SUBCELLULAR LOCATION: SECRETED (ISOFORM 1) OR INTRACELLULAR
CC       (ISOFORMS 2, 3 AND 4).
CC   -!- ALTERNATIVE PRODUCTS: 4 isoforms; 1 (shown here), 2/icIL-1ra,
CC       3/icIL-1ra type II and 4; are produced by alternative splicing.
CC   -!- TISSUE SPECIFICITY: THE INTRACELLULAR FORM OF IL-1RA IS
CC       PREDOMINANTLY EXPRESSED IN EPITHELIAL CELLS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   -!- DATABASE: NAME=R&D Systems' cytokine source book: IL1RN;
CC       WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=205".
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M55646; AAA59138.1; -.
DR   EMBL; M63099; AAB41943.1; -.
DR   EMBL; X52015; CAA36262.1; -.
DR   EMBL; X53296; CAA37386.1; -.
DR   EMBL; X64532; CAA45832.1; -.
DR   EMBL; U65590; AAB92268.1; -.
DR   EMBL; U65590; AAB92270.1; -.
DR   EMBL; X84348; CAA59087.1; -.
DR   EMBL; U65590; AAB92269.1; -.
DR   EMBL; AF043143; AAC39672.1; -.
DR   PIR; A30368; A30368.
DR   PIR; A37822; A37822.
DR   PIR; S08160; S08160.
DR   PIR; S08159; S08159.
DR   PIR; A40956; A40956.
DR   PIR; A39386; A39386.
DR   PDB; 1ITN; 30-APR-94.
DR   PDB; 2IRT; 15-OCT-94.
DR   PDB; 1IRP; 27-FEB-95.
DR   PDB; 1ILR; 07-FEB-95.
DR   PDB; 1ILT; 01-APR-95.
DR   PDB; 1IRA; 17-JUN-98.
DR   Aarhus/Ghent-2DPAGE; 7104; IEF.
DR   Aarhus/Ghent-2DPAGE; 7105; IEF.
DR   MIM; 147679; -.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Glycoprotein; Signal; Alternative splicing; 3D-structure.
FT   SIGNAL        1     25
FT   CHAIN        26    177       INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT                                 PROTEIN.
FT   DISULFID      91    141
FT   CARBOHYD     109    109       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC       1     21       MEICRGLRSHLITLLLFLFHS -> MAL (IN
FT                                 ISOFORM 2).
FT   VARSPLIC       1     21       MEICRGLRSHLITLLLFLFHS -> MALADLYEEGGGGGGE
FT                                 GEDNADSK (IN ISOFORM 3).
FT   VARSPLIC       1     34       MISSING (IN ISOFORM 4).
SQ   SEQUENCE   177 AA;  20055 MW;  D1690776A7394057 CRC64;


  Query Match             22.1%;  Score 183.5;  DB 1;  Length 177;
  Best Local Similarity   30.6%;  Pred. No. 4e-12;
  Matches   45;  Conservative   26;  Mismatches   49;  Indels   27;  Gaps    3;

Qy      15 IQDINHRVWVLQDQTLIA-------VPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGL 67
           | |:| : : |::  |:|       |  ::::  | |                : ::||:
Db      40 IWDVNQKTFYLRNNQLVAGYLQGPNVNLEEKIDVVPI-------------EPHALFLGI 85

Qy      68 NGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWF 127
           :|  :|| | | ||:  |||:  :| ||    :  | | |  | ||  ::||| | ||||
Db      86 HGGKMCLSCVKSGDETRLQLEAVNITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWF 145

Qy     128 IAVSSEGGCPLILTQELGKANTTDFGL 154
           :  : |   |: ||       |  | |:
Db     146 LCTAMEADQPVSLT------NMPDEGV 166


RESULT   5
IL1X_PIG
ID   IL1X_PIG       STANDARD;      PRT;   177 AA.
AC   Q29056;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
```

```
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE   (IRAP).
GN   IL1RN OR IRAP1.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CROSSBREED; TISSUE=Lung;
RA   Yin J., Murtaugh M.P.;
RT   "Characterization of IRAP in morphine treated pig.";
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC       RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L38849; AAA99424.1; -.
DR   HSSP; P18510; 1IRA.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Glycoprotein; Signal.
FT   SIGNAL        1     25       BY SIMILARITY.
FT   CHAIN        26    177       INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT                                PROTEIN.
FT   DISULFID      91    141      BY SIMILARITY.
FT   CARBOHYD     109    109      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   177 AA;  20093 MW;  2114DC6119A9D5F9 CRC64;


  Query Match             21.5%;  Score 178.5;  DB 1;  Length 177;
  Best Local Similarity   32.4%;  Pred. No. 1.3e-11;
  Matches   44;  Conservative   20;  Mismatches   47;  Indels   25;  Gaps    2;

Qy      15 IQDINHRVWVLQDQTLIA---------VPRKDRMSPVTIALISCRHVETLEKDRGNPIYL 65
           | |:| : : |::  |:|         :  |  : ||                : ::|
Db      40 IWDVNQKTFYLRNNQLVAGYLQGPNTKLEEKIDVVPV----------------EPHFVFL 83

Qy      66 GLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPG 125
           |::|  ||| | | ||:  |||   :| ||    |  | | |  | ||  ::||| | ||
Db      84 GIHGGKLCLSCVKSGDEMKLQLDAVNITDLRKNSEQDKRFTFIRSDSGPTTSFESAACPG 143

Qy     126 WFIAVSSEGGCPLILT 141
           ||:  : |   |: ||
Db     144 WFLCTALEADQPVGLT 159


RESULT   6
IL1B_SHEEP
ID   IL1B_SHEEP     STANDARD;      PRT;   266 AA.
AC   P21621;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Interleukin-1 beta precursor (IL-1 beta).
GN   IL1B.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92119335; PubMed=1840515;
RA   Seow H.F., Rothel J.S., David M.J., Wood P.R.;
RT   "Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.";
RL   DNA Seq. 1:423-426(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91088326; PubMed=2263490;
RA   Fiskerstrand C., Sargan D.;
RT   "Nucleotide sequence of ovine interleukin-1 beta.";
RL   Nucleic Acids Res. 18:7165-7165(1990).
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC   -!- SUBUNIT: MONOMER.
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X54796; CAA38566.1; -.
DR   EMBL; X56972; CAA40293.1; -.
DR   PIR; S13092; S13092.
DR   PIR; S13810; S13810.
DR   PIR; S23010; S23010.
DR   HSSP; P01584; 5I1B.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP        1    113
FT   CHAIN       114    266       INTERLEUKIN-1 BETA.
FT   CONFLICT     14     14       Y -> C (IN REF. 2).
FT   CONFLICT     55     55       Q -> K (IN REF. 2).
FT   CONFLICT     64     64       V -> A (IN REF. 2).
FT   CONFLICT    145    145       P -> L (IN REF. 2).
SQ   SEQUENCE   266 AA;  30717 MW;  BDED07B58224AB78 CRC64;


  Query Match             20.9%;  Score 173.5;  DB 1;  Length 266;
  Best Local Similarity   30.8%;  Pred. No. 7.5e-11;
  Matches   48;  Conservative   27;  Mismatches   62;  Indels   19;  Gaps    4;

Qy       2 EKALKIDTPQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGN 61
           :|:| :|:|             ||:    : :| ::    |   :     |:  |:|
Db     128 QKSLVLDSP-----------CVLK---ALHLPSQEMSREVVFCM---SFVQGEERDNKI 169

Qy      62 PIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESV 121
           |: ||:   || | | | || |||||:| |   :| :    | |:|| ::      ||||
Db     170 PVALGIRDKNLYLSCVKKGDTPTLQLEEVD-PKVYPKRNMEKRFVFYKTEIKNTVEFESV 228
```

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Qy    122 AFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
          :| |:|: |     |: | :  |  : |||  :  |
Db    229 LYPNWYISTSQIEEKPVFLGRFRGGQDITDFRMETL 264
```

```
RESULT   7
IL1X_BOVIN
ID   IL1X_BOVIN     STANDARD;      PRT;   174 AA.
AC   O77482;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE   (IRAP).
GN   IL1RN.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98305607; PubMed=9643454;
RA   Kirisawa R., Fukuda T., Yamanaka H., Hagiwara K., Goto M., Obata Y.,
RA   Yoshino T., Iwai H.;
RT   "Enzymatic amplification and expression of bovine interleukin-1
RT   receptor antagonist cDNA.";
RL   Vet. Immunol. Immunopathol. 62:197-208(1998).
CC   -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC       RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB005148; BAA31854.1; -.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Glycoprotein; Signal.
FT   SIGNAL        1     23       BY SIMILARITY.
FT   CHAIN        24    174       INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT                                 PROTEIN.
FT   DISULFID     89    139       BY SIMILARITY.
FT   CARBOHYD    107    107       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   174 AA;  19926 MW;  1E56E7F224FF851F CRC64;
```

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  Query Match             20.8%;  Score 172.5;  DB 1;  Length 174;
  Best Local Similarity   30.6%;  Pred. No. 5.6e-11;
  Matches   41;  Conservative   25;  Mismatches   47;  Indels   21;  Gaps    2;

Qy      15 IQDINHRVWVLQDQTLIA-------VPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGL 67
           | |:| ::: |::  |:|          ::::  | |               : ::||:
Db      38 IWDVNQKIFYLRNNQLVAGYLQGPNTKLEEKIDVVPI-------------EPHTMFLGI 83

Qy      68 NGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWF 127
           :|  ||| | | ||:  |:|:  :| ||    |  | | |    :|  ::||| | ||||
Db      84 HGGKLCLACVKSGDEIKLKLEAVNITDLNQNREQDKRFAFIRFDNGPTTSFESAACPGWF 143

Qy     128 IAVSSEGGCPLILT 141
           :  | |   |: ||
Db     144 LCTSLEADQPVGLT 157
```

```
RESULT   8
IL1X_RABIT
ID   IL1X_RABIT     STANDARD;      PRT;   177 AA.
AC   P26890;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE   (IRAP).
GN   IL1RN OR IL1RA.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94165101; PubMed=7509813;
RA   Cominelli F., Bortolami M., Pizarro T.T., Monsacchi L., Ferretti M.,
RA   Brewer M.T., Eisenberg S.P., Ng R.K.;
RT   "Rabbit interleukin-1 receptor antagonist. Cloning, expression,
RT   functional characterization, and regulation during intestinal
RT   inflammation.";
RL   J. Biol. Chem. 269:6962-6971(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Hamada H., Mulligan R.C.;
RL   Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93052512; PubMed=1427977;
RA   Goto F., Goto K., Miyata T., Ohkawara S., Takao T., Mori S.,
RA   Furukawa S., Maeda T., Iwanaga S., Shimonishi Y., Yoshinaga M.;
RT   "Interleukin-1 receptor antagonist in inflammatory exudate cells of
RT   rabbits. Production, purification and determination of primary
RT   structure.";
RL   Immunology 77:235-244(1992).
CC   -!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC       RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; S68977; AAB30093.1; -.
DR   EMBL; M57526; AAA31374.1; -.
DR   EMBL; D21832; BAA04860.1; -.
DR   PIR; A54377; A54377.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   PRINTS; PR00264; INTERLEUKIN1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Glycoprotein; Signal.
FT   SIGNAL        1     25       BY SIMILARITY.
FT   CHAIN        26    177       INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT                                 PROTEIN.
FT   DISULFID     91    141       BY SIMILARITY.
FT   CARBOHYD    109    109       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   177 AA;  20214 MW;  F5BC087F097FFEAF CRC64;
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  Query Match             20.5%;  Score 170.5;  DB 1;  Length 177;
  Best Local Similarity   30.6%;  Pred. No. 9.3e-11;
  Matches   44;  Conservative   21;  Mismatches   52;  Indels   27;  Gaps    3;
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Qy      15 IQDINHRVWVLQDQTLIA-------VPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGL 67
           | |:| : : |::  |:|         ::|:  | :                ::||:
Db      40 IWDVNQKTFYLRNNQLVAGYLQGPNAKLEERIDVVPL--------------EPQLLFLGI 85

Qy      68 NGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWF 127
              ||| | | ||:  | |:  :| ||    |  | | |  | ||  :|||| : ||||
Db      86 QRGKLCLSCVKSGDKMKLHLEAVNITDLGKNKEQDKRFTFIRSNSGPTTTFESASCPGWF 145

Qy     128 IAVSSEGGCPLILTQELGKANTTD 151
           :  : |   |: ||      || |
Db     146 LCTALEADQPVSLT------NTPD 163


RESULT   9
IL1B_CEREL
ID   IL1B_CEREL     STANDARD;      PRT;   266 AA.
AC   P51745;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Interleukin-1 beta precursor (IL-1 beta).
GN   IL1B.
OS   Cervus elaphus (Red deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Cervinae; Cervus.
OX   NCBI_TaxID=9860;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lockhart E.A.;
RL   Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION AND PROLIFERATION, AND FIBROBLAST GROWTH FACTOR
CC       ACTIVITY. IL-1S ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS
CC       (BY SIMILARITY).
CC   -!- SUBUNIT: MONOMER (By similarity).
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U20500; AAA62234.1; -.
DR   HSSP; P01584; 1HIB.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP        1    113       BY SIMILARITY.
FT   CHAIN       114    266       INTERLEUKIN-1 BETA.
SQ   SEQUENCE   266 AA;  30629 MW;  4F40B4E6F0D9F060 CRC64;


  Query Match             20.1%;  Score 167;  DB 1;  Length 266;
  Best Local Similarity   31.4%;  Pred. No. 3.6e-10;
  Matches   49;  Conservative   25;  Mismatches   64;  Indels   18;  Gaps    5;

Qy      14 SIQDINHRVWVLQDQ----TLIAVP--------RKDRMSPVTIALISCRHVETLEKDRGN 61
           ::| :| :   |||:     ::| |            ||   :  :|   |:  |:|
Db     115 AVQSVNCK---LQDREQNSLVLASPCVLKALHLLSQEMSREVVFCMS--FVQAEERDNKI 169

Qy      62 PIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESV 121
           |: ||:   |  | | | || |||||:| |   :| :    | |:|| ::      ||||
Db     170 PVALGIRDKNQYLSCVKKGDTPTLQLEEVD-PKVYPKRNMEKRFVFYKTEIKDTVEFESV 228

Qy     122 AFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
           :| |:|: |     |: |    |  : ||| :  |
Db     229 LYPNWYISTSHPEEKPVFLGHFRGGQDITDFRMETL 264


RESULT  10
IL1B_BOVIN
ID   IL1B_BOVIN     STANDARD;      PRT;   266 AA.
AC   P09428;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Interleukin-1 beta precursor (IL-1 beta).
GN   IL1B.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89016591; PubMed=3262866;
RA   Leong S.R., Flaggs G.M., Lawman M., Gray P.W.;
RT   "The nucleotide sequence for the cDNA of bovine interleukin-1 beta.";
RL   Nucleic Acids Res. 16:9054-9054(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88318652; PubMed=3261832;
RA   Maliszewski C.R., Baker P.E., Schoenborn M.A., Davis B.S., Cosman D.,
RA   Gillis S., Cerretti D.P.;
RT   "Cloning, sequence and expression of bovine interleukin 1 alpha and
RT   interleukin 1 beta complementary DNAs.";
RL   Mol. Immunol. 25:429-437(1988).
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC   -!- SUBUNIT: MONOMER.
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M35589; AAA30585.1; -.
DR   EMBL; X12498; CAA31018.1; -.
DR   EMBL; M37211; AAA30584.1; -.
DR   PIR; JL0010; ICBO1B.
DR   PIR; S01380; S01380.
DR   HSSP; P01584; 1HIB.
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DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP        1    113
FT   CHAIN       114    266       INTERLEUKIN-1 BETA.
FT   CONFLICT    252    252       A -> G (IN REF. 2).
SQ   SEQUENCE   266 AA;  30774 MW;  9D1EF8F575070586 CRC64;


  Query Match             19.7%;  Score 163.5;  DB 1;  Length 266;
  Best Local Similarity   36.8%;  Pred. No. 8.3e-10;
  Matches   39;  Conservative   16;  Mismatches   50;  Indels    1;  Gaps    1;

Qy      52 VETLEKDRGNPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQ 111
           |:  |:|   |: ||:   || | | | || |||||:| |   :| :    | |:|| ::
Db     160 VQGEERDNKIPVALGIKDKNLYLSCVKKGDTPTLQLEEVD-PKVYPKRNMEKRFVFYKTE 218

Qy     112 SGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
                ||||  :| |:|: |     |: |       : ||| :  |
Db     219 IKNTVEFESVLYPNWYISTSQIEERPVFLGHFRAGQDITDFRMETL 264


RESULT  11
IL1B_CAPHI
ID   IL1B_CAPHI     STANDARD;      PRT;   266 AA.
AC   P79162;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Interleukin-1 beta precursor (IL-1 beta).
GN   IL1B.
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Capra.
OX   NCBI_TaxID=9925;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Takakura H., Hashimoto O., Mori Y., Tatsumi M.;
RT   "Molecular cloning and expression of caprine IL-1alpha and
RT   IL-1beta.";
RL   Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS
CC       (BY SIMILARITY).
CC   -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; D63351; BAA09675.1; -.
DR   HSSP; P01584; 1HIB.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP        1    113       BY SIMILARITY.
FT   CHAIN       114    266       INTERLEUKIN-1 BETA.
SQ   SEQUENCE   266 AA;  30769 MW;  59F7B39BD1D4DDA5 CRC64;


  Query Match             19.6%;  Score 162.5;  DB 1;  Length 266;
  Best Local Similarity   31.4%;  Pred. No. 1.1e-09;
  Matches   49;  Conservative   25;  Mismatches   63;  Indels   19;  Gaps    4;

Qy       2 EKALKIDTPQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGN 61
             :|:| :|:|              ||:   |::      ||   :  :|   |:  |:|
Db     128 QKSLVLDSP-----------CVLKALHLLS----QEMSREVVFCMS--FVQGEERDNKI 169

Qy      62 PIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESV 121
           |: ||:   || |   | || |||||:| |   :| :    | |:|| ::      ||||
Db     170 PVALGIRDKNLYLSWVKKGDTPTLQLEEVD-PKVYPKRNMEKRFVFYKTEIKNTVEFESV 228

Qy     122 AFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
             :| |:|: |     |: |    |  : ||| :  |
Db     229 LYPNWYISTSQIEEKPVFLGHFRGGQDITDFRMETL 264


RESULT  12
IL1B_PIG
ID   IL1B_PIG       STANDARD;      PRT;   267 AA.
AC   P26889;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Interleukin-1 beta precursor (IL-1 beta).
GN   IL1B.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93314975; PubMed=8325511;
RA   Huether M.J., Lin G., Smith D.M., Murtaugh M.P., Molitor T.W.;
RT   "Cloning, sequencing and regulation of an mRNA encoding porcine
RT   interleukin-1 beta.";
RL   Gene 129:285-289(1993).
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC   -!- SUBUNIT: MONOMER.
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M86725; AAA02584.1; -.
DR   PIR; JN0724; JN0724.
DR   HSSP; P01584; 1HIB.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP        1    114       BY SIMILARITY.
FT   CHAIN       115    267       INTERLEUKIN-1 BETA.
SQ   SEQUENCE   267 AA;  30404 MW;  7F6B92B784D5086F CRC64;


  Query Match             18.7%;  Score 155;  DB 1;  Length 267;
  Best Local Similarity   22.8%;  Pred. No. 6.5e-09;
  Matches   52;  Conservative   34;  Mismatches   66;  Indels   76;  Gaps    7;

Qy       5 LKIDTPQRGSIQ-DINHRVW---VLQDQTLIAVPRKDRMSPVT---------------- 43
           | : : : ||||  |:|::|   : |  ::|    |   :| :
Db      39 LDLGSLRNGSIQLQISHQLWNKSIRQMVSVIVAVEKPMKNPSSQAFCDDDQKSIFSFIFE 98

Qy      44 ---IALISCR-------HVETLE----------------------------------- 56
              | | :|        :|:::|
Db      99 EEPIILETCNDDFVCDANVQSMECKLQDKDHKSLVLAGPHMLKALHLLTGDLKREVVFCM 158

Qy      57 -----KDRGN--PIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYH 109
                 |  |  |: ||: | || | |    : |||||:: |    | : :  | |:||
Db     159 SFVQGDDSNNKIPVTLGIKGKNLYLSCVMKDNTPTLQLEDID-PKRYPKRDMEKRFVFYK 217

Qy     110 SQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
           ::      |||  :| |:|: |     |: |    |: : ||| : :|
Db     218 TEIKNRVEFESALYPNWYISTSQAEQKPVFLGNSKGRQDITDFTMEVL 265


RESULT  13
IL1B_MACFA
ID   IL1B_MACFA     STANDARD;      PRT;   268 AA.
AC   P79182;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Interleukin-1 beta precursor (IL-1 beta).
GN   IL1B.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Thymus;
RA   Totsuka K., Takakura H., Hashimoto O., Tatsumi M.;
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
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CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC   -!- SUBUNIT: MONOMER.
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC       SECRETORY PROTEINS.
CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC   ---------------------------------------------------------------------
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CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D63353; BAA09677.1; -.
DR   HSSP; P01584; 1HIB.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP        1    116       BY SIMILARITY.
FT   CHAIN       117    268       INTERLEUKIN-1 BETA.
SQ   SEQUENCE   268 AA;  30425 MW;  CFB7266E3E2C05B4 CRC64;


  Query Match             17.5%;  Score 145.5;  DB 1;  Length 268;
  Best Local Similarity   34.5%;  Pred. No. 6.4e-08;
  Matches   39;  Conservative   15;  Mismatches   56;  Indels    3;  Gaps    2;

Qy      46 LISCRHVETLEKDRGNPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSF 105
           : |   |:  | :   |: |||   || | |   |:|||||:  |  : | : :  | |
Db     157 VFSMSFVQGEESNDKIPVALGLKAKNLYLSCVLKDDKPTLQLESVDPKN-YPKKKMEKRF 215

Qy     106 LFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTMLF 158
           :|   :      |||  || |:|: |     |: |    |  : |||  || |
Db     216 VFNKIEINNKLEFESAQFPNWYISTSQAESMPVFLGGTRGGQDITDF--TMQF 266


RESULT  14
IL1B_MACMU
ID   IL1B_MACMU     STANDARD;      PRT;   269 AA.
AC   P48090;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Interleukin-1 beta precursor (IL-1 beta).
GN   IL1B.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and
RT   nonhuman primates.";
RL   J. Immunol. 155:3946-3954(1995).
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC       IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC       THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC   -!- SUBUNIT: MONOMER.
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
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CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
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CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U19845; AAA86709.1; -.
DR   HSSP; P01584; 1HIB.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT   PROPEP        1    116       BY SIMILARITY.
FT   CHAIN       117    269       INTERLEUKIN-1 BETA.
SQ   SEQUENCE   269 AA;  30481 MW;  A7CD59EBAC120EC7 CRC64;


  Query Match             17.5%;  Score 145.5;  DB 1;  Length 269;
  Best Local Similarity   34.5%;  Pred. No. 6.5e-08;
  Matches   39;  Conservative   15;  Mismatches   56;  Indels    3;  Gaps    2;

Qy      46 LISCRHVETLEKDRGNPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSF 105
           : |   |:  | :   |: |||   || | |    |:|||||:  |  : | : :  | |
Db     157 VFSMSFVQGEESNDKIPVALGLKAKNLYLSCVLKDDKPTLQLESVDPKN-YPKKKMEKRF 215

Qy     106 LFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTMLF 158
           :|   :      |||  || |:|: |     |: |    |  : |||  || |
Db     216 VFNKIEINNKLEFESAQFPNWYISTSQAENMPVFLGGTRGGQDITDF--TMQF 266


RESULT  15
IL1B_HUMAN
ID   IL1B_HUMAN     STANDARD;      PRT;   269 AA.
AC   P01584; Q96HE5; Q9UCT6;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Interleukin-1 beta precursor (IL-1 beta) (Catabolin).
GN   IL1B.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85088517; PubMed=6083565;
RA   Auron P.E., Webb A.C., Rosenwasser L.J., Mucci S.F., Rich A.,
RA   Wolff S.M., Dinarello C.A.;
RT   "Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:7907-7911(1984).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85240547; PubMed=2989698;
RA   March C.J., Mosley B., Larsen A., Cerretti D.P., Braedt G., Price V.,
RA   Gillis S., Henney C.S., Kronheim S.R., Grabstein K., Conlon P.J.,
RA   Hopp T.P., Cosman D.;
RT   "Cloning, sequence and expression of two distinct human interleukin-1
RT   complementary DNAs.";
RL   Nature 315:641-647(1985).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87040762; PubMed=3490654;
RA   Clark B.D., Collins K.L., Gandy M.S., Webb A.C., Auron P.E.;
RT   "Genomic sequence for human prointerleukin 1 beta: possible evolution
RT   from a reverse transcribed prointerleukin 1 alpha gene.";
RL   Nucleic Acids Res. 14:7897-7914(1986).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87248099; PubMed=2954882;
RA   Bensi G., Raugei G., Palla E., Carinci V., Buonamassa D.T., Melli M.;
RT   "Human interleukin-1 beta gene.";
RL   Gene 52:95-101(1987).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90249285; PubMed=2635664;
RA   Kotenko S.V., Bulenkov M.T., Veiko V.P., Epishin S.M., Lomakin I.B.,
RA   Emel'Yanov A.V., Kozlov A.P., Konusova V.G., Kotov A.Y.,
RA   Kurbatova T.V., Reshetnikov V.L., Simbirtsev A.S., Ketlinskii S.A.,
RA   Vinetskii Y.P.;
RT   "Cloning of the cDNA coding for human prointerleukin-1 alpha and
RT   prointerleukin-1 beta.";
RL   Dokl. Akad. Nauk SSSR 309:1005-1008(1989).
RN   [6]
RP   SEQUENCE FROM N.A.
RA   Webb A.C., Dinarello C.A., Rosenwasser L.J., Mucci S.F., Rich A.,
RA   Wolff S.M., Auron P.E.;
RT   "Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.";
RL   Adv. Gene Technol. 22:339-340(1985).
RN   [7]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87156769; PubMed=3493774;
RA   Nishida T., Nishino N., Takano M., Kawai K., Bando K., Masui Y.,
RA   Nakai S., Hirai Y.;
RT   "cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell
RT   line.";
RL   Biochem. Biophys. Res. Commun. 143:345-352(1987).
RN   [8]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
RN   [9]
RP   SEQUENCE OF 117-128.
RX   MEDLINE=88184226; PubMed=3281727;
RA   Zsebo K.M., Wypych J., Yuschenkoff V.N., Lu H., Hunt P., Dukes P.P.,
RA   Langley K.E.;
RT   "Effects of hematopoietin-1 and interleukin 1 activities on early
RT   hematopoietic cells of the bone marrow.";
RL   Blood 71:962-968(1988).
RN   [10]
RP   SEQUENCE OF 114-135.
RC   TISSUE=Skin;
RX   MEDLINE=92013781; PubMed=1919436;
RA   Mizutani H., Schechter N., Lazarus G., Black R.A., Kupper T.S.;
RT   "Rapid and specific conversion of precursor interleukin 1 beta (IL-1
RT   beta) to an active IL-1 species by human mast cell chymase.";
RL   J. Exp. Med. 174:821-825(1991).
RN   [11]
RP   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX   MEDLINE=88211543; PubMed=3259176;
RA   Priestle J.P., Schar H.-P., Grutter M.G.;
RT   "Crystal structure of the cytokine interleukin-1 beta.";
RL   EMBO J. 7:339-343(1988).
RN   [12]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=90099325; PubMed=2602367;
RA   Priestle J.P., Schar H.-P., Grutter M.G.;
RT   "Crystallographic refinement of interleukin 1 beta at 2.0-A
RT   resolution.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:9667-9671(1989).
RN   [13]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
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RX   MEDLINE=90064532; PubMed=2585509;
RA   Finzel B.C., Clancy L.L., Holland D.R., Muchmore S.W.,
RA   Watenpaugh K.D., Einspahr H.M.;
RT   "Crystal structure of recombinant human interleukin-1 beta at 2.0-A
RT   resolution.";
RL   J. Mol. Biol. 209:779-791(1989).
RN   [14]
RP   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF COMPLEX WITH RECEPTOR.
RX   MEDLINE=97215903; PubMed=9062193;
RA   Vigers G.P., Anderson L.J., Caffes P., Brandhuber B.J.;
RT   "Crystal structure of the type-I interleukin-1 receptor complexed
RT   with interleukin-1beta.";
RL   Nature 386:190-194(1997).
RN   [15]
RP   STRUCTURE BY NMR.
RX   MEDLINE=90321925; PubMed=2372550;
RA   Driscoll P.C., Gronenborn A.M., Wingfield P.T., Clore G.M.;
RT   "Determination of the secondary structure and molecular topology of
RT   interleukin-1 beta by use of two- and three-dimensional heteronuclear
RT   15N-1H NMR spectroscopy.";
RL   Biochemistry 29:4668-4682(1990).
RN   [16]
RP   STRUCTURE BY NMR.
RX   MEDLINE=91159409; PubMed=2001363;
RA   Clore G.M., Wingfield P.T., Gronenborn A.M.;
RT   "High-resolution three-dimensional structure of interleukin 1 beta in
RT   solution by three- and four-dimensional nuclear magnetic resonance
RT   spectroscopy.";
RL   Biochemistry 30:2315-2323(1991).
CC   -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC       THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC       MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC       IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
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CC   -!- SUBUNIT: MONOMER.
CC   -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC   -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC       PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC       OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
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CC   -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
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CC   ---------------------------------------------------------------------
DR   EMBL; M15840; AAA74137.1; -.
DR   EMBL; X02532; CAA26372.1; -.
DR   EMBL; K02770; AAA36106.1; -.
DR   EMBL; X04500; CAA28185.1; -.
DR   EMBL; X56087; CAA39567.1; -.
DR   EMBL; M54933; AAA59136.1; -.
DR   EMBL; M15330; AAA59135.1; -.
DR   EMBL; BC008678; AAH08678.1; -.
DR   PIR; A01848; ICHU1B.
DR   PIR; A25542; A25542.
DR   PIR; A29019; A29019.
DR   PIR; B27616; B27616.
DR   PIR; S19626; S19626.
DR   PDB; 111B; 15-OCT-92.
DR   PDB; 2I1B; 15-JUL-93.
DR   PDB; 4I1B; 15-JAN-93.
DR   PDB; 5I1B; 15-OCT-94.
DR   PDB; 6I1B; 15-OCT-92.
DR   PDB; 7I1B; 15-OCT-92.
DR   PDB; 21BI; 15-APR-92.
DR   PDB; 31BI; 15-APR-92.
DR   PDB; 41BI; 15-JUL-92.
DR   PDB; 1HIB; 31-JAN-94.
DR   PDB; 1IOB; 17-AUG-96.
DR   PDB; 1ITB; 04-FEB-98.
DR   PDB; 9ILB; 06-JAN-99.
DR   MIM; 147720; -.
DR   InterPro; IPR002348; IL1_HBGF.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   PRINTS; PR00262; IL1HBGF.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen;
KW   3D-structure.
FT   PROPEP        1    116
FT   CHAIN       117    269       INTERLEUKIN-1 BETA.
FT   CONFLICT      6      6       K -> E (IN REF. 2, 6 AND 8).
FT   CONFLICT     20     20       D -> H (IN REF. 7).
FT   CONFLICT    111    111       E -> Q (IN REF. 7).
FT   CONFLICT    177    177       G -> A (IN REF. 7).
FT   CONFLICT    214    214       R -> P (IN REF. 7).
FT   STRAND      121    128
FT   TURN        129    130
FT   STRAND      132    138

  Query Match             17.3%;  Score 143.5;  DB 1;  Length 269;
  Best Local Similarity   34.5%;  Pred. No. 1e-07;
  Matches   39;  Conservative   15;  Mismatches   56;  Indels    3;  Gaps    2;

Qy      46 LISCRHVETLEKDRGNPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSF 105
           : |   |:  | :   |: |||   || | |    |:|||||:  |  : | : :  | |
Db     157 VFSMSFVQGEESNDKIPVALGLKEKNLYLSCVLKDDKPTLQLESVDPKN-YPKKKMEKRF 215

Qy     106 LFYHSQSGRNSTFESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTMLF 158
           :|   :      |||  || |:|: |     |: |    |  : |||  || |
Db     216 VFNKIEINNKLEFESAQFPNWYISTSQAENMPVFLGGTKGGQDITDF--TMQF 266


Search completed: June 20, 2002, 15:11:20
Job time: 445 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 20, 2002, 15:10:54 ; Search time 61.16 Seconds
(without alignments)
446.913 Million cell updates/sec

Title: US-09-763-498-13
Perfect score: 830
Sequence: 1 MEKALKIDTPQRGSIQDINH.....ILTQELGKANTTDFGLTMLF 158

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	826	99.5	158	4	Q9UHA7	Q9uha7 homo sapien
2	466.5	56.2	169	4	Q9NZH8	Q9nzh8 homo sapien
3	463	55.8	160	11	Q9JLA2	Q9jla2 mus musculu
4	384	46.3	157	4	Q9UHA5	Q9uha5 homo sapien
5	333	40.1	183	11	Q9D6Z6	Q9d6z6 mus musculu
6	210	25.3	192	4	Q9UHA6	Q9uha6 homo sapien
7	210	25.3	218	4	Q9NZH6	Q9nzh6 homo sapien
8	210	25.3	218	4	Q9HBF3	Q9hbf3 homo sapien
9	201	24.2	164	4	Q9NZH7	Q9nzh7 homo sapien
10	185.5	22.3	155	4	Q9UBH0	Q9ubh0 homo sapien
11	184	22.2	267	13	O73909	O73909 gallus gall
12	183.5	22.1	159	4	Q96GD6	Q96gd6 homo sapien
13	180.5	21.7	176	6	Q9BEH0	Q9beh0 canis famil
14	172.5	20.8	177	6	Q9GMZ4	Q9gmz4 tursiops tr
15	170.5	20.5	176	6	Q9GKK2	Q9gkk2 canis famil
16	169	20.4	152	4	Q969H5	Q969h5 homo sapien
17	167.5	20.2	155	11	Q9QYY1	Q9qyy1 mus musculu
18	167.5	20.2	156	11	Q9JIG2	Q9jig2 mus musculu
19	166.5	20.1	144	4	Q9BYX1	Q9byx1 homo sapien
20	159.5	19.2	267	6	Q29082	Q29082 sus scrofa
21	154.5	18.6	260	13	Q9YGD3	Q9ygd3 oncorhynchu
22	151.5	18.3	178	4	Q9HBF2	Q9hbf2 homo sapien
23	146	17.6	261	13	Q90W84	Q90w84 dicentrarch
24	144.5	17.4	283	13	Q9PVZ5	Q9pvz5 xenopus lae
25	144	17.3	266	6	Q9TTK1	Q9ttk1 tursiops tr
26	143.5	17.3	153	4	O43645	O43645 homo sapien
27	143.5	17.3	269	4	Q96HE5	Q96he5 homo sapien
28	138	16.6	272	13	Q9DDF2	Q9ddf2 cyprinus ca
29	136	16.4	267	11	Q91ZL5	Q91zl5 sigmodon hi
30	136	16.4	276	13	O57398	O57398 cyprinus ca
31	136	16.4	276	13	Q9PW18	Q9pw18 cyprinus ca
32	133.5	16.1	272	13	Q9DDF3	Q9ddf3 cyprinus ca
33	124.5	15.0	254	13	Q9PT12	Q9pt12 oncorhynchu
34	123.5	14.9	253	13	Q90W32	Q90w32 sparus aura
35	121	14.6	599	11	Q91WP7	Q91wp7 mus musculu
36	107	12.9	72	6	O77771	O77771 equus cabal
37	94	11.3	118	6	Q9TSJ0	Q9tsj0 equus cabal
38	87	10.5	64	13	Q98SG5	Q98sg5 scophthalmu
39	82.5	9.9	65	6	Q9TV37	Q9tv37 equus cabal
40	81	9.8	256	10	Q9FX11	Q9fx11 arabidopsis
41	81	9.8	348	10	Q9FVW3	Q9fvw3 arabidopsis
42	79	9.5	747	5	Q9N9L5	Q9n915 leishmania
43	78	9.4	478	5	Q93759	Q93759 caenorhabdi
44	78	9.4	603	10	Q9SQT8	Q9sqt8 arabidopsis
45	76	9.2	728	4	Q9BRZ1	Q9brz1 homo sapien

ALIGNMENTS

RESULT 1
Q9UHA7
ID Q9UHA7 PRELIMINARY; PRT; 158 AA.
AC Q9UHA7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE FIL1 EPSILON.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092888; PubMed=10625660;
RA Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
RA Sims J.E.;
RT "Four New Members Expand the IL-1 Superfamily.";
RL J. Biol. Chem. 275:1169-1175(2000).
DR EMBL; AF201831; AAF25211.1; -.
DR HSSP; P18510; 1ILR.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 158 AA; 17684 MW; 469AC84306B0E280 CRC64;

Query Match 99.5%; Score 826; DB 4; Length 158;
Best Local Similarity 99.4%; Pred. No. 6.7e-81;
Matches 157; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 MEKALKIDTPQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRG 60
           ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MEKALKIDTPQQGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRG 60

Qy      61 NPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFES 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 NPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFES 120
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Qy    121 VAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTMLF 158
          |||||||||||||||||||||||||||||||||||||
Db    121 VAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTMLF 158


RESULT   2
Q9NZH8
ID   Q9NZH8      PRELIMINARY;      PRT;   169 AA.
AC   Q9NZH8;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN-1 HOMOLOG 1 (INTERLEUKIN-1 EPSILON).
GN   IL1E.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20209405; PubMed=10744718;
RA   Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA   Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA   Young P.R.;
RT   "Identification and initial characterization of four novel members of
RT   the interleukin-1 family.";
RL   J. Biol. Chem. 275:10308-10314(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=AIRWAY EPITHELIAL CELLS INDUCED WITH TNF ALPHA, AND IFN;
RA   Debets R., Timans J., Zurawski S., Bazan J.F., Kastelein R.A.;
RT   "Novel IL-1 family member IL-1e responds through the orphan IL-1R-
RT   related protein 2; response is antagonized by IL-1d.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF200492; AAF69248.1; -.
DR   EMBL; AF206696; AAG35670.1; -.
DR   HSSP; P18510; 1ITN.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
SQ   SEQUENCE   169 AA;  18721 MW;  F00A9243706F4154 CRC64;


  Query Match             56.2%;  Score 466.5;  DB 4;  Length 169;
  Best Local Similarity   59.9%;  Pred. No. 3e-42;
  Matches   88;  Conservative   24;  Mismatches   34;  Indels    1;  Gaps    1;

Qy     10 PQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNG 69
          |  |:| |:| :|| || | |:|||| | ::|||:|:|:|:: | ||: ||:||||||:
Db     22 PITGTINDLNQQVWTLQGQNLVAVPRSDSVTPVTVAVITCKYPEALEQGRGDPIYLGIQN 81

Qy     70 LNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIA 129
               :|| | |||:||||||||: ||||| |||||| |||| :::|| || |||||| ||||
Db     82 PEMCLYCEKVGEQPTLQLKEQKIMDLYGQPEPVKPFLFYRAKTGRTSTLESVAFPDWFIA 141

Qy    130 VSSEGGCPLILTQELGKANTTDFGLTM 156
           ||:   |:||| ||||:  | | | :
Db    142 -SSKRDQPIILTSELGKSYNTAFELNI 167


RESULT   3
Q9JLA2
ID   Q9JLA2      PRELIMINARY;      PRT;   160 AA.
AC   Q9JLA2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN-1 HOMOLOG 1 (INTERLEUKIN-1 EPSILON) (INTERLEUKIN 1
DE   SUPERFAMILY 1, EPSILON).
GN   IL1F6 OR FIL1 OR IL1E.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20209405; PubMed=10744718;
RA   Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA   Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA   Young P.R.;
RT   "Identification and initial characterization of four novel members of
RT   the interleukin-1 family.";
RL   J. Biol. Chem. 275:10308-10314(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Debets R., Timans J., Zurawski S., Bazan J.F., Kastelein R.A.;
RT   "Novel IL-1 family member IL-1e responds through the orphan IL-1R-
RT   related protein 2; response is antagonized by IL-1d.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AF200493; AAF69249.1; -.
DR   EMBL; AF206697; AAG35671.1; -.
DR   EMBL; AK004061; BAB23147.1; -.
DR   HSSP; P01584; 1HIB.
DR   MGD; MGI:1859324; Il1f6.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
SQ   SEQUENCE   160 AA;  18015 MW;  AA0434D68FF62F4A CRC64;


  Query Match             55.8%;  Score 463;  DB 11;  Length 160;
  Best Local Similarity   54.5%;  Pred. No. 6.6e-42;
  Matches   85;  Conservative   30;  Mismatches   41;  Indels    0;  Gaps    0;

Qy      2 EKALKIDTPQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGN 61
          || |:  :|    :||:: |||:||:  | ||||::  |||| }: |::::||| :||:
Db      4 EKELRAASPSLRHVQDLSSRVWILQNNILTAVPRKEQTVPVTITLLPCQYLDTLETNRGD 63

Qy     62 PIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESV 121
          | |:|:     || | | |:|| ||| | :||::||: |||| |||| :|| ||||
Db     64 PTYMGVQRPMSCLFCTKDGEQPVLQLGEGNIMEMYNKKEPVKASLFYHKKSGTTSTFESA 123

Qy    122 AFPGWFIAVSSEGGCPLILTQELGKANTTDFGLTML 157
          ||||||||| |:| ||||||||||:   ||| : ::
Db    124 AFPGWFIAVCSKGSCPLILTQELGEIFITDFEMIVV 159


RESULT   4
Q9UHA5
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ID   Q9UHA5      PRELIMINARY;      PRT;   157 AA.
AC   Q9UHA5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   FIL1 ETA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20092888; PubMed=10625660;
RA   Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
RA   Sims J.E.;
RT   "Four New Members Expand the IL-1 Superfamily.";
RL   J. Biol. Chem. 275:1169-1175(2000).
DR   EMBL; AF201833; AAF25213.1; -.
DR   HSSP; P10749; 2MIB.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
SQ   SEQUENCE   157 AA;  17702 MW;  7A54F3D7557A3EE3 CRC64;
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  Query Match           46.3%;  Score 384;  DB 4;  Length 157;
  Best Local Similarity 49.0%;  Pred. No. 2e-33;
  Matches   71;  Conservative   29;  Mismatches   45;  Indels    0;  Gaps    0;

Qy      10 PQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNG 69
           |:  :|:|    ||||   :||| |    : |||: ||:|| |  :|::|| :|||: |
Db       9 PKSYAIRDSRQMVWVLSGNSLIAAPLSRSIKPVTLHLIACRDTEFSDKEKGNMVYLGIKG 68

Qy      70 LNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFIA 129
            :||| ||::  :||||||||:||||| : :  | |||:|:: |  | |:||::||||||
Db      69 KDLCLFCAEIQGKPTLQLKEKNIMDLYVEKKAQKPFLFFHNKEGSTSVFQSVSYPGWFIA 128

Qy     130 VSSEGGCPLILTQELGKANTTDFGL 154
           |:  | |: ||:| |  | |:| |
Db     129 TSTTSGQPIFLTKERGITNNTNFYL 153
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RESULT   5
Q9D6Z6
ID   Q9D6Z6      PRELIMINARY;      PRT;   183 AA.
AC   Q9D6Z6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   2310043N20RIK PROTEIN.
GN   2310043N20RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=TONGUE;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK009787; BAB26505.1; -.
DR   HSSP; P01584; 1HIB.
DR   MGD; MGI:1916927; 2310043N20Rik.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
SQ   SEQUENCE   183 AA;  20878 MW;  A3ACE339FB96F02F CRC64;
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  Query Match           40.1%;  Score 333;  DB 11;  Length 183;
  Best Local Similarity 44.4%;  Pred. No. 7.1e-28;
  Matches   64;  Conservative   25;  Mismatches   55;  Indels    0;  Gaps    0;

Qy       9 TPQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLN 68
             :|:   : |    ||||   || |||  : : || ::||:||  |  :  :|| ::||:
Db      34 SPRNYRVHDSQQMVWWLTGNTLTAVPASNNVKPVILSLIACRDTEFQDVKKGNLVFLGIK 93

Qy      69 GLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWFI 128
             ||| | ::  :|||||||  |||:|| : :  |:|||||   |  | |:|| :|||||
Db      94 NRNLCFCCVEMEGKPTLQLKEVDIMNLYKERKAQKAFLFYHGIEGSTSVFQSVLYPGWFI 153

Qy     129 AVSSEGGCPLILTQELGKANTTDF 152
           | ||     :||| : ||   |:|
Db     154 ATSSIERQTIILTHQRGKLVNTNF 177
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RESULT   6
Q9UHA6
ID   Q9UHA6      PRELIMINARY;      PRT;   192 AA.
AC   Q9UHA6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   FIL1 ZETA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20092888; PubMed=10625660;
RA   Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
RA   Sims J.E.;
RT   "Four New Members Expand the IL-1 Superfamily.";
RL   J. Biol. Chem. 275:1169-1175(2000).
DR   EMBL; AF201832; AAF25212.1; -.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
SQ   SEQUENCE   192 AA;  21543 MW;  4AF584C81802F612 CRC64;
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  Query Match           25.3%;  Score 210;  DB 4;  Length 192;
  Best Local Similarity 36.7%;  Pred. No. 1.2e-14;
  Matches   54;  Conservative   26;  Mismatches   61;  Indels    6;  Gaps    4;

Qy      10 PQRGSIQDINHRVWVLQDQTLIAVPRKDRMSP-VTIALISCRHVETLEKDRGNPIYLGLN 68
           |:: || | :|:| ||    ||||| |: : | :  || |   : :   ::|:|| ||::
Db      31 PKKFSIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALAS--SLSSASAEKGSPILLGVS 88

Qy      69 GLNLCLMCAKVGDQ--PTLQLKEKDIMDLYNQPEPV-KSFLFYHSQSGRNSTFESVAFPG 125
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              || | |    |  |:||||:: :| |  | |   : |:|| :| |  :  || | ||
Db     89 KGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPG 148

Qy    126 WFIAVSSEGGCPLILTQELGKANTTDF 152
          |||  |     |: :| :       :|
Db    149 WFICTSCNCNEPVGVTDKFENRKHIEF 175


RESULT   7
Q9NZH6
ID   Q9NZH6      PRELIMINARY;      PRT;   218 AA.
AC   Q9NZH6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN-1 HOMOLOG 4 (IL-1X PROTEIN) (INTERLEUKIN-1-RELATED PROTEIN
DE   LONG ISOFORM A).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=FETAL LUNG, FETAL TESTIS, FETAL B-CELL, AND FETAL COLON;
RX   MEDLINE=20209405; PubMed=10744718;
RA   Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA   Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA   Young P.R.;
RT   "Identification and initial characterization of four novel members of
RT   the interleukin-1 family.";
RL   J. Biol. Chem. 275:10308-10314(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON CARCINOMA;
RA   Manoj P.P., Mantovani A., Muzio M.;
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Pan G., Risser P., Mao W., Baldwin D.T., Zhong A.W., Yansura D.,
RA   Lewis L., Eigenbrot C., Henzle W.J., Vandlen R., Filvaroff E.;
RT   "IL-1H, an interleukin-1-related protein that binds IL-18 receptor/IL-
RT   1Rrp.";
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF200496; AAF69252.1; -.
DR   EMBL; AF167368; AAG29344.1; -.
DR   EMBL; AF251118; AAG14420.1; -.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
SQ   SEQUENCE   218 AA;  24126 MW;  96E089310D2CEA68 CRC64;


  Query Match             25.3%;  Score 210;  DB 4;  Length 218;
  Best Local Similarity   36.7%;  Pred. No. 1.4e-14;
  Matches   54;  Conservative   26;  Mismatches   61;  Indels    6;  Gaps    4;

Qy      10 PQRGSIQDINHRVWVLQDQTLIAVPRKDRMSP-VTIALISCRHVETLEKDRGNPIYLGLN 68
           |:: || | :|:| ||    |||| |: : | :  || |   : :   ::|:|| ||::
Db      57 PKKFSIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALAS--SLSSASAEKGSPILLGVS 114

Qy      69 GLNLCLMCAKVGDQ--PTLQLKEKDIMDLYNQPEPV-KSFLFYHSQSGRNSTFESVAFPG 125
              || | |   |  |:||||:: :| |  | |   : |:|| :| |  :  || | ||
Db     115 KGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPG 174

Qy     126 WFIAVSSEGGCPLILTQELGKANTTDF 152
          |||  |     |: :| :       :|
Db     175 WFICTSCNCNEPVGVTDKFENRKHIEF 201


RESULT   8
Q9HBF3
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ID   Q9HBF3      PRELIMINARY;      PRT;   218 AA.
AC   Q9HBF3;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN-1-RELATED PROTEIN LONG ISOFORM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21066552; PubMed=11145836;
RA   Pan G., Risser P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E.,
RA   Yansura D., Lewis L., Eigenbrot C., Henzel W.J., Vandlen R.;
RT   "IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-
RT   1Rrp.";
RL   Cytokine 13:1-7(2001).
DR   EMBL; AF251119; AAG14421.1; -.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
SQ   SEQUENCE   218 AA;  24138 MW;  76E09C35093DEA63 CRC64;


  Query Match             25.3%;  Score 210;  DB 4;  Length 218;
  Best Local Similarity   36.7%;  Pred. No. 1.4e-14;
  Matches   54;  Conservative   26;  Mismatches   61;  Indels    6;  Gaps    4;

Qy      10 PQRGSIQDINHRVWVLQDQTLIAVPRKDRMSP-VTIALISCRHVETLEKDRGNPIYLGLN 68
           |:: || | :|:| ||    |||| |: : | :  || |   : :   ::|:|| ||::
Db      57 PKKFSIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALAS--SLSSASAEKGSPILLGVS 114

Qy      69 GLNLCLMCAKVGDQ--PTLQLKEKDIMDLYNQPEPV-KSFLFYHSQSGRNSTFESVAFPG 125
              || | |   |  |:||||:: :| |  | |   : |:|| :| |  :  || | ||
Db     115 KGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFIFYRAQVGSWNMLESAAHPG 174

Qy     126 WFIAVSSEGGCPLILTQELGKANTTDF 152
          |||  |     |: :| :       :|
Db     175 WFICTSCNCNEPVGVTDKFENRKHIEF 201


RESULT   9
Q9NZH7
ID   Q9NZH7      PRELIMINARY;      PRT;   164 AA.
AC   Q9NZH7;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   INTERLEUKIN-1 HOMOLOG 2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=OSTEOCLASTOMA;
RX   MEDLINE=20209405; PubMed=10744718;
RA   Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA   Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA   Young P.R.;
RT   "Identification and initial characterization of four novel members of
RT   the interleukin-1 family.";
RL   J. Biol. Chem. 275:10308-10314(2000).
DR   EMBL; AF200494; AAF69250.1; -.
DR   InterPro; IPR000975; Interleukin_1.
DR   SMART; SM00125; IL1; 1.
SQ   SEQUENCE   164 AA;  18521 MW;  F0D2099F4A357A0A CRC64;


  Query Match             24.2%;  Score 201;  DB 4;  Length 164;
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  Best Local Similarity   44.7%;  Pred. No. 9.4e-14;
  Matches   38;  Conservative   17;  Mismatches   30;  Indels    0;  Gaps    0;

Qy      10 PQRGSIQDINHRVWVLQDQTLIAVPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGLNG 69
           |:  :|:|    ||||   :||| |    : |||: ||:||  |  :|::|| :|||: |
Db       9 PKSYAIRDSRQMVWVLSGNSLIAAPLSRSIKPVTLHLIACRDTEFSDKEKGNMVYLGIKG 68

Qy      70 LNLCLMCAKVGDQPTLQLKEKDIMD 94
            :||| ||::  :|||||| :   |
Db      69 KDLCLFCAEIQGKPTLQLKLQGSQD 93


RESULT  10
Q9UBH0
ID   Q9UBH0      PRELIMINARY;      PRT;   155 AA.
AC   Q9UBH0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   FIL1 DELTA (INTERLEUKIN-1 LIKE PROTEIN 1) (INTERLEUKIN-1 RECEPTOR
DE   ANTAGONIST HOMOLOG 1) (INTERLEUKIN-1 DELTA).
GN   IL1HY1 OR IL1L1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20092888; PubMed=10625660;
RA   Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
RA   Sims J.E.;
RT   "Four New Members Expand the IL-1 Superfamily.";
RL   J. Biol. Chem. 275:1169-1175(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99443727; PubMed=10512743;
RA   Mulero J.J., Pace A.M., Nelken S.T., Loeb D.B., Correa T.R.,
RA   Drmanac R., Ford J.E.;
RT   "IL1HY1: A Novel Interleukin-1 Receptor Antagonist Gene.";
RL   Biochem. Biophys. Res. Commun. 263:702-706(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RA   Barton J.L., di Giovine F.S., Symons J.A., Nicklin M.J.H.;
RT   "A tissue specific interleukin-1 receptor antagonist homolog from the
RT   IL1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18ra activities.";
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Barton J.L., Herbst R., Bosisio D., Nicklin M.J.H.;
RT   "A tissue specific interleukin-1 receptor antagonist homolog from the
RT   IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18ra activities.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20322477; PubMed=10866108;
RA   Mulero J.J., Nelken S.T., Ford J.E.;
RT   "Organization of the Human Interleukin-1 Receptor Antagonist Gene
RT   IL1HY1.";
RL   Immunogenetics 51:425-428(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RA   Debets R., Timans J.C., Zurawski S., Sana T.R., Bazan F.,
RA   Kastelein R.A.;
RT   "Novel IL-1 ligands IL-1d and IL-1e use IL-1R related protein 2.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF201830; AAF25210.1; -.
DR   EMBL; AF186094; AAF02757.1; -.
DR   EMBL; AJ242737; CAB59822.1; -.
DR   EMBL; AJ242738; CAB59823.1; -.
DR   EMBL; AJ271338; CAB67704.1; -.
DR   EMBL; AF216693; AAF76981.1; -.
DR   EMBL; AF230377; AAF91274.1; -.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
KW   Receptor.
SQ   SEQUENCE   155 AA;  16962 MW;  B96DB5EFA2612E25 CRC64;


  Query Match             22.3%;  Score 185.5;  DB 4;  Length 155;
  Best Local Similarity   44.8%;  Pred. No. 4.1e-12;
  Matches   43;  Conservative   13;  Mismatches   35;  Indels    5;  Gaps    3;

Qy      61 NPIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFES 120
           :|: ||: | : || |  || :||| |:  :||:||   :  ||| ||    |  |:|||
Db      55 SPVILGVQGGSQCLSCG-VGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFES 113

Qy     121 VAFPGWFIAVSSEGGCPLILTQ--ELG--KANTTDF 152
           |:||||:    |   |: |||  | |   |  |||
Db     114 AAYPGWFLCTVPEADQPVRLTQLPENGGWNAPITDF 149


RESULT  11
O73909
ID   O73909      PRELIMINARY;      PRT;   267 AA.
AC   O73909;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   INTERLEUKIN-1BETA.
GN   IL-1BETA OR IL1B.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Weining K.C., Sick C., Kaspers B., Staeheli P.;
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LINE N;
RA   Kaiser P., Rothwell L., Goodchild M., Bumstead N.;
RT   "Chicken interleukin-1b: an evolutionary bridge between fish and
RT   mammals.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Y15006; CAA75239.1; -.
DR   EMBL; AJ245728; CAC04510.1; -.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   InterPro; IPR003502; Interleukin_1_prop.
DR   Pfam; PF00340; IL1; 1.
DR   Pfam; PF02394; IL1_propep; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
FT   CHAIN       106    267       INTERLEUKIN-1BETA.
SQ   SEQUENCE   267 AA;  29822 MW;  3EF72164E4D40B64 CRC64;


  Query Match             22.2%;  Score 184;  DB 13;  Length 267;
  Best Local Similarity   32.7%;  Pred. No. 1.1e-11;
  Matches   54;  Conservative   25;  Mismatches   66;  Indels   20;  Gaps    6;

Qy       4 ALKIDTPQRGSIQDINHRVWVLQDQT-LIAV----PRKDRMSPVTIALISCRHVETLEKD 58
           | :    |   | ||| : :||:  | |:|:    |   :   : |||   |
Db     108 AFRYTRSQSFDIFDINQKCFVLESPTQLVALHLQGPSSSQKVRLNIALYRPR------GP 161

Qy      59 RGN------PIYLGLNGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQS 112
           ||:      |: ||: |  | : |   | :|||||:| |:|   :  | : |:||   |
Db     162 RGSAGTGQMPVALGIKGYKLYMSCVMSGTEPTLQLEEADVMRDIDSVE-LTRFIFYRLDS 220
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Qy     113 GRNST--FESVAFPGWFIAVSSEGGCPLILTQELGKANTTDFGLT 155
           |  ||| |||||||  | :   |: :| :  : |   : |:
Db     221 PTEGTTRFESAAFPGWFICTSLQPRQPVGITNQPDQVNIATYKLS 265


RESULT  12
Q96GD6
ID   Q96GD6      PRELIMINARY;      PRT;   159 AA.
AC   Q96GD6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN 1 RECEPTOR ANTAGONIST.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PANCREATIC ADENOCARCINOMA;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC009745; AAH09745.1; -.
KW   Receptor.
SQ   SEQUENCE   159 AA;  17888 MW;  C1D66CDF0D2F7B44 CRC64;


  Query Match             22.1%;  Score 183.5;  DB 4;  Length 159;
  Best Local Similarity   30.6%;  Pred. No. 6.9e-12;
  Matches   45;  Conservative   26;  Mismatches   49;  Indels   27;  Gaps    3;

Qy      15 IQDINHRVWVLQDQTLIA-------VPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGL 67
           | |:| : : |::  |:|       |  ::::  | |              : ::||:
Db      22 IWDVNQKTFYLRNNQLVAGYLQGPNVNLEEKIDVVPI-------------EPHALFLGI 67

Qy      68 NGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWF 127
           :|  :|| | | ||:  |||:  :| ||    :  | | |  | ||  ::||| | ||||
Db      68 HGGKMCLSCVKSGDETRLQLEAVNITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWF 127

Qy     128 IAVSSEGGCPLILTQELGKANTTDFGL 154
           :  : |   }: ||       |  | |:
Db     128 LCTAMEADQPVSLT------NMPDEGV 148


RESULT  13
Q9BEH0
ID   Q9BEH0      PRELIMINARY;      PRT;   176 AA.
AC   Q9BEH0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN-1 RECEPTOR ANTAGONIST.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Shin I.-S., Youn H.-Y.;
RT   "Molecular cloning of canine interleukin-1 receptor antagonist (IL-
RT   1ra).";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY026462; AAK01472.1; -.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Receptor.
SQ   SEQUENCE   176 AA;  19922 MW;  8486CA54A240212B CRC64;


  Query Match             21.7%;  Score 180.5;  DB 6;  Length 176;
  Best Local Similarity   30.6%;  Pred. No. 1.6e-11;
  Matches   41;  Conservative   25;  Mismatches   47;  Indels   21;  Gaps    2;

Qy      15 IQDINHRVWVLQDQTLIA-------VPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGL 67
           | |:| : : |::  |:|          ::::  | :                : ::||:
Db      40 IWDVNQKTFYLRNNQLVAGYLQGSNTKLEEKLDVVPV-------------EPHAVFLGI 85

Qy      68 NGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWF 127
           :|  ||| | | ||:  |||:  :| ||    :  | | |  | ||  ::||| | ||||
Db      86 HGGKLCLACVKSGDETRLQLEAVNITDLSKNKDQDKRFTFILSDSGPTTSFESAACPGWF 145

Qy     128 IAVSSEGGCPLILT 141
           :  : |   |: ||
Db     146 LCTALEADRPVSLT 159


RESULT  14
Q9GMZ4
ID   Q9GMZ4      PRELIMINARY;      PRT;   177 AA.
AC   Q9GMZ4;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN-1 RECEPTOR ANTAGONIST.
GN   IL-1RA.
OS   Tursiops truncatus (Atlantic bottle-nosed dolphin).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC   Tursiops.
OX   NCBI_TaxID=9739;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21109087; PubMed=11182153;
RA   Inoue Y., Itou T., Jimbo T., Syouji Y., Ueda K., Sakai T.;
RT   "Molecular cloning and functional expression of bottle-nosed dolphin
RT   (Tursiops truncatus) interleukin-1 receptor antagonist.";
RL   Vet. Immunol. Immunopathol. 78:131-141(2001).
DR   EMBL; AB038268; BAB11806.1; -.
DR   HSSP; P18510; 1IRA.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; 1.
KW   Receptor.
SQ   SEQUENCE   177 AA;  19923 MW;  6FD19A06C09B131B CRC64;


  Query Match             20.8%;  Score 172.5;  DB 6;  Length 177;
  Best Local Similarity   31.3%;  Pred. No. 1.2e-10;
  Matches   42;  Conservative   24;  Mismatches   47;  Indels   21;  Gaps    2;

Qy      15 IQDINHRVWVLQDQTLIA-------VPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGL 67
           | |:| : : |::  |:|          ::::  | |                : ::||:
Db      40 IWDVNQKTFYLRNNQLVAGYLQGPNTKLEEKIDVVPI-------------EPHAMFLGI 85

Qy      68 NGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWF 127
           :|  ||| | | ||:  | |:  :| || :  |  | | |  | ||  ::||| | ||||
Db      86 HGGKLCLACVKSGDEIKLGLEPVNITDLNSSKEEDKRFAFIRSDSGPTTSFESAACPGWF 145

Qy     128 IAVSSEGGCPLILT 141
           :  : |   |: ||
Db     146 LCTALETDQPVGLT 159


RESULT  15
Q9GKK2
ID   Q9GKK2      PRELIMINARY;      PRT;   176 AA.
AC   Q9GKK2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
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DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   INTERLEUKIN-1 RECEPTOR ANTAGONIST.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21109092; PubMed=11182158;
RA   Campbell S.E., Nasir L., Argyle D.J., Gault E.A., Duthie S.,
RA   Bennett D.;
RT   "Cloning of canine IL-1ra, TNFR and TIMP-2.";
RL   Vet. Immunol. Immunopathol. 78:207-214(2001).
DR   EMBL; AF216526; AAG36777.1; -.
DR   HSSP; P18510; 1ILR.
DR   InterPro; IPR000975; Interleukin_1.
DR   Pfam; PF00340; IL1; 1.
DR   ProDom; PD002536; Interleukin_1; 1.
DR   SMART; SM00125; IL1; 1.
DR   PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
KW   Receptor.
SQ   SEQUENCE   176 AA;  19938 MW;  8486CA54A254206B CRC64;


  Query Match             20.5%;  Score 170.5;  DB 6;  Length 176;
  Best Local Similarity   29.9%;  Pred. No. 1.9e-10;
  Matches   40;  Conservative   25;  Mismatches   48;  Indels   21;  Gaps    2;

Qy      15 IQDINHRVWVLQDQTLIA-------VPRKDRMSPVTIALISCRHVETLEKDRGNPIYLGL 67
           | |:| : : |::  |:|          ::::  | :              : ::||:
Db      40 IWDVNQKTFYLRNNQLVAGYLQGSNTKLEEKLDVVPV-------------EPHAVFLGI 85

Qy      68 NGLNLCLMCAKVGDQPTLQLKEKDIMDLYNQPEPVKSFLFYHSQSGRNSTFESVAFPGWF 127
           :|  ||| | | ||:  |||:  :| ||    :  | | |  | ||  ::||| | ||||
Db      86 HGGKLCLACVKSGDETRLQLEAVNITDLSKNKDQDKRFTFILSDSGPTTSFESAACPGWF 145

Qy     128 IAVSSEGGCPLILT 141
           :  : |    : ||
Db     146 LCTALEADRLVSLT 159


Search completed: June 20, 2002, 15:10:55
Job time: 466 sec
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